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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

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NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by
5 such polynucleotides, along with uses for these polynucleotides and proteins, for example
in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines,
10 such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured
rapidly over the past decade. The now routine hybridization cloning and expression
cloning techniques clone novel polynucleotides "directly" in the sense that they rely on
information directly related to the discovered protein (i.e., partial DNA/amino acid
sequence of the protein in the case of hybridization cloning; activity of the protein in the
15 case of expression cloning). More recent "indirect" cloning techniques such as signal
sequence cloning, which isolates DNA sequences based on the presence of a now
well-recognized secretory leader sequence motif, as well as various PCR-based or low
stringency hybridization-based cloning techniques, have advanced the state of the art by
making available large numbers of DNA/amino acid sequences for proteins that are
20 known to have biological activity, for example, by virtue of their secreted nature in the
case of leader sequence cloning, by virtue of their cell or tissue source in the case of
PCR-based techniques, or by virtue of structural similarity to other genes of known
biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications
25 in, for example, diagnostics, forensics, gene mapping; identification of mutations
responsible for genetic disorders or other traits, to assess biodiversity, and to produce
many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

30 The compositions of the present invention include novel isolated polypeptides, novel
isolated polynucleotides encoding such polypeptides, including recombinant DNA

molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

5 The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

10 The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO:
15 1-739. The polypeptides sequences are designated SEQ ID NO: 740-1478. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

20 The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-739 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by
25 SEQ ID NO:1-739. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-739 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

 The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-739. The sequence
30 information can be a segment of any one of SEQ ID NO:1-739 that uniquely identifies or represents the sequence information of SEQ ID NO:1-739.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-739 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-739 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-739; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1 - 739; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1- 739. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-739; (b) a nucleotide sequence encoding any one of the

amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-739; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein,

and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The

invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products.

Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid

which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-739. The sequence information can be a segment of any one of SEQ ID NO:1-739 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-739. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-

mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully
5 matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

10 Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1/4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an
15 array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

20 The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously
25 linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

30 The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to

naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may
5 change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

10 The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological
15 macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic
20 acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect,
25 or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of
30 glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134

-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or
5 provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS),
10 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium
15 pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result
20 in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the
25 substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no
30 more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment,

by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

5 Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-739 ; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:740-1478; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of
10 any one of SEQ ID NO:740-1478. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-739 ; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide
15 recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 740-1478. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic
20 domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or
25 partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known
30 methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification

and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-739 can be obtained by screening appropriate cDNA or genomic DNA
5 libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-739 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-739 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and
10 sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including
15 nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are
20 nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-739, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or
25 20 nucleotides or more that are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on
30 unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-739, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-739 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-739, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the

nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent
5 degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

10 Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA,
15 amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the
20 mature protein coding sequences corresponding to any one of SEQ ID NO:1-739, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

25 A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and
30 the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide.

In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell.

Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-739 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-739 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example,

pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-739, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:740-1478 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-739 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding

region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences
 5 which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO:1-739), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid
 10 molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or
 15 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase
 20 the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil,
 25 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil,
 30 beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine,

pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a

2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

5 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a
10 mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO:1-739). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a
15 SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences
20 complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the
25 base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the
30 deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to

allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

5 PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial
10 restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by
15 the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity.
20 PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite
25 coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively,
30 chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If

linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a

suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be
5 used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography
10 (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains
15 include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced
20 therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the
25 invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be
30 comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations

of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:740-1478 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-739 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-739 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO:740-1478 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:740-1478 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:740-1478.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the

disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein

which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present
5 invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in
10 which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a
15 full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but
20 are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that retain biological/immunological activity
25 include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial
30 libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models

that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

5 In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:740-1478.

10 The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

15 The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

25 Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other

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immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for
5 baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an
10 insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or
15 cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using
20 such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin
25 (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven,
30 Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE

IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST

(Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990)).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into

pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction
5 may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a
10 ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation,
15 restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to
20 complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding
25 a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of
30 normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states

involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression

by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a

tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in

disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

5 Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased
10 protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to
15 express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed
20 or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals,
25 preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals,
30 are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

5 The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease
10 states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known
15 sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or
20 potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

25 The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which
30 the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of

course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic

compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions
5 of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19;
10 Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node
15 cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto.
20 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and
25 Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986;
30 Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John

Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

15 **4.10.4 STEM CELL GROWTH FACTOR ACTIVITY**

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia
5 inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type,
10 expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the
15 culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

20 Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to
25 create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present
30 invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune

disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. *Proc. Natl. Acad. Sci, U.S.A.*, 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., *Blood*, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative

disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

5 Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a
10 tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or
15 ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo*
20 for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

 The compositions of the present invention may also be useful for proliferation of
25 neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and
30 localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager

syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the

polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and
5 murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by
10 suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and
15 persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing
20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that
25 destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration
30 of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a

subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or

eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient
5 by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic
10 acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation
15 signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2
20 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene
25 encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome
30 tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology

154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may

also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

5 The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

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4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial
15 cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well
20 as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell
25 population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

30 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the

migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a

polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer
5 may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and
10 pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast
15 cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in
20 the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and
25 Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant
30 cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of

tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the

5 polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan,

10 Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog),

15 Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

20 In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to

25 reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York,

30 NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in

Boyden Chamber assays as described in Pilkington et al., *Anticancer Res.*, 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., *Intl. J. Dev. Biol.*, 40: 1189-97 (1999) and Li et al., *Clin. Exp.*

- 5 Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor,
10 receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation,
15 cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without
20 limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those
25 described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., *Proc. Natl. Acad. Sci. USA* 84:6864-6868, 1987; Bierer et al., *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein et al., *J. Exp. Med.*
30 169:149-160 1989; Stoltenborg et al., *J. Immunol. Methods* 175:59-68, 1994; Stitt et al., *Cell* 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

5 Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in
10 Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

15

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in
20 solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One
25 may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or
30 modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3)

combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or
5 compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves.
10 Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of
15 particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997);
20 Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay
25 are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin
30 or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity

of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

5 The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding
10 partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for
15 receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression
20 library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides,
25 oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host
30 cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins

involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

5 **4.10.15 ANTI-INFLAMMATORY ACTIVITY**

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells
10 involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic
15 inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or
20 material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or
25 inflammatory disease, an antiproliferative agent such as for acute or chronic mylogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of
30 a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not

limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B.

5 Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or
10 polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention
15 include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- 20 (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by
25 human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or
30 amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody

binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

5 In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and
10 including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

15 **4.10.18 OTHER ACTIVITIES**

 A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other
20 parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting
25 the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells
30 in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related

diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences

of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity

of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, 5 IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), 10 insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active 15 ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or 20 anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

25 As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of 30 the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers

to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions.

When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or

cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the

pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art.

Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon

dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The

5 compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing

10 and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic

15 fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active

20 ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the

25 compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives,

30 for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological

effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

5 The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T
10 cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with
15 co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

 The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other
20 pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the
25 art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

 The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the
30 patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each

individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure

proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients

of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating

concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50} .

Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%.

In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , $F_{ab'}$ and $F_{(ab')_2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain.

Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 4, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below:

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide

primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D.

- 5 Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition",
10 as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a
15 particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing
20 antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human
25 mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse
30 myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or

survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures

such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536

(1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found
5 neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The
10 humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

15 Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol
20 Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human
25 B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be
30 made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely

inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. 5 (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al, (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman 10 animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's 15 genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the 20 XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal 25 antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. 30 Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to

prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)2} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)2} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan).

Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as
5 homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science
10 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab' -TNB derivatives is then
15 reconverted to the Fab' -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab' -TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and
20 chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and
25 normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol.
30 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody

homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc γ R), such as Fc γ RI (CD64), Fc γ RII (CD32) and Fc γ RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

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5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in

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vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolacca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcumin,

crocin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

5 Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl)
10 hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid
15 (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

 In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the
20 circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

 In one application of this embodiment, a nucleotide sequence of the present
25 invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these
30 categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to

create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-739 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-739 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for

commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample.

5 Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise
10 contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying
15 for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available
20 hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science
25 Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described
30 method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein

extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more
5 containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a
10 quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes,
15 labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

25

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of
30 inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of

the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

5 Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-739, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- 10 (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

 In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a

15 polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

 Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide

20 of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

 Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for

25 a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

 Compounds identified via such methods can include compounds which modulate

30 the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds

identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard
5 assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling
10 techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected
15 or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In
20 Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be
25 randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA.
30 Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or

can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-739. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO:1-739 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection

of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes.

5 Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein
10 may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of
15 chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science
20 (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

25 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to
30 those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers.

Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated
5 herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be
10 purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound
15 to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem.
20 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond
25 joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

30 More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M

1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC),
5 dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

10 It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent
15 phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA
20 probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of
25 Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

30 One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6,

incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside
5 phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC
10 inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification
15 methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 µl of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

20 Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful
25 alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*II, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be
30 suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate

(all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

5 Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

10 The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the
15 exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon
20 the scope of the invention are those which appear in the appended claims.

 All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1 EXAMPLE 1

25 Novel Nucleic Acid Sequences Obtained From Various Libraries

 A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers
30 specific for the vector sequences which flank the inserts. Clones from cDNA libraries were

spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. Chromatograms were base called and assembled using a software suite from University of Washington, Seattle containing three applications designated PHRED, PHRAP, and CONSED. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-739 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 120, gb pri 120, UniGene version 120, and Genpept 120) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 120, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and

contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for SEQ ID NO: 1-739 are shown in Table 2.

Tables 1, 2, and 3 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-739. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homologue for each assemblage and contains the translated amino acid sequences for which the assemblage encodes. Table 2 also shows homologues with identifiable functions for SEQ ID NO: 1-739. The polypeptides were predicted using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of translated novel polynucleotides to known polynucleotides (W.R. Pearson, Methods in Enzymology, Vol. 183: pp. 63-98, (1990), herein incorporated by reference). Table 3 shows the predicted amino acid sequence corresponding to the novel nucleic acid contig sequences.

Table 1 - Tissue Sources

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	28 46 54 62 95 117 134 175 188-189 324 330 337 356 369 371 378 386 389 396 432 435-436 468 472-473 476-477 483 486 518 538-539 543 545 557 565 571 573 578 582 598 613-614 619 627 632 634 639 687 709
adult brain	GIBCO	ABD003	5 12 46 52 57 66 79 91 97 134 144 148 150 162 164 172 175-176 181 186 193 250 323 325-327 330 334 338 362 367 369 371 378-379 386 388-389 392 396-397 399-401 403 416 422 435 444 449 451 454 461 463-464 468 472-473 483 486 494 506 511 513 516 520 523-524 526 529 533 536-537 539 545 548 552 556 558-559 562-563 565 567 569 573-574 576 579-580 582-584 590 593-594 598 602 606 613-614 619- 621 623-624 627 634 637 641 646 648 659 675 688-689 694 696-698 703 714 729
adult brain	Clontech	ABR001	57 162 164 227 266 316 334 356 367 385 438 468 512 524 528 557 582 590 621 627 631 634 689 714
adult brain	Clontech	ABR006	189 228 385 438 571 584 632 650 677
adult brain	Clontech	ABR008	1 3 5 11-25 31-32 46-47 55-57 59

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			61 65-67 69 75 79 91 103 108 111 113-114 126 132 150 160 162 164 171-172 186 188-189 193 202-203 206 210-212 220 222-224 227-229 233 235-236 243-247 251-252 257 264-266 268 275 313 324 328-331 334-335 338-339 343 346-347 351 355 357 359-361 365 367 370-371 378 380 382 386-389 391 396 399- 400 402 406 413 419-420 423 426 432 434 437-438 442 446 448-449 459-460 465 468 470 472-473 475 481-483 487 489-490 495-497 499 501 503-504 507-509 511 520 524 526 528 532-533 536 539-540 543- 546 551-552 556-557 563 565-567 569 572-573 576-577 579-580 582 584 586 590-591 593 595-597 599- 602 604 610-616 620-621 624-625 627-628 632 634 637-638 641 643- 644 646-647 650 653-657 660-662 668 672 675 677-678 680-681 688- 689 691 693 695-696 698 706-707 709 711 713-727 729 731 733-734 736 738-739
adult brain	Clontech	ABR011	334 476 634 677
adult brain	BioChain	ABR012	379 587
adult brain	Invitrogen	ABR013	334 634
adult brain	Invitrogen	ABT004	3 19 57 62 66 75 110 122 150 160 162 167 171 176 186 197 203 211 230 232 259 328-331 334 369 382 389 394 400 406 417 426 429 442 457 472 483-484 492 511 514 529 531 534 537 540 553 558 562 572 580 582-584 590 604 611 613 615 622 637 639 643-644 648 688-689 692 695
cultured preadipo- cytes	Strategene	ADP001	16 37-39 66 109 120 141 144 193 273 316 331 333 338 389 415 429 442 444 464-465 475 489 501 511 513 531 534 539-540 545-546 557 583-584 590 596 602 607 613 615 619 622 629 632 634 643
adrenal gland	Clontech	ADR002	4-5 12 48 53 57 162 164 172 186 188 192 196 203 207 213 258 316 330-331 333 339 354 356-357 369 383 385 388 392 395 402 406 411 415 434 454-455 465 468 473 475 477 491 498 501 509 511 517 528- 529 532 537-539 542 545 558 560 565 567 576-577 586 600 606 615 621 624 627 632 634 647 653 660 667 683 689 696 714

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult heart	GIBCO	AHR001	28 39 57 64-65 75 79 89 97-98 108 117 134 144 157 159-160 164-166 169 171 174 184 192-193 203 207 220 243 256 258 266-267 281 314 316 318 328-329 331 338-339 341 346 348 354 356-357 366-367 369 371 377-379 382 385-386 388 393 395-396 399-401 403 415 420 422 425 431-432 435-436 445 451 459 465 472-473 477 483 486 488 490 496 501 503 508 515 519-520 526 528 531 533-534 537-538 540-541 544 546 552 556-557 562-563 566- 571 573 576-581 583-584 586-587 594 602 606 608 611 613-615 618 620-621 626-628 632 634 641 643 646 648 653 659 667 676 678 687 689 696 703-704 708 711 714 729- 730
adult kidney	GIBCO	AKD001	3 28-29 48 56-57 67 79 84 93 106 117 134 138 140 144 156 160-164 168-170 172 177 183 188-189 192- 193 199 203 207 235 251 257 275 319 321-323 328-330 337 346-347 349 354-356 360 367-369 371 375 378-381 383-386 388-389 392 396- 397 399 401 404 407 409 411-412 415-416 420-422 427 432 436-437 439-440 444 451-456 458-459 464- 465 468 470 472-473 477 481 483 486-487 492 496 501 503 505-506 508 511 513-516 518 524 526 529 533 535 537-541 543 545-546 548 552 557 559-560 562-563 565-569 572-574 576-577 579-587 589-591 593-594 602 604-607 613-614 617- 618 620-624 627-628 630 632-635 637-638 640-642 644-645 652 662 664 667-668 677 682 685 687 689 694-696 698 703 716 723 728-729 732 734
adult kidney	Invitrogen	AKT002	92 136 154 160 164 178 271 314 347 353 360 367 376 378-379 386 391 402 409 423 432 449 451 477 490 494 503 526 528 531 534 538-539 541 545-546 559 566 579 584 588 594 602 613 621 624 632 647 652 689
adult lung	GIBCO	ALG001	56-57 67 69 98 113 134 144 164 172 191-192 270 321 328 338 369 371 374 378 380 388-389 396 405 411 416 424 443-444 456 473-474 482- 483 497 508 518 529 531 534 536

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			540 552 556 559 563 568 573 579-580 585-586 588-589 593 601-602 606 612-613 618 634 662 667 685 696 702 726 729-730
lymph node	Clontech	ALN001	28 57 79 113 164 172 179 193 240 325 332 367 378-379 386 388 402 485 526 580 586 603 613-614 621-622 628 634 662 667 686 734
young liver	GIBCO	ALV001	3 24 28 54 60 117 134 137 154 160 193 196 242 273 316 328-329 334 351 354 370-371 388 392 395-396 401 406 411 415 432 435 439 448 454-455 477 483 486-487 495 506 509 514 518 523-524 526 529 531 534 537-538 540 544 548 566 568 571 573 579 587-588 591 594 602 621 641 645 686 713 723
adult liver	Invitrogen	ALV002	3 24 27 56-57 65-66 71 79 92 97 106 134 140 164 192 200 214 220 232 240 242 271-272 291 313 316 328 347 349-350 353 355 357 368-369 371-372 378-379 381-382 385 397 430 435 448 457 459 471-472 475 485 487 502 505-506 511 520 530-531 533-534 537 540-541 543 548 566 574-575 579 582 588 590 612 623 640 648-649 681 687 689 710 714
adult ovary	Invitrogen	AOV001	3 10 14 28 54 56-58 62 65-66 68 73 75 79 98 127 144 154 162 164-165 172-174 182 186 188-189 192-196 206 213 224 234-235 241 243 248 253 261 273 275 289 314 316 321-322 325-327 329-331 333-334 336-338 340 343 345-348 354-357 367 369 371-372 378 382 386 388 395-397 399-402 404 407 411 415-416 419-420 425 427 429 431 435-437 441 444 451 453-459 465 468-470 472-475 481 485 490 494 496 501 503 509-510 513 517-518 522-524 526 528-529 531-534 537-542 545-546 548 552 554 556-557 559-560 562-563 565 567-569 572-579 581-582 584-588 590-591 593-598 602-604 606 611-615 618 620-623 627 629 631-632 635-638 643 647 652-654 657 659 661-662 667 674-675 677-678 682 684 689 693 695-698 703 705-707 714 717-718 723 729 731 738
adult placenta	Clontech	APL001	172 224 239 363 371 392 437 531 534 622 690 696

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
placenta	Invitrogen	APL002	57 66 122 161 172 241 326 329 334 369 388 407 427 429 436 459 464 506 508 511 539 541 545 566 573 575 590 597 637 648 690
adult spleen	GIBCO	ASP001	28 57 65 78 93 95 117 134 156-157 172 186 188 194 214 273 314 319 331 334 338 344 354 371 374 392 436 457 471-473 478-479 481 483 515 526 528-529 541 548 557 559 563 565 569 573 585-587 603 606 613 615 618 621-622 627 632 634 637 643 654 671 689 696-698 701 712 739
testis	GIBCO	ATS001	3 67 134 160 192 235 327 329 337 342 371 375 378 380-381 396 399 415 431 436 441 451 472 477-478 483 486 494 496 503 522 524 526 531 533-534 538 541-542 546 548 557 568 573 577 579 581 584 594 596 618 641 658 662 689 700 714 729-730
adult bladder	Invitrogen	BLD001	28 57 112 161 164 172 192 194 250 334 354 370 397 404 487 513 526 531 534 545 572 599 602 620 634 651 659 672 689 713 725
bone marrow	Clontech	BMD001	10-11 28 31 54 57 62 75 78-83 88 131-133 135-137 141-143 157 159 164 171-173 176-177 187-189 192 195 200 202 205 207 218 225 282 314-318 325 330 334-335 337 346- 348 367 369 372 378 383 386 388 395 401 405 412-413 416 422 436 442-443 447 449 455 465 472 475 477 503 516 523 528-529 533-534 539 545 551 556 559 563 565-567 571 573-574 576 579-586 594 601- 602 606 613 620-623 628-629 634 638 642-643 646 656 659 666 686 689 691 696 698-699 703 705 714 720 726 729
bone marrow	Clontech	BMD002	2 15 23 35 49 54 57 59 78 81 114 156-157 164 171-172 189-190 202 223 240 325 334 346 357 367 379 381-382 388 397 412 454 465 482 490 509 516 526 535 537 563 566 579 595 600 638 640-641 654-655 676 689 714
adult colon	Invitrogen	CLN001	48 79 94 138 162 167 189 333 368- 369 375 386 404 409 414 435-436 455 470 525 541 548 553 567 603 634 656 659 689 694 721
adult cervix	BioChain	CVX001	3 28 35 54 57 79 83 95 97 113 117 154 162 164 172 176 220 235 248-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			249 321 327 329 333 338 346 348 354 356 362 367-368 371 374-375 378-379 386 388-389 395 401-402 404 407 420 429 431 437 443 451 459 468 475 477 479 483 485 490 493-494 496 506 508 511 517 526 528 531 534 544 550 552 559 566 569 571-573 575-576 581-583 588 590 593-594 604 606 614 622 628 631-635 639 661-662 675 689 692 695 715 718 738
endothelial cells	Strategene	EDT001	3 28 31 39 54 58 65-66 79 89 144 160 173 187 189 191 193 197-199 207 220 230 267 273 314 324 326 329-331 336 347 354 369 372 378- 379 384 386 388 391-394 396-397 399 401 407 420 422 429 431-432 435-437 444 449 451 455 459 465 472 474-475 481-482 486 490 499- 501 503 506 511 513 515-517 520 522-524 528 531-534 538-539 541 545-546 548 550 552 557 559-560 563 565 567 569 571 573 577 579- 580 583-584 587-590 593-594 596- 597 599 602 611 614-615 618 620- 621 624 630 632-634 637-638 642- 643 647-648 651 675 677 680 682 694 696-698 703 708 714 719 724- 725 728-730 734
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	38 41-45 118-121 164 198 292-312
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM003	43 164 295
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM004	121 164 306 482
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM006	293

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
esophagus	BioChain	ESO002	513 526
fetal brain	Clontech	FBR001	57 468 563 634
fetal brain	Clontech	FBR004	162 186 254 265 491 582
fetal brain	Clontech	FBR006	1-2 5-6 11-12 22-23 49 57 62 73 94 103 114 162 164 172 189 193 203 218 240 244 251-252 259 279 330- 331 334-335 346-347 351 367 378 386 388-389 399 413 420 422 424 434 442 444 448 465 468 470 472- 473 490 496 501 503-504 511 520 524 528 532-533 539 544-546 548 551 553 563 571 573 576 587 591 601 613 615-616 620-621 628 634 641 644 648 653 657 662 672-673 689 691 698 706 714 718 725-728 733 735-739
fetal brain	Clontech	FBRs03	444 587
fetal brain	Invitrogen	FBT002	17 66 157 162 164 186 190 193 250 270 324 331 334-335 338 346 354- 355 374 382 389-390 426 429-430 437 442 453 467 471 475 481 485 491 507-508 513-514 526 528 532 540 544 548 550 552-553 557-558 563 565-566 590 593 602 612 615 637 641 648 654 662 672 676 692 703
fetal heart	Invitrogen	FHR001	57 75 164 547
fetal kidney	Clontech	FKD001	57 164 172 179 188 194 208 218 230 240 250 330 334 369 388 401 413 439 454 465 529 546 550 573 576 581 583 594-596 602 634 648 667 676 689 698 706
fetal kidney	Clontech	FKD002	2 560
fetal kidney	Invitrogen	FKD007	565 596-597
fetal lung	Clontech	FLG001	75 164 355 386 428 455 513 524 528 631 689
fetal lung	Invitrogen	FLG003	30 157 162 169 188 243 253 256 283 330 392 400-401 404 407 424 428 435-436 479 506 508 520 530-531 534 572 578 584 602 611 613 631 654 658 662 676 689 701 716
fetal lung	Clontech	FLG004	371
fetal liver-spleen	Columbia University	FLS001	2-3 5 26 29 31 35 48 54-58 60 62 65 67 70 74-77 79-80 84-87 89 92 96 98-100 104 117 122-130 138 140 144-158 160 162 164 172-173 185- 186 188-189 192-194 196 199-200 207 214 218-219 237-238 241 269 273 280 282 314-316 318-322 324 327 329-331 334-335 337 340 345 348-350 354-358 363-364 367-371

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			373 375 377-380 382-383 385-386 388 394-396 399 402 409 411-412 418 420-422 424 427 431 435-437 440 442 448-451 453 455 459 461 464-465 470 472-473 475 477-478 480-485 488-490 501 503 505-506 509 511-513 515-518 520 522-524 526-534 538-539 541 543-547 549- 550 552-553 556-557 559-564 566- 567 569 571 573 576 578-580 582- 587 589 591-594 596-597 599-600 602 611-615 618 620-625 627-628 631-636 638 641-642 646 648 651 659-660 662-664 667-668 675-678 680-681 684 689-690 696-698 709 714 723 738
fetal liver-spleen	Columbia University	FLS002	15 31-32 39-40 47-49 52 56 60 65 69 72 75 78 84 97-98 100 104 115 123 138 140 144 146 152-153 157 161 164 172-173 182 188 194 196 199 220 241-242 246 249 253 255 266 273-275 280-281 288-291 314- 316 318-319 321-322 324 329-331 336-339 343 347-350 353-354 357- 358 363 367 369-370 372 374 378- 380 382-383 386 388-389 393-397 399 405 407 409-410 412 421 424 432 435 439 448 450-451 453-457 459 461 464-465 470 472-475 477 479-481 483 485 488 490 497 501 503 506 509 511-513 516-518 520 524 527-528 531-532 534 539 541- 546 556 559-560 565-566 569 571 574 576 579 582-586 588 590 597- 599 602-604 606 615 618 620-621 623 625 627 632-634 639 641 644 648 666-668 675-676 681 684 689- 690 696-697 701 703 714 719 723 734-735
fetal liver-spleen	Columbia University	FLS003	60 79 157 190 690
fetal liver	Invitrogen	FLV001	3 27 35 48 50 56-57 66 75 92 94 105 157 161 164 176 189 209 220 243 272 324 328 333 335 353 369- 370 381 392 396 429-430 435 439- 440 442 444 465 471 483 487 502 506 513-514 519 534-535 537 548 554 566 568 576-577 580 582 590 613 621 645 648-649 689
fetal liver	Clontech	FLV002	343
fetal muscle	Invitrogen	FMS001	51 79 97 108-110 166 194 196 266 341 352 380 389 402 407 444 464

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			475 501 513 524 546 552 554 560 570 572 598 605 628 634 649 675 703-704 714 737
fetal muscle	Invitrogen	FMS002	524
fetal skin	Invitrogen	FSK001	31 33 35 48 57 63 67 75 112-114 117 157 162 164 172 178 180 188 196 220 243 254 319 324 328 330 333-334 367 369 371 375 379-383 386 388-389 400 404 407 412 419- 420 429 444 455 472-473 491 499 503 508 511 514 517 522-524 529 531 534 537 540 542 547 552 554 556-557 560 563 565 567 571-572 574 576 579 590 596 599 616 621 625 627 631-632 634 639-640 648 653-654 662 689 708 714
fetal skin	Invitrogen	FSK002	501 537
fetal spleen	BioChain	FSP001	465 729
umbilical cord	BioChain	FUC001	27-28 35 57 68 83 105 136 157 159- 160 164 188 191 225 279 315-316 321 328 334 363 367 369 378-379 383 386 388-389 392 397 406-407 413 415-416 427 440 449 455 458 461 464-465 468 473-475 479 485- 486 488 490 496 514 517 522 524 526 528-529 531 533-534 538 540 546 550 552 556-558 572 582 584- 585 587-588 594-597 602 606 613 616 618-619 631 634 637 651 689 696 698 706 729
fetal brain	GIBCO	HFB001	3 5 22 26 46 53 66 73 94 117 134 139 164 172-173 188-189 212 215 230-231 248 251 262 288-289 316 325 329-331 334 337-338 348 352 365-367 369 371 377-379 385-386 388 392 394 396 400 403 420 422 429 437 444-446 449 451 455 459 461-463 466-468 472-473 475 477 481 483 485-486 488 490-491 496 503-504 506 513 523-524 529 532- 533 539-541 545 548 550 552 557- 560 563 565-566 569 571 576-577 579-580 583-584 586 590 593-594 596-599 601-602 604 606 611 613 615 618 621-623 627-628 634-635 637 641 643 647 662 664-665 667 675 677 680 689 695-697 703 726
macrophage	Invitrogen	HMP001	97 518 532 569
infant brain	Columbia University	IB2002	28 46 56-57 59 67 75 78 109 117 122 129 144 157 162 164-165 172 176 180 190 193 212 220 226 236-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			237 251 261-262 316 318 324 328-330 334-335 337 340 354-356 361 364-365 367 369 371-373 377-380 382 385-386 389 392 395 397 400 411 416 421-422 429 432 436 438 444 448 451 456 464-465 469 471-475 484 486 496 504-506 511 520 524 526 529 531 533-534 537-540 544-546 548 553 556 558 562 565 567 576 579-580 582 584 586 589-590 593 597-598 602 613-614 618 620-621 627-628 632 634 636 641 650 654 659 662 667 683 689 721 730
infant brain	Columbia University	IB2003	46 54 75 109 156 164 220 244 251 314 324-325 331 335 340 361-362 367 369 377-379 400 408 438 442 456 460 464 469 472 496 506 523-524 526 529 538 540 544-545 547 558 560-562 565 567 569 579 584 598 602 613 615 621 627 632 634 637 639 650 738
infant brain	Columbia University	IBM002	262 340 432 436 438 472 531 534 569 613 634
infant brain	Columbia University	IBS001	162 231 283 331 369 385 438 444 472 506 513 523 531 534 580 615 636 689
lung, fibroblast	Stratagene	LFB001	28 54 57 65 172 188 233 321 331 340 347 367 369 378-379 388 401 451 459 475 479 503 511 522 524 532 534 559-560 573 580 583 587 597 615 632 634 638 686 689 708
lung tumor	Invitrogen	LGT002	3 7 21 24 26 28 31 54 56-57 62-63 66 92-93 101 109 112 162 164 171-172 176 183 188-189 192-193 196 201-202 223 230 235 259 273-274 316 321 329-331 333-334 338 345 347-348 356 367 369 371-372 378-379 381-382 386 388-390 396 399-404 406 409 416 424-425 427 429 432 436-437 439 451 455-456 459 464-465 467 473 475 484-486 490 499 502-503 506 508 511 513-514 517-518 522 524 526 528 531-532 534-535 538-539 541 543-546 553 557-559 563 567-568 571 573 575-576 579-580 585-588 590-591 593-594 598 601-604 609 611-613 615 621 627-628 631-632 636-637 645 648 651-652 654 662 667 672 677 681 683 689 698 701-702 714 718 724 726 729 734
lymphocytes	ATCC	LPC001	4 31-32 35 57 65-66 70 110 116 156

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			162 164 230 243 250 282 287 326 328-330 334 336 346-347 359 378 386 388 397 407 414 416 419 472 497 520 525 539 545 549 551 582 590 606 615 618 621 631 634 686 692 698 701 714
leukocyte	GIBCO	LUC001	4 7 9-11 23 28 31 35 39 54 65 75- 76 79 90 97 110 117 134 152 157 159 162 164-167 171 173 176 188 193 199 204 207 220 244 253 255 314 316 318 321 324 326 329-330 337-339 346-347 352 354 356 367 369 371 378-379 382 388-389 392 396-397 400-402 405 415-416 420 422 429 432 435-436 443-444 449 454-455 457-459 465 479 481-486 491 497 501 503-504 506 508 511 514 516 520 523-525 529 532-533 535 538-539 545 548 552-554 556 559-560 562-563 565-566 569 571- 573 576 579 581 585-587 590 593- 594 598 600-602 604 606-609 613- 614 618 620-622 624 627 630 632- 634 636 638 643 645 660-662 667 678 682 684 686 689 691 693 696- 698 714 726
leukocyte	Clontech	LUC003	11 54 97 152 164 330 479 546 564- 565 593 613 627 634 646 696 729
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	2 57 67 79 164 171-173 188 193 196 232 321 337 341 346 367 379-380 388 407 427 454 472 477 482 501 520 539 545 552 556 579 588 593 598 611 621 631 648 665 714 730
mammary gland	Invitrogen	MMG001	3 20-21 29 31 54 56-57 63-66 79 94 109 112-113 117 122 125 138 141 154 160 162 164 172 176 186 189 192 204 214 220-221 232 238 251 255 257 273 276-278 324 326 328- 331 333 335 337 341-343 347 354- 355 357 367-371 374-375 379 382- 386 388-392 397 399-400 404 406- 408 410-411 425 431 435-436 444 451 455 457 459 461 464-465 470- 471 475 479 483 485 487-488 491 501 506-508 511 513-519 523-524 526 529 531-532 534-535 537 539- 540 542-545 552-554 557-560 563 566 569 572 577 580 584 587-588 590 597-598 602 604-605 609 611 613 615 624 627 631-634 637 639- 640 643 648-649 654 664 669-670 672-673 676-679 681 689 691-695 697-698 706 714 731 734 737

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
induced neuron cells	Strategene	NTD001	36 57 164 284 388 397 420 481 485 501 524 528-529 539 542 545 560 571 579 582 595 602 620 637 654 667 689 730
retinoid acid induced neuronal cells	Strategene	NTR001	524 584 693
neuronal cells	Strategene	NTU001	36-38 120 204 331 351 354 357 386 388 399 411 442 459 516 533 539 545 565 586 606 615 621 637-638 642 646 648 714 730
placenta	Clontech	PLA003	503 579 690
prostate	Clontech	PRT001	15 40 65 164 187 207 229 337 348 367 375 377-378 395 406 416 428 458 468 476 511 524 526 531 534 538 555 559 563 576 584 597 613 622 624 631 642 667 672 677 684 724 734
rectum	Invitrogen	REC001	57 67 164 260 331 343 370-371 380 382 384 404 409 436 444 475 485 498 513 524 526 540 542 552 554 581 615 619 624 627 634 654 659 671 689 714
salivary gland	Clontech	SAL001	21 84 106-107 152 179 238 246 255 273 287 371 378 383 401 407 420 455 475 477 509 512 515 521 541 548 565 570-571 573-574 589 606 628 634 636 652 689 703 738
skin fibroblast	ATCC	SFB002	192
skin fibroblast	ATCC	SFB003	464
small intestine	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711
skeletal muscle	Clontech	SKM001	3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738
spinal cord	Clontech	SPC001	10 54 57 66 75 100 102 114 144 164 175 193 199 215-216 325 334 337 367 370 380 385-386 406 411-413 419 429 466 470 486 518 526 529 531 534 574 579 585 587 590 604 620-621 631-632 634 642 644 648 659 688-689 691 693 695
adult spleen	Clontech	SPLc01	478 572
stomach	Clontech	STO001	26 90 164 218 358 369 386 468 475

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			485 526 532 569 576 579 581 586 603 631 634 677 682 689
thalamus	Clontech	THA002	17 31 57 66 109 127 164 217-218 262 315-316 324 330 357 369 386 388 400 406 435 456 459 464 468- 469 515-516 537 540-541 556 566 574 590 611 622 631 634 644 648 656 677-678 680
thymus	Clontech	THM001	6 15 26 54 79 164 172 187 193 201 264 291 315 329 331 351 356 367 397-398 401 407 412 424 427 429 435-436 443 451 474 478 482 549 563 565 567 569 576 578 581-582 610 615 621 631-632 634 648 662 667 669 679 689 693 696
thymus	Clontech	THMc02	3-6 8 11 16 18 34 58-59 67 132 149 162 164 167 172-173 186 188-189 193 200 203 216 223 232 239 255 263 265 319-320 331 333-334 355 359 370 373 377-380 382 387-390 393 395 398-399 402 404 408 420 427 434 436 467 475-476 503 508 518 524 526 532 540 560 563 565 571-572 576-577 579 582 598 601 603 612-613 615 621 627 632 634 639 641 648 651 657 659 662 672 677-678 684-686 689 696 699 706 714-716 722 726-729 732
thyroid gland	Clontech	THR001	5 29-30 40 54 57 66 72 79 117 144 160 164 166 170 172 176 183 188- 189 208-209 219 230 285-286 314 318 327 331 335 338 344 347 354 363 367 375 377-380 382 384-386 388 393 397 399 401-403 419 422 429 436 442 444 451 456 458-461 464 467-468 470 472-473 476-477 481 488 494 503 508-509 511 516 519-521 524 528-529 533 537-538 543 548 557 559-560 563 565-566 571-574 576 582 585 587 590-591 593-594 596-597 606 614-615 620- 621 623-624 627 631-634 640 650- 651 653 662 667 669-670 675 679 689 708 712 714
trachea	Clontech	TRC001	156 164 171 240 375 378 390 400 422 468 484 565 574 581 585 587 631 654 689 714
uterus	Clontech	UTR001	65 77 79 101 164 220 367 369 451 468 526 530 533 548 554 559 562 568 573 582 594 637 648 689

Table 2 - Nearest Neighbor Results

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
1	1000	gi7021484	Mus musculus	secretory carrier membrane protein 4	567	85
2	10017	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	848	100
3	10020	gi1065967	Caenorhabditis elegans	similar to other protein phosphatases 1, 2A and 2B	325	36
4	10024	G03460	Homo sapiens	Human secreted protein,	439	98
5	10032	Y12505	Homo sapiens	Human 5' EST secreted protein	136	87
6	10042	Y29511	Homo sapiens	Human lung tumour protein SAL-25 1st predicted amino acid sequence.	701	100
7	1006	Y92324	Homo sapiens	Human alpha-2-delta-D polypeptide from splice variant 1.	763	100
8	10064	gi4589375	Homo sapiens	Gab2	425	58
9	1007	gi7018398	Homo sapiens		151	75
10	1008	gi896065	Homo sapiens	protein that is immuno-reactive with anti-PTH polyclonal antibodies	1226	99
11	10088	gi3779244	Homo sapiens	Metallo-protease 1	1512	98
12	10089	gi2947232	Homo sapiens	membrane associated guanylate kinase 2	523	100
13	10091	gi3347863	Mus musculus	cAMP-specific cyclic	223	54

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				nucleotide phosphodiesterase PDE8; MMPDE8		
14	10098	gi69793 11	Homo sapiens	cysteine-rich repeat-containing protein S52 precursor	1068	100
15	10102	G01395	Homo sapiens	Human secreted protein,	297	88
16	10103	gi85473 3	Rattus norvegicus	casein kinase 1 gamma 1 isoform	293	84
17	10104	Y60017	Homo sapiens	Human endometrium tumour EST encoded protein 77.	154	100
18	10108	G03290	Homo sapiens	Human secreted protein,	215	97
19	10110	gi72922 99	Drosophila melanogaster	CG1271 gene product	208	46
20	10111	gi45123 34	Rattus norvegicus	Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha	822	89
21	10113	Y41694	Homo sapiens	Human PRO382 protein sequence.	633	97
22	10114	gi34907 5	Rattus norvegicus	calmodulin-binding protein	531	99
23	10116	gi16298 1	Bos taurus	endozepine-related protein precursor	937	87
24	10121	gi89797 43	Canis familiaris	Band4.1-like5 protein	643	100
25	10126	Y99420	Homo sapiens	Human PRO1486 (UNQ755) amino acid sequence	607	100
26	1013	gi80475 0	Homo sapiens	protein tyrosine	614	73

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				phosphatase		
27	10136	W02105	Homo sapiens	Human L-asparaginase.	1243	98
28	10142	Y35924	Homo sapiens	Extended human secreted protein sequence,	862	89
29	10148	gi3334982	Homo sapiens	R27216_1	329	98
30	1015	G02485	Homo sapiens	Human secreted protein,	120	72
31	10154	gi10798804	Homo sapiens	sperm antigen	2607	98
32	10175	Y96864	Homo sapiens	SEQ. ID. 37 from WO0034474.	536	100
33	10196	gi553621	Homo sapiens	profilaggrin	346	39
34	10198	gi1419016	Mus musculus	odorant receptor	281	53
35	10200	Y57903	Homo sapiens	Human transmembrane protein HTMPN-27.	448	100
36	10208	gi4062492	Escherichia coli		505	100
37	10212	gi882529	Escherichia coli	ORF_f141	625	96
38	10213	gi4062778	Escherichia coli	Hypothetical protein HI0761	773	98
39	10214	gi6693832	Rattus norvegicus	opioid growth factor receptor	661	44
40	10227	G01360	Homo sapiens	Human secreted protein,	384	100
41	10236	gi1651257	Escherichia coli	.	373	100
42	10241	gi2769262	Escherichia coli	catabolite gene activator protein	178	96
43	10245	gi1789539	Escherichia coli	orf, hypothetical protein	679	98
44	10246	gi882492	Escherichia coli	ORF_o179	488	97
45	10247	gi1742149	Escherichia coli	Sn-glycerol-3-phosphate	323	100

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				transport system permease protein UgpA.		
46	10282	Y29817	Homo sapiens	Human synapse related glycoprotein 2.	521	96
47	1031	gi6435130	Mus musculus	putative E1-E2 ATPase	990	86
48	1040	gi854124	Homo sapiens	Human giant larvae homologue	471	63
49	1043	gi3882285	Homo sapiens	KIAA0782 protein	154	61
50	1051	gi178216	Homo sapiens	anion exchange protein 1	172	100
51	1053	Y76748	Homo sapiens	Human protein kinase homologue, PKH-1.	180	92
52	1062	gi965014	Mus musculus	ADAM 4 protein precursor	492	65
53	1063	gi2393880	Drosophila melanogaster	A-kinase anchor protein DAKAP550	580	60
54	1066	gi2746788	Caenorhabditis elegans	contains similarity to transacylases	607	35
55	107	G00357	Homo sapiens	Human secreted protein,	183	77
56	1071	gi9105937	Xylella fastidiosa	Acetylglutamate kinase	505	36
57	1085	R95913	Homo sapiens	Neural thread protein.	257	55
58	1086	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	387	58
59	1088	gi4589642	Homo sapiens	KIAA0999 protein	873	99
60	109	gi763431	Homo sapiens	KIAA0999 protein	360	85
61	1095	Y94907	Homo sapiens	Human secreted	701	97

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				protein clone cal06_19x protein sequence		
62	1102	Y07096	Homo sapiens	Colon cancer associated antigen precursor sequence.	1982	100
63	1105	Y84907	Homo sapiens	A human proliferation and apoptosis related protein.	983	91
64	1108	gi1398903	Mus musculus	Ca ²⁺ dependent activator protein for secretion	1307	89
65	1109	Y91524	Homo sapiens	Human secreted protein sequence encoded by gene 74	2400	99
66	1113	gi1657462	Sus scrofa	calcium/calmodulin-dependent protein kinase II isoform gamma-E	1348	94
67	1117	Y32169	Homo sapiens	Human growth-associated protease inhibitor heavy chain precursor.	2831	97
68	1118	gi3063517	Homo sapiens		1138	98
69	1125	gi8248285	Homo sapiens	sphingosine kinase type 2 isoform	1290	98
70	1132	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein sequence	437	59
71	1143	gi45806	Homo sapiens	prepro-major	209	40

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		77		basic protein homolog		
72	1146	gi182395	Homo sapiens	focal adhesion kinase	131	87
73	1161	W90962	Homo sapiens	Human CSGP-2 protein.	931	100
74	117	W69428	Homo sapiens	Human secreted protein bp537_4.	159	93
75	1170	gi34339	Homo sapiens		586	87
76	1175	gi7960243	Homo sapiens	SNARE protein kinase SNAK	308	100
77	118	gi5360093	Homo sapiens	NY-REN-18 antigen	178	96
78	1183	gi292037	Homo sapiens	helix-loop-helix phosphoprotein	361	91
79	1193	gi1899186	Rattus norvegicus	polysialyltransferase	171	76
80	1195	gi1399462	Homo sapiens	serine/threonine-protein kinase PRP4h	208	71
81	1198	gi181535	Homo sapiens	defensin precursor	150	71
82	1201	gi5668935	Rattus norvegicus	plasma membrane Ca ²⁺ ATPase isoform 1kb	244	73
83	1207	gi6224868	Homo sapiens	TANK binding kinase TBK1	716	86
84	1210	gi179646	Homo sapiens	complement component C1s	242	61
85	1211	gi1483187	Homo sapiens		296	65
86	1214	gi7800638	Streptococcus pneumoniae	PspA	121	37
87	123	Y44810	Homo sapiens	Human Aspartic Protease-2 (NHAP-2).	218	93
88	1259	gi2116672	Homo sapiens	EAR-1r	128	70
89	1266	gi7243125	Homo sapiens	KIAA1372 protein	403	53
90	1270	gi1289445	Homo sapiens	diacylglycerol kinase epsilon DGK	125	96

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
91	1290	gi1429371	Drosophila melanogaster	ubiquitin-specific protease	470	41
92	1291	Y66755	Homo sapiens	Membrane-bound protein PRO1185.	993	100
93	1296	gi9652087	Homo sapiens	scavenger receptor cysteine-rich type 1 protein M160 precursor	1183	99
94	1299	gi7300398	Drosophila melanogaster	CG7683 gene product	397	40
95	1317	gi3695115	Rattus norvegicus	CL1AA	216	100
96	132	gi187171	Homo sapiens	12-lipoxygenase	176	97
97	1330	Y12482	Homo sapiens	Human 5' EST secreted protein	65	44
98	1336	gi10798814	Homo sapiens	MLTK-beta	2366	99
99	135	gi456090	Homo sapiens	effector cell protease receptor 1	190	74
100	1356	gi193057	Mus musculus	envelope polyprotein precursor	131	36
101	1369	gi458657	Homo sapiens	glucocorticoid receptor alpha-2	596	89
102	1392	gi8493519	Mus musculus	nuclear localization signal binding protein	145	59
103	1408	gi3127051	Rattus norvegicus	potassium channel regulatory protein KChAP	176	84
104	141	gi6453613	Mus musculus	putative protein kinase	204	33
105	1424	gi2982501	Homo sapiens	neuropathy target esterase	769	100
106	143	W50033	Homo sapiens	Human immunity related factor.	1201	98
107	1431	gi10644	Heterodera	hypothetical	133	36

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		565	glycines	esophageal gland cell secretory protein 10		
108	1441	gi3044086	Myxococcus xanthus	unknown	149	32
109	1444	gi7248381	Homo sapiens	adaptor protein p130Cas	1615	97
110	1447	Y65168	Homo sapiens	Human 5' EST related polypeptide	403	97
111	1457	W19919	Homo sapiens	Human Ksr-1 (kinase suppressor of Ras).	227	77
112	1471	G02532	Homo sapiens	Human secreted protein,	97	59
113	1473	gi6062874	Homo sapiens	candidate tumor suppressor protein DICE1	581	100
114	1474	Y64896	Homo sapiens	Human 5' EST related polypeptide	197	100
115	1483	gi436218	Homo sapiens	KIAA0037	295	76
116	1486	gi5852834	Homo sapiens	bridging integrator-2	133	64
117	149	gi3327162	Homo sapiens	KIAA0674 protein	2243	98
118	1503	gi1736785	Escherichia coli	.	1270	97
119	1506	gi4062298	Escherichia coli	YhhI protein	612	90
120	1513	gi4062346	Escherichia coli	.	556	94
121	1514	gi216609	Escherichia coli	PhoQ protein	661	90
122	1523	gi5712756	Rattus norvegicus	calcium transporter CaT1	1178	90
123	1527	gi1853980	Mus musculus	glucocorticoid receptor interacting protein 1	171	84
124	1536	Y17227	Homo sapiens	Human secreted	452	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				protein (clone yal-1).		
125	154	gi8515090	Pinus taeda	putative arabinogalactan protein	81	40
126	1544	gi3879933	Caenorhabditis elegans	Similarity to Xenopus F-spondin precursor (PIR Acc. No. comes from this gene	134	34
127	1554	gi6523817	Homo sapiens	SlR protein	255	84
128	1555	gi6635205	Homo sapiens	beta-ureidopropionase	210	90
129	1556	Y39286	Homo sapiens	Phosphodiesterase 10 (PDE10) clone FB93a.	161	61
130	1564	gi8977945	Streptomyces coelicolor A3(2)	putative secreted serine protease	231	45
131	1576	gi3025828	Rattus norvegicus	signal transducer and activator of transcription 4	183	97
132	1578	gi5106572	Homo sapiens	transcriptional activator SRCAP	758	98
133	1579	gi8575527	Homo sapiens	toll-like receptor 8	595	99
134	158	gi406058	Mus musculus	protein kinase	168	70
135	1580	gi63340	Gallus gallus	c-Rml	231	90
136	1588	gi2217931	Homo sapiens	PKU-alpha	127	92
137	1589	gi1272422	Mus musculus	Phosphoinositide 3-kinase	720	99
138	159	gi2224629	Homo sapiens	KIAA0344	215	43
139	1600	gi1016012	Rattus norvegicus	neural cell adhesion protein BIG-2 precursor	543	93
140	161	gi6649583	Homo sapiens	kidney and liver proline	1651	98

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				oxidase 1		
141	1612	gi406113	Rattus norvegicus	protein kinase I	125	89
142	1615	gi219992	Homo sapiens	phSR2	150	78
143	1620	gi5714636	Homo sapiens	serine/threonine protein kinase Kp78 splice variant CTAK75a	126	71
144	1644	Y13352	Homo sapiens	Amino acid sequence of protein PRO228.	2542	100
145	1647	Y99444	Homo sapiens	Human PRO1575 (UNQ781) amino acid sequence	704	100
146	1650	gi3789765	Homo sapiens	transmembrane receptor UNC5C	271	100
147	1663	W75258	Homo sapiens	Fragment of human secreted protein encoded by gene 26.	163	96
148	1665	gi10432431	Homo sapiens	secreted modular calcium-binding protein	1428	99
149	1671	gi6708169	Mus musculus	inositol phosphatase eSHIPD183	169	97
150	1672	Y68773	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-5.	1030	99
151	1678	gi6063017	Homo sapiens	tousled-like kinase 1	132	86
152	1680	gi3510603	Homo sapiens	nuclear receptor co-repressor N-CoR	278	80
153	1692	gi1546084	Homo sapiens	farnesol receptor HRR-1	165	100
154	1698	gi520469	Oryctolagus cuniculus	597 aa protein related to	177	94

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				Na/glucose cotransporters		
155	1702	gi10432382	Homo sapiens		519	95
156	1704	Y91668	Homo sapiens	Human secreted protein sequence encoded by gene 73	214	75
157	1708	gi3080757	Mus musculus	growth factor independence-1B	457	78
158	1716	gi29653	Homo sapiens	putative oncogene	220	92
159	173	gi3452473	Rattus norvegicus	serine/threonine protein kinase TAO1	699	100
160	1731	Y27581	Homo sapiens	Human secreted protein encoded by gene No. 15.	774	100
161	1732	gi9652087	Homo sapiens	scavenger receptor cysteine-rich type 1 protein M160 precursor	1025	98
162	174	Y35923	Homo sapiens	Extended human secreted protein sequence,	1691	100
163	1740	Y53014	Homo sapiens	Human secreted protein clone fn189_13 protein sequence	337	60
164	1748	gi7770237	Homo sapiens	PRO2822	218	93
165	1751	gi8979825	Homo sapiens		306	50
166	1755	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone	1184	62

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				3TW).		
167	1762	gi7380947	Homo sapiens	Gem-interacting protein	1545	99
168	1776	gi5912265	Homo sapiens	hypothetical protein	224	100
169	1777	Y70461	Homo sapiens	Human membrane channel protein-11 (MECHP-11).	413	95
170	1781	R26060	Homo sapiens	Growth Factor Receptor Bound protein GRB-1.	398	98
171	1796	gi10312169	Homo sapiens	serine carboxypeptidase 1 precursor protein	1381	99
172	180	gi3002527	Homo sapiens	neuronal thread protein AD7c-NTP	477	61
173	182	gi7385131	Homo sapiens	HBV pX associated protein-8; XAP-8	2066	82
174	1820	G03249	Homo sapiens	Human secreted protein,	370	97
175	1822	gi473969	Oryctolagus cuniculus	one of the members of sodium-glucose cotransporter family	1048	90
176	1829	gi10440355	Homo sapiens	FLJ00012 protein	310	96
177	1832	gi165650	Oryctolagus cuniculus	phosphorylase kinase beta-subunit	146	96
178	1834	W75132	Homo sapiens	Human secreted protein encoded by gene 11 clone HCENJ40.	423	47
179	1837	gi60369	Saimiriine herpesvirus 2	ORF 48-EDLF5-sim. to EBV BRRF2	615	71

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
180	1859	gi9989696	Homo sapiens	ROR2 protein	645	87
181	1880	gi7340847	Mus musculus	chondroitin 4-sulfotransferase	275	40
182	1881	gi7573291	Homo sapiens		298	100
183	1890	gi3149950	Homo sapiens	ST1C2	183	94
184	1899	gi2143260	Homo sapiens	Phosphoinositide 3-kinase	346	98
185	19	gi1808582	Homo sapiens	U2AF1-RS2	224	46
186	192	G03192	Homo sapiens	Human secreted protein,	267	86
187	1922	gi485858	Mus musculus	IB3/5-polypeptide	1206	78
188	1945	gi37261	Homo sapiens		1402	97
189	195	W67863	Homo sapiens	Human secreted protein encoded by gene 57 clone HFEBF41.	551	98
190	1957	gi406738	Homo sapiens	Shb	263	44
191	1969	Y41701	Homo sapiens	Human PRO708 protein sequence.	975	98
192	1970	gi3979817	Caenorhabditis elegans	Weak similarity to Human tyrosine-protein kinase, CSK	254	49
193	1973	G00796	Homo sapiens	Human secreted protein,	365	98
194	1985	gi4558637	Homo sapiens	Putative homolog of hypoxia inducible factor three alpha	1420	99
195	1986	gi4455015	Homo sapiens	host cell factor homolog	367	50

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Water man Score	% Identity
				LCP		
196	2	G02532	Homo sapiens	Human secreted protein,	106	85
197	2004	gi10503935	Homo sapiens	type A calpain-like protease	961	100
198	2023	gi1651341	Escherichia coli	.	1075	97
199	2025	Y71069	Homo sapiens	Human membrane transport protein, MTRP-14.	540	100
200	2038	gi8572543	Homo sapiens	membrane-associated lectin type-C	686	98
201	2041	gi37400	Homo sapiens	trk-2h polypeptide	228	89
202	2043	W75096	Homo sapiens	Human secreted protein encoded by gene 40 clone HNEDJ57.	290	38
203	2068	G03394	Homo sapiens	Human secreted protein,	595	97
204	2072	gi2116552	Rattus norvegicus	cationic amino acid transporter 3	1025	85
205	2076	gi157409	Drosophila melanogaster	fat protein	369	39
206	2078	gi1054940	Gallus gallus	CSH-PTP2	605	94
207	2084	gi9663128	Homo sapiens	hypothetical protein	874	99
208	2088	gi10567590	Homo sapiens	sodium bicarbonate cotransporter-like protein	609	100
209	2089	gi1789001	Escherichia coli	putative ATP-binding component of a transport system	961	98
210	2097	Y70460	Homo sapiens	Human membrane channel	258	96

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				protein-10 (MECHP-10)		
211	2108	gi3207508	Rattus norvegicus	hexokinase	767	74
212	2111	gi6330233	Homo sapiens	KIAA1176 protein	3710	99
213	2118	W74797	Homo sapiens	Human secreted protein encoded by gene 68 clone HKIXR69.	156	96
214	2134	gi1780991	Homo sapiens	branched chain acyl-CoA oxidase	209	97
215	2146	gi7688148	Homo sapiens	hypothetical protein	1038	100
216	2149	gi2280485	Homo sapiens	KIAA0376	917	100
217	2153	gi1842429	Rattus norvegicus	ankyrin binding cell adhesion molecule neurofascin	592	88
218	2155	gi6526791	Homo sapiens	Eps15R	1126	100
219	2161	gi7300427	Drosophila melanogaster	CG7709 gene product	200	33
220	2163	Y52296	Homo sapiens	Human isomerase homologue-3 (HIH-3).	186	91
221	2173	W34526	Homo sapiens	hTCP protein fragment.	164	93
222	2178	gi3360512	Rattus norvegicus	Citron-K kinase	299	94
223	2180	Y74008	Homo sapiens	Human prostate tumor EST fragment derived protein #195.	261	41
224	2184	gi53041	Mus musculus		130	41
225	2186	gi401774	Homo sapiens	ribosomal protein S6 kinase 3	142	64
226	2190	gi577295	Homo sapiens	The hal225 gene product is related to human alpha-	176	100

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				glucosidase.		
227	2210	gi20553 92	Rattus norvegicus	transmembrane receptor UNC5H1	620	90
228	2214	gi78617 33	Homo sapiens	low density lipoprotein receptor related protein-deleted in tumor	1360	98
229	2223	gi79591 89	Homo sapiens	KIAA1464 protein	884	99
230	223	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	300	77
231	2233	gi78395 87	Homo sapiens	organic anion transporting polypeptide 14	1092	99
232	2237	gi10440 400	Homo sapiens	FLJ00033 protein	1212	99
233	2251	gi59237 86	Homo sapiens	zinc metallo-protease ADAMTS6	277	44
234	2256	W63698	Homo sapiens	Human secreted protein 18.	516	100
235	2259	gi46787 22	Homo sapiens	hypothetical protein	387	36
236	2262	Y33741	Homo sapiens	Beta-secretase.	793	99
237	2265	gi70185 45	Homo sapiens	hypothetical protein	608	94
238	2271	gi41861 83	Homo sapiens	unknown	684	53
239	2273	gi72430 35	Homo sapiens	KIAA1327 protein	1031	100
240	2280	gi58096 78	Homo sapiens	sperm membrane protein BS-63	342	95
241	2286	gi62246 91	Homo sapiens	Na ⁺ /sulfate cotransporter SUT-1	1221	99
242	2291	gi20762 1	Rattus norvegicus	uromodulin	345	50
243	2292	gi72963 04	Drosophila melanogaster	CG5274 gene product	272	35
244	2294	Y28503	Homo sapiens	HGFH3 Human Growth Factor	320	98

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				Homologue 3.		
245	2296	W88799	Homo sapiens	Polypeptide fragment encoded by gene 45.	223	86
246	2303	gi7110160	Homo sapiens	guanine nucleotide exchange factor	1212	99
247	2306	gi6434874	Mus musculus	calcium/calmodulin dependent protein kinase kinase alpha	576	84
248	2309	Y95433	Homo sapiens	Human calcium channel SOC-2/CRAC-1 C-terminal polypeptide.	1203	99
249	2313	gi7300943	Drosophila melanogaster	CG4677 gene product	689	79
250	2318	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	202	59
251	2329	G01772	Homo sapiens	Human secreted protein,	311	84
252	2330	Y41729	Homo sapiens	Human PRO1071 protein sequence.	886	99
253	2342	gi3786430	Caenorhabditis elegans		268	42
254	2350	gi930104	Homo sapiens	protein-tyrosine phosphatase	571	79
255	2359	gi9392591	Homo sapiens	CC chemokine CCL28	679	99
256	2361	gi1666689	Mus musculus	alpha-NAC, muscle-specific form gp220	357	41
257	2374	G03172	Homo sapiens	Human secreted protein,	112	78
258	2387	gi1399197	Homo sapiens	pyruvate dehydrogenase kinase isoform 4	201	85
259	2401	G01757	Homo sapiens	Human	612	99

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				secreted protein,		
260	2409	gi181123	Homo sapiens	cleavage signal 1 protein	194	86
261	2431	gi7018547	Homo sapiens	hypothetical protein	473	50
262	2432	gi4826496	Homo sapiens		327	39
263	2467	G03667	Homo sapiens	Human secreted protein,	640	97
264	2471	gi7688148	Homo sapiens	hypothetical protein	1284	91
265	2478	gi790819	Homo sapiens	polycystic kidney disease-associated protein	615	90
266	2484	gi3327080	Homo sapiens	KIAA0633 protein	1747	99
267	249	G03793	Homo sapiens	Human secreted protein,	139	65
268	2490	gi6467371	Homo sapiens	thyrotropin-releasing hormone degrading ectoenzyme	757	98
269	25	G03203	Homo sapiens	Human secreted protein,	137	65
270	2504	gi4097712	Homo sapiens	HBV associated factor	166	74
271	2506	gi2072784	Homo sapiens	Na ⁺ /nucleoside cotransporter	201	95
272	2507	gi5924007	Homo sapiens		335	38
273	2510	gi7717385	Homo sapiens	beta-site APP-cleaving enzyme 2, EC 3.4.23.	383	89
274	2523	gi339709	Homo sapiens		150	96
275	253	gi36615	Homo sapiens	serine/threonine protein kinase	391	77
276	2533	gi45896	Homo sapiens	KIAA0985	191	61

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		14		protein		
277	2536	gi2088685	Caenorhabditis elegans	strong similarity to the CDC2/CDX subfamily of ser/thr protein kinases	419	55
278	2544	gi1002425	Mus musculus	YSPL-1 form 2	280	80
279	2568	Y41738	Homo sapiens	Human PRO541 protein sequence.	379	49
280	2580	gi3004482	Rattus norvegicus	putative integral membrane transport protein	382	49
281	2593	gi7300049	Drosophila melanogaster	CG4525 gene product	582	50
282	2600	gi4530437	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	334	90
283	2625	gi8099652	Homo sapiens	toll-like receptor 9 form A	761	96
284	2641	gi148019	Escherichia coli	tolA	692	100
285	2667	gi1750387	Pseudomonas aeruginosa	Carbamoyl-phosphate synthetase large subunit	143	76
286	2670	gi4883437	Mus musculus	RNA binding protein	139	92
287	2673	Y66656	Homo sapiens	Membrane-bound protein PRO943.	1869	98
288	2676	gi3885978	Mus musculus	mismatch-specific thymine-DNA glycosylate	123	88
289	2680	gi6453438	Homo sapiens	hypothetical protein	465	82
290	2682	gi18417	Mus musculus	GATA-5	527	77

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Water man Score	% Identity
		56		cardiac transcription factor		
291	2684	gi98449 20	Homo sapiens	nicotinic acetylcholine receptor subunit alpha 10	294	88
292	2695	gi17897 64	Escherichia coli	putative transport	879	98
293	2697	gi34922 9	Escherichia coli	peripheral membrane protein	936	99
294	2698	gi40621 94	Escherichia coli	.	737	100
295	2700	gi52924 0	Escherichia coli	homoserine kinase	578	100
296	2704	gi15528 31	Escherichia coli	hypothetical	420	100
297	2712	gi17896 72	Escherichia coli	putative ATP- binding component of a transport system	262	100
298	2716	gi40624 09	Escherichia coli	Transmembrane protein dppC	382	100
299	2719	gi30497 6	Escherichia coli	matches PS00017: ATP_GTP_A and PS00301: EFACTOR_GTP; similar	921	95
300	2724	gi14585 6	Escherichia coli	nmpC	647	97
301	2725	gi17894 73	Escherichia coli	putative transport protein	312	100
302	2728	gi18055 61	Escherichia coli		222	97
303	2729	gi43248	Escherichia coli		655	91
304	2744	gi39629 9	Escherichia coli	similar to E. coli pyruvate formate-lyase activating enzyme	675	100
305	2749	gi17426 48	Escherichia coli	.	592	100
306	2752	gi40622	Escherichia	Sensor kinase	357	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		36	coli	CitA		
307	2762	gi1787795	Escherichia coli	putative LACI-type transcriptional regulator	342	100
308	2764	gi1799743	Escherichia coli	putative LACI-type transcriptional regulator	151	84
309	2768	gi405964	Escherichia coli	yohG	534	94
310	2774	gi4062338	Escherichia coli	.	387	97
311	2790	gi4062338	Escherichia coli	.	420	86
312	2800	gi1789805	Escherichia coli	putative transport	572	100
313	2811	gi5305333	Mus musculus	protein kinase Myak-S	421	49
314	2827	gi10047251	Homo sapiens	KIAA1588 protein	531	97
315	2830	G02872	Homo sapiens	Human secreted protein,	185	62
316	2836	gi191175	Cricetulus sp.	cAMP-dependent protein kinase alpha-catalytic subunit	1677	97
317	2851	gi558846	Homo sapiens	BCL2/adeno-virus E1B 19kD-interacting protein 3	220	61
318	2856	gi3882211	Homo sapiens	KIAA0745 protein	232	93
319	2866	gi6329708	Homo sapiens	KIAA1119 protein	1331	91
320	2874	gi2853033	Mus musculus	tousled-like kinase	203	82
321	2882	gi10185134	Schizosaccharomyces pombe	hypothetical zinc-finger protein	318	42
322	2886	G03797	Homo sapiens	Human secreted protein,	140	69
323	2899	gi4240325	Homo sapiens	KIAA0918 protein	170	53

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
324	2906	Y94988	Homo sapiens	Human secreted protein vll_1,	1738	100
325	2920	gi9453735	Homo sapiens		1926	100
326	2925	gi6434876	Homo sapiens	CDK4-binding protein p34SEI1	1210	100
327	2930	gi3941320	Schistosoma japonicum	myosin	208	28
328	2934	Y31645	Homo sapiens	Human transport-associated protein-7 (TRANP-7).	642	63
329	2955	G01165	Homo sapiens	Human secreted protein,	528	99
330	2967	gi7263960	Homo sapiens		466	100
331	2980	gi4589530	Homo sapiens	KIAA0943 protein	1849	94
332	2994	G03812	Homo sapiens	Human secreted protein,	124	61
333	2996	gi9857400	Homo sapiens	tumor endothelial marker 1 precursor	2666	98
334	2999	Y66697	Homo sapiens	Membrane-bound protein PRO1383.	2254	100
335	3	gi6289072	Homo sapiens	JM24 protein	930	100
336	3008	Y45219	Homo sapiens	Human CASB47 protein.	557	92
337	3013	gi5262678	Homo sapiens	hypothetical protein	1747	100
338	3041	Y73335	Homo sapiens	HTRM clone 1850120 protein sequence.	1315	99
339	306	gi4868443	Mesocricetus auratus	Mx-interacting protein kinase PKM	1867	95
340	3061	gi433338	Homo sapiens	protein-tyrosine kinase	3934	94

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
341	309	Y76145	Homo sapiens	Human secreted protein encoded by gene 22.	1313	99
342	3095	gi7300159	Drosophila melanogaster	CG14899 gene product	190	57
343	3098	gi532056	Homo sapiens	protein-tyrosine-phosphatase	2641	86
344	3105	gi285987	Homo sapiens	mitochondrial outer membrane protein 19	192	71
345	3118	gi9929935	Macaca fascicularis	hypothetical protein	180	61
346	3124	gi8131903	Mus musculus	transient receptor potential-related protein	226	100
347	3126	Y02370	Homo sapiens	Polypeptide identified by the signal sequence trap method.	261	100
348	3166	gi7290860	Drosophila melanogaster	CG1531 gene product	534	42
349	3175	gi6649583	Homo sapiens	kidney and liver proline oxidase 1	1752	95
350	3176	gi7208438	Homo sapiens	long-chain 2-hydroxy acid oxidase HAOX2	1048	95
351	3188	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	243	57
352	3191	gi7105926	Homo sapiens	calcium channel alpha2-delta3 subunit	300	96
353	3208	gi10334774	Homo sapiens	MUCDHL-FL	613	98
354	3226	Y87209	Homo sapiens	Human secreted protein sequence	3147	99

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
355	3235	gi6715135	Homo sapiens	Fanconi anemia, complementation group F	1947	99
356	3257	gi5441615	Canis familiaris	zinc finger protein	326	42
357	3282	G03002	Homo sapiens	Human secreted protein,	211	61
358	3289	gi3288457	Homo sapiens	PI3-kinase	5832	97
359	3296	gi7770139	Homo sapiens	PRO1722	293	64
360	3298	gi2198815	Ambystoma tigrinum	electrogenic Na ⁺ bicarbonate cotransporter; NBC	1278	52
361	3303	gi4028015	Homo sapiens	potassium channel	1881	92
362	3305	gi5902966	Homo sapiens	very large G-protein coupled receptor-1	1770	100
363	3308	gi219944	Homo sapiens	The first in-frame ATG codon is located at nucleotides NPPase.	3967	86
364	3325	gi3510234	Homo sapiens	R31237_1, partial CDS	192	94
365	3341	W78899	Homo sapiens	Human UNC-5 homologue UNC5H-1.	1614	90
366	3342	gi1478205	Mus musculus	PNG protein	341	70
367	3350	gi2739460	Bos taurus	regulator of G-protein signaling 7	2263	98
368	3372	gi7671663	Homo sapiens		375	79
369	338	Y84322	Homo sapiens	A human cardiovascular system associated protein kinase-3.	2606	100
370	3383	gi10441	Homo sapiens	protein	1127	100

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		382		kinase		
371	3395	gi530823	Homo sapiens	epidermal growth factor receptor kinase substrate	402	47
372	3405	Y29332	Homo sapiens	Human secreted protein clone pe584_2 protein sequence.	1220	94
373	3408	gi3334741	Homo sapiens	shal-type potassium channel	2888	90
374	345	gi4539527	Homo sapiens	NAALADase L protein	600	72
375	346	Y95434	Homo sapiens	Human calcium channel SOC-3/CRAC-2 C-terminal polypeptide.	1802	99
376	3470	gi9798452	Homo sapiens	putative capacitative calcium channel	277	100
377	3482	gi3818572	Homo sapiens	cAMP-specific phosphodiesterase 8B; PDE8B1; 3',5'-cyclic nucleotide phosphodiesterase	2353	96
378	3492	gi1665825	Homo sapiens		3878	99
379	3530	gi505100	Homo sapiens	KIAA0066	3637	100
380	3533	Y32169	Homo sapiens	Human growth-associated protease inhibitor heavy chain precursor.	2860	99
381	3545	gi6624133	Homo sapiens		449	98
382	3549	gi1469193	Homo sapiens	The KIAA0135 gene is related to	5374	99

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Water man Score	% Identity
				pim-1 oncogene.		
383	3595	gi63301 90	Homo sapiens	KIAA1169 protein	1893	100
384	3601	gi80891 5	Homo sapiens	tumor necrosis factor receptor type 1 associated protein	992	99
385	3612	gi53054 48	Mus musculus	SH2-B PH domain containing signaling mediator 1 gamma isoform	1439	92
386	3613	Y32194	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 266775.	1438	100
387	3621	gi89784 9	Mus musculus	ubiquitinating enzyme E2-230 kDa	393	68
388	3624	R47858	Homo sapiens	Human LDL receptor Domains 1 and 2.	2895	100
389	3625	Y57949	Homo sapiens	Human transmembrane protein HTPN- 73.	1868	100
390	3626	W69342	Homo sapiens	Secreted protein of clone CJ424_9.	442	94
391	3627	gi65371 36	Homo sapiens	putative organic anion transporter	982	92
392	3630	Y06886	Homo sapiens	HWHHJ20 polypeptide.	1109	91
393	3642	gi48864 67	Homo sapiens	hypothetical protein	570	52
394	3645	gi95884 02	Homo sapiens		598	98
395	3647	Y12050	Homo sapiens	Human 5' EST secreted protein	517	98

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
396	3653	Y70018	Homo sapiens	Human Protease and associated protein-12 (PPRG-12).	2232	99
397	3676	W67818	Homo sapiens	Human secreted protein encoded by gene 12 clone HMSJJ74.	338	100
398	3677	gi32093	Homo sapiens	HGMP07J	650	52
399	3681	Y48443	Homo sapiens	Human prostate cancer-associated protein 140.	803	93
400	3682	gi46917 26	Homo sapiens	ARF GTPase-activating protein GIT1	2435	91
401	3688	gi66938 24	Homo sapiens	ubiquitin-specific protease	1995	99
402	3689	Y94927	Homo sapiens	Human secreted protein clone ck213_12 protein sequence	530	81
403	3690	gi18716 12	Oryctolagus cuniculus	ryanodine receptor	594	95
404	3706	gi60027 14	Homo sapiens	membrane-type serine protease 1	2630	94
405	3714	gi26957 08	Homo sapiens	SPOP	553	81
406	3720	gi93092 93	Homo sapiens	asc-type amino acid transporter 1	566	95
407	3726	gi10440 381	Homo sapiens	FLJ00026 protein	1023	69
408	373	gi57146 96	Mus musculus	alpha 2 delta calcium channel subunit	243	95
409	3788	gi69112 19	Homo sapiens	type II membrane serine protease	841	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
410	3789	Y45023	Homo sapiens	Human sensory transduction G-protein coupled receptor-B3.	1084	95
411	3790	gi1524088	Homo sapiens	Polio virus receptor protein	1508	99
412	3801	gi6723675	Homo sapiens	mitotic kinase-like protein-1	2035	99
413	3803	gi968973	Homo sapiens	mitotic kinase-like protein-1	332	86
414	3820	gi1770478	Homo sapiens	NK receptor	1988	99
415	3831	gi2781386	Homo sapiens		1493	99
416	3837	gi9367840	Homo sapiens	neuronal apoptosis inhibitory protein 2	2243	99
417	385	gi1526978	Homo sapiens	ryanodine receptor 2	149	96
418	3856	gi995654	Homo sapiens	interleukin-11 receptor	147	100
419	386	gi4960038	Mus musculus	T2K protein kinase homolog	669	66
420	3861	Y74129	Homo sapiens	Human prostate tumor EST fragment derived protein #316.	842	98
421	3883	gi6635205	Homo sapiens	beta-ureidopropionase	1576	100
422	3898	gi37231	Homo sapiens	DNA topoisomerase II	8436	99
423	3921	gi8648881	Homo sapiens	putative organic anion transporter	131	100
424	3932	gi8575775	Homo sapiens	KRAB zinc finger protein	1935	99
425	3934	gi4689128	Homo sapiens	SIH003	127	92
426	3963	gi3212996	Homo sapiens		339	64
427	3974	G03790	Homo sapiens	Human	232	63

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				secreted protein,		
428	3983	gi181971	Homo sapiens	vascular endothelial growth factor	433	85
429	3999	gi1657464	Sus scrofa	calcium/calmodulin-dependent protein kinase II isoform gamma-G	484	75
430	4001	gi6572230	Homo sapiens		329	100
431	4009	gi2143260	Homo sapiens	phosphoinositide 3-kinase	521	99
432	401	gi6572379	Homo sapiens		1372	56
433	4020	gi2815624	Homo sapiens	tumor necrosis factor superfamily member LIGHT	1252	100
434	4024	Y21166	Homo sapiens	Human bcl2 proto-oncogene mutant protein fragment 14.	84	40
435	4040	Y57285	Homo sapiens	Human GPCR protein (HGPRP) sequence (clone ID 2214673).	1726	99
436	4057	W74873	Homo sapiens	Human secreted protein encoded by gene 145 clone HFXHL79.	531	100
437	4066	G03714	Homo sapiens	Human secreted protein,	92	70
438	4067	gi8331760	Homo sapiens	LUL protein	1077	92
439	4078	Y57900	Homo sapiens	Human transmembrane protein HTPPN-24.	996	100
440	4120	gi18715	Homo sapiens	mitogen-	927	100

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		39		activated protein kinase phosphatase 4		
441	4123	gi5360125	Homo sapiens	NY-REN-58 antigen	140	100
442	4130	gi6289072	Homo sapiens	JM24 protein	604	100
443	4133	gi8575527	Homo sapiens	toll-like receptor 8	755	100
444	4166	gi6118555	Homo sapiens	DEAD-box protein abstrakt	2512	100
445	4167	gi3800830	Rattus norvegicus	putative four repeat ion channel	615	93
446	4172	gi7209676	Homo sapiens	potassium channel Kv8.1	369	100
447	4185	gi5305405	Homo sapiens	Na ⁺ /H ⁺ exchanger isoform 2	1769	100
448	4197	gi2811122	Xenopus laevis	NaDC-2	524	69
449	4203	Q89840_aal	Homo sapiens	Human death associated protein DAP-3.	198	97
450	4262	gi5901478	Marmota marmota	olfactory receptor	209	92
451	4276	gi32456	Homo sapiens	protein-tyrosine phosphatase	3270	99
452	4283	R41231	Homo sapiens	GAT-2 transporter gene.	477	100
453	4331	gi3171912	Homo sapiens	RAMP2	443	98
454	4340	gi8118223	Homo sapiens	unknown	1330	100
455	4351	gi1754515	Rattus norvegicus	aminopeptidase -B	2050	92
456	4354	Y57906	Homo sapiens	Human transmembrane protein HTPPN-30.	1402	100
457	4385	gi5596433	Homo sapiens	candidate tumor suppressor protein NOC2	509	97

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Access- ion No.	Species	Description	Smith - Water man Score	% Identity
458	4388	W78140	Homo sapiens	Human secreted protein encoded by gene 15 clone HSDES04.	100	94
459	4405	Y48226	Homo sapiens	Human prostate cancer-associated protein 12.	1246	99
460	441	gi29153 6	Bovine herpesvirus 1	BICP4	106	35
461	4417	gi65625 33	Homo sapiens	sialin	939	100
462	4419	gi18415 55	Homo sapiens	NG5	146	33
463	4443	gi49613 9	Mus musculus	AMPA selective glutamate receptor	262	94
464	4470	gi72483 81	Homo sapiens	adaptor protein p130Cas	2592	100
465	4482	gi73299 79	Homo sapiens	apoptosis regulator	2071	100
466	4487	gi67066 59	Homo sapiens		405	100
467	4491	gi98373 41	Homo sapiens	CamKI-like protein kinase	1044	100
468	4492	Y42751	Homo sapiens	Human calcium binding protein 2 (CaBP-2).	586	99
469	4497	gi61797 40	Homo sapiens	paraneoplastic cancer-testis-brain antigen	352	37
470	4502	gi63297 42	Homo sapiens	KIAA1124 protein	327	100
471	4519	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence	1563	100
472	4526	Y08008	Homo sapiens	Human HLIG-1 protein.	4023	99
473	4547	gi45895 62	Homo sapiens	KIAA0959 protein	4165	99
474	4554	gi13810 29	Mus musculus		1164	77

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
475	4555	gi2792366	Homo sapiens	unknown protein IT12	4461	99
476	457	Y70551	Homo sapiens	Human latent transforming growth factor-beta binding protein 3 (I).	1825	100
477	4571	gi5360115	Homo sapiens	NY-REN-45 antigen	869	100
478	4613	Y05868	Homo sapiens	Human Toll protein PRO358.	2413	100
479	4614	Y27129	Homo sapiens	Human bone marrow-derived polypeptide (clone OAF038-Leu).	1815	100
480	4622	G03789	Homo sapiens	Human secreted protein,	173	53
481	4667	gi7673638	Danio rerio	Dedd1	446	48
482	4670	gi402649	Homo sapiens	c-rel	2309	100
483	4683	Y68773	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-5.	2234	99
484	4698	Y73470	Homo sapiens	Human secreted protein clone yd141_1 protein sequence	746	100
485	4724	gi6456846	Homo sapiens	hypothetical protein	1101	99
486	4734	gi3334982	Homo sapiens	R27216_1	1151	80
487	4814	gi6274473	Homo sapiens	pregnancy-induced growth inhibitor	1348	100
488	4819	Y07825	Homo sapiens	Human secreted protein fragment #4 encoded from	117	67

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Access- ion No.	Species	Description	Smith - Water man Score	% Identity
				gene 28.		
489	4821	Y81498	Homo sapiens	Human foetal bone-derived growth factor-like protein.	1200	100
490	4851	gi56894 91	Homo sapiens	KIAA1077 protein	4364	99
491	4872	gi59119 53	Homo sapiens	hypothetical protein	3723	99
492	4902	B08917	Homo sapiens	Human secreted protein sequence encoded by gene 27	717	100
493	5006	gi43577 4	Homo sapiens	receptor tyrosine kinase isoform FLT4 long, FLT41 {C-terminal}	385	100
494	5007	Y93951	Homo sapiens	Amino acid sequence of a Brainiac-5 polypeptide.	804	100
495	5027	gi35487 91	Homo sapiens	R33590_1	1606	100
496	5029	gi56895 27	Homo sapiens	KIAA1095 protein	5722	99
497	5033	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	166	66
498	5040	Y95019	Homo sapiens	Human secreted protein vq1_1,	258	92
499	5061	gi13044 34	Pseudorabies virus	EP0	85	38
500	5081	gi40380 81	Homo sapiens	vascular endothelial cell growth inhibitor	134	100
501	5129	gi31691 58	Homo sapiens	BC269730_2	2340	99
502	5139	gi40628 56	Homo sapiens	HEXIM1 protein	293	47
503	5174	gi93685	Homo sapiens	140up gene	576	90

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		40		product		
504	524	G00329	Homo sapiens	Human secreted protein,	565	100
505	5291	Y92515	Homo sapiens	Human OXRE-12.	1271	98
506	5335	gi72961 58	Drosophila melanogaster	CG3862 gene product	753	46
507	5346	Y94987	Homo sapiens	Human secreted protein vjl_1,	849	100
508	5379	gi71445 06	Homo sapiens	cytokine-inducible SH2-containing protein	1353	99
509	5441	gi80965 51	Homo sapiens	similar to mouse Ehm2	1516	100
510	549	Y22113	Homo sapiens	Human ZSMF-3 protein sequence.	294	62
511	5542	Y76267	Homo sapiens	Fragment of human secreted protein encoded by gene 11.	1066	100
512	5560	G03790	Homo sapiens	Human secreted protein,	103	36
513	5696	gi79203 98	Homo sapiens	PTOV1	1904	91
514	5704	B08930	Homo sapiens	Human secreted protein sequence encoded by gene 2	987	100
515	5758	W18878	Homo sapiens	Human protein kinase C inhibitor, IPKC-1.	368	100
516	5760	gi65621 76	Homo sapiens	hypothetical protein	425	100
517	5763	Y41706	Homo sapiens	Human PRO381 protein sequence.	441	100
518	5787	Y57907	Homo sapiens	Human transmembrane protein HTMPN-31.	952	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
519	5823	gi9800242	rat cytomegalovirus Maastricht	pr5	153	36
520	5886	gi1781037	Mus musculus	neuronal tyrosine threonine phosphatase 1	1135	52
521	5924	W69221	Homo sapiens	Human parotid secretory protein.	710	96
522	5960	Y91529	Homo sapiens	Human secreted protein sequence encoded by gene 79	1300	99
523	5962	W69784	Homo sapiens	Protein Kinase C Inhibitor-like Protein (IPKC-2).	395	100
524	5969	Y79141	Homo sapiens	Human haemopoietic stem cell regulatory protein SCML13.	1205	79
525	5976	gi780310	Homo sapiens	natural killer associated transcript 4	1808	91
526	6002	gi2104553	Homo sapiens		4367	67
527	6008	Y66765	Homo sapiens	Membrane-bound protein PRO1384.	822	100
528	6020	gi1911548	Homo sapiens	cytochrome c-like polypeptide	322	50
529	6036	W71362	Homo sapiens	Human cytokine/steroid receptor protein.	353	51
530	6070	Y42750	Homo sapiens	Human calcium binding protein 1 (CaBP-1).	626	100
531	6075	gi10732648	Homo sapiens	angiopoietin-like protein	2164	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				PP1158		
532	6106	gi2217970	Homo sapiens	p40	1349	96
533	6420	W82000	Homo sapiens	Human adult brain secreted protein dm26_2.	929	100
534	6434	gi10732648	Homo sapiens	angiopoietin-like protein PP1158	2164	100
535	6439	gi189701	Homo sapiens	endothelial cell growth factor	376	100
536	6463	Y41720	Homo sapiens	Human PRO792 protein sequence.	360	82
537	6466	gi4884084	Homo sapiens	hypothetical protein	538	100
538	6508	gi5442030	Homo sapiens	aminopeptidase	2317	96
539	6570	gi5921491	Homo sapiens		1591	99
540	6719	gi31847	Homo sapiens	glypican	1625	87
541	6772	Y65432	Homo sapiens	Human 5' EST related polypeptide	180	53
542	6789	gi537292	Homo sapiens	ICH-1L	1556	100
543	6805	gi4454702	Homo sapiens	HSPC007	634	84
544	6833	gi1890660	Homo sapiens	protein tyrosine phosphatase receptor omicron	5726	87
545	6834	gi5921491	Homo sapiens		1746	88
546	6851	gi2407641	Homo sapiens	neuropilin	3968	98
547	6868	gi6714641	Drosophila melanogaster	MAP kinase phosphatase	218	49
548	6876	Y13138	Homo sapiens	Human secreted protein encoded by 5' EST	414	76
549	688	Y73463	Homo sapiens	Human secreted protein clone	701	98

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				yk199_1 protein sequence		
550	6897	gi5815180	Homo sapiens	unknown	509	97
551	690	gi10645186	Homo sapiens	meningioma-expressed antigen 5s splice variant	522	100
552	6909	W78149	Homo sapiens	Human secreted protein encoded by gene 24 clone HSVBF78.	485	100
553	6924	Y35923	Homo sapiens	Extended human secreted protein sequence,	514	99
554	6937	G03798	Homo sapiens	Human secreted protein,	281	70
555	6951	gi511857	Homo sapiens	prostate-specific antigen	364	95
556	7008	G03200	Homo sapiens	Human secreted protein,	548	98
557	7009	Y22213	Homo sapiens	Human V201 protein sequence.	856	100
558	7057	gi6003654	Homo sapiens	brain specific membrane-anchored protein BSMAP	1814	100
559	7098	W27291	Homo sapiens	Human H1075-1 secreted protein 5' end.	712	100
560	7114	gi3212110	Homo sapiens	prefoldin subunit 1	534	98
561	712	gi4558641	Homo sapiens	P85B_HUMAN; PTDINS-3-KINASE P85-BETA	470	74
562	7215	gi4868366	Homo sapiens	delta-6 fatty acid desaturase	2437	100

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
563	7244	Y12445	Homo sapiens	Human 5' EST secreted protein	428	100
564	7248	gi311376	Homo sapiens	Humig	633	100
565	7252	gi5689531	Homo sapiens	KIAA1097 protein	5240	100
566	7292	gi5106998	Homo sapiens	HSPC040 protein	580	100
567	7306	Y32201	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2057886.	1974	95
568	7338	Y73880	Homo sapiens	Human prostate tumor EST fragment derived protein #67.	1566	100
569	736	gi10178317	Homo sapiens		1468	100
570	737	G00851	Homo sapiens	Human secreted protein,	522	98 .
571	740	W85610	Homo sapiens	Secreted protein clone eh80_1.	1115	87
572	7400	Y93948	Homo sapiens	Amino acid sequence of a lectin ss3939 polypeptide.	1982	98
573	7415	gi3043670	Homo sapiens	KIAA0573 protein	2392	100
574	7429	Y40864	Homo sapiens	A human glutathione-S-transferase (hGST) protein.	1183	99
575	7458	Y53643	Homo sapiens	A bone marrow secreted protein designated BMS6.	554	99
576	7516	gi4468311	Homo sapiens		1146	99
577	7526	gi4138922	Homo sapiens	promyelocytic leukemia zinc finger	3571	99

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				protein; kruppel-like zinc finger protein; PLZF		
578	7571	G02915	Homo sapiens	Human secreted protein,	209	100
579	7614	W74726	Homo sapiens	Human secreted protein fg949_3.	1879	100
580	7663	gi5912548	Homo sapiens		1634	100
581	7686	gi4929711	Homo sapiens	CGI-121 protein	870	100
582	7714	gi388765	Homo sapiens	phospholipase D	4428	99
583	7724	G03933	Homo sapiens	Human secreted protein,	570	100
584	7834	gi8919166	Homo sapiens	mesenchymal stem cell protein DSC92	1133	100
585	7855	Y48505	Homo sapiens	Human breast tumour-associated protein 50.	684	100
586	7870	Y13372	Homo sapiens	Amino acid sequence of protein PRO223.	2559	100
587	7871	Y91689	Homo sapiens	Human secreted protein sequence encoded by gene 93	768	100
588	7892	gi34659	Homo sapiens	macrophage inflammatory protein-2alpha precursor	532	100
589	7927	gi32575	Homo sapiens		183	91
590	7944	gi1657458	Sus scrofa	calcium/calmodulin-dependent protein kinase II isoform gamma-B	2744	100
591	7947	G01131	Homo sapiens	Human	574	96

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Water man Score	% Identity
				secreted protein,		
592	800	gi30214 28	Homo sapiens	neutral sphingomyelina se	167	68
593	8055	gi49296 37	Homo sapiens	CGI-84 protein	1038	100
594	8082	gi46790 14	Homo sapiens	HSPC014	715	100
595	8127	gi99556 93	Homo sapiens	twisted gastrulation protein	905	95
596	8174	gi55322 94	Homo sapiens	MUM2	767	100
597	8178	gi45305 87	Homo sapiens	TADA1 protein	1132	100
598	8215	R66278	Homo sapiens	Therapeutic polypeptide from glioblastoma cell line.	830	100
599	8263	Y48371	Homo sapiens	Human prostate cancer- associated protein 68.	713	98
600	827	gi31723 37	Cavia porcellus	phospholipase B	955	73
601	828	Y29517	Homo sapiens	Human lung tumour protein SAL-82 predicted amino acid sequence.	833	94
602	8294	gi49297 67	Homo sapiens	CGI-149 protein	1085	100
603	8313	gi57714 20	Homo sapiens	group IID secretory phospholipase A2	852	100
604	832	Y86260	Homo sapiens	Human secreted protein HELHN47,	319	78
605	8357	gi41913 58	Mus musculus	claudin-7	164	47
606	8373	gi19452 71	Homo sapiens	protein phosphatase 6	1666	100
607	8379	gi58529	Homo sapiens		1226	100

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		81		cardiotrophin-like cytokine CLC		
608	8380	gi3402216	Homo sapiens	protein	974	100
609	8386	gi386988	Homo sapiens	oncostatin M	1297	99
610	8418	Y70210	Homo sapiens	Human TANGO 130 protein.	722	98
611	8442	G01895	Homo sapiens	Human secreted protein,	490	95
612	8457	G04048	Homo sapiens	Human secreted protein,	450	98
613	8458	W97119	Homo sapiens	S-adenosyl-L-methyltransferase (SAM-MT) protein.	1484	100
614	8469	gi7159799	Homo sapiens		255	100
615	8480	gi4589530	Homo sapiens	KIAA0943 protein	1998	100
616	8521	gi5726235	multiple sclerosis associated retrovirus element	unknown protein U5/2	250	82
617	857	gi9663958	Homo sapiens	cysteinyl leukotriene CysLT2 receptor	612	99
618	8574	gi6841260	Homo sapiens	HSPC305	1049	100
619	8606	gi3367707	Homo sapiens	scrapie responsive protein 1	544	100
620	8632	G01158	Homo sapiens	Human secreted protein,	502	100
621	8646	gi3882249	Homo sapiens	KIAA0764 protein	2175	100
622	8666	Y66196	Homo sapiens	Human bladder tumour EST encoded protein 54.	1080	95
623	8675	gi9963908	Homo sapiens	NPD009	432	96
624	8683	G04018	Homo sapiens	Human	469	98

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				secreted protein,		
625	8708	gi1633564	Homo sapiens	C8	364	98
626	8720	gi8248465	Homo sapiens	hepatocellular carcinoma-associated antigen 56A	191	69
627	8756	Y94984	Homo sapiens	Human secreted protein vell_1,	369	97
628	8765	Y00346	Homo sapiens	Fragment of human secreted protein encoded by gene 2.	1068	97
629	8783	Y27918	Homo sapiens	Human secreted protein encoded by gene No. 123.	1051	95
630	8804	Y25426	Homo sapiens	Human SIGIRR protein.	887	100
631	8838	Y99409	Homo sapiens	Human PRO1343 (UNQ698) amino acid sequence	1279	100
632	8851	W74785	Homo sapiens	Human secreted protein encoded by gene 56 clone HSAXS65.	454	100
633	8853	W75116	Homo sapiens	Human secreted protein encoded by gene 60 clone HILCJ01.	245	95
634	8857	gi2565196	Homo sapiens	non-functional folate binding protein	479	74
635	8859	Y02690	Homo sapiens	Human secreted protein encoded by gene 41c lone	600	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				HSZAF47.		
636	8901	Y86491	Homo sapiens	Human gene 59-encoded protein fragment,	548	99
637	8907	W88745	Homo sapiens	Secreted protein encoded by gene 30 clone HTSEV09.	2004	99
638	8934	W75088	Homo sapiens	Human secreted protein encoded by gene 32 clone HAGBB70.	421	98
639	8960	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	267	72
640	8979	Y76143	Homo sapiens	Human secreted protein encoded by gene 20.	1374	98
641	8980	Y11433	Homo sapiens	Human 5' EST secreted protein	466	100
642	8986	G02626	Homo sapiens	Human secreted protein,	306	100
643	8987	G02093	Homo sapiens	Human secreted protein,	486	97
644	8995	Y12908	Homo sapiens	Human 5' EST secreted protein	181	100
645	9035	Y71108	Homo sapiens	Human Hydrolase protein-6 (HYDRL-6).	800	100
646	9062	gi8886005	Homo sapiens	lysophosphatidic acid acyltransferase-delta	523	100
647	9074	Y25761	Homo sapiens	Human	1366	99

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				secreted protein encoded from gene 51.		
648	9075	Y73336	Homo sapiens	HTRM clone 1852290 protein sequence.	1591	100
649	9098	Y57878	Homo sapiens	Human transmembrane protein HTPMPN-2.	516	100
650	9109	gi23903	Homo sapiens	63kDa protein kinase	1141	97
651	911	gi32456	Homo sapiens	protein-tyrosine phosphatase	2591	100
652	912	gi1136743	Homo sapiens	human P5	212	46
653	9163	Y34129	Homo sapiens	Human potassium channel K+Hnov28.	377	71
654	9164	Y41324	Homo sapiens	Human secreted protein encoded by gene 17 clone HNF1Y77.	1083	99
655	9173	gi6851256	Mus musculus	protein tyrosine phosphatase-like protein PTPLB	631	93
656	9187	Y66721	Homo sapiens	Membrane-bound protein PRO511.	1173	95
657	9190	W40378	Homo sapiens	Human breast cancer protein CH14-2a16-1 from 2.0 kB DNA fragment #2.	792	81
658	9194	Y02781	Homo sapiens	Human secreted protein.	462	70
659	9210	G02994	Homo sapiens	Human secreted protein,	166	80

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
660	9222	G02520	Homo sapiens	Human secreted protein,	186	43
661	9230	gi6706554	Homo sapiens	inositol 1,4,5-trisphosphate 3-kinase B	1315	95
662	9258	gi522145	Homo sapiens	B-cell growth factor	120	56
663	9260	G04072	Homo sapiens	Human secreted protein,	138	51
664	9271	gi6690095	Homo sapiens	tetraspanin protein	317	67
665	9272	gi163042	Bos taurus	factor activating exoenzyme S	444	72
666	9275	gi401774	Homo sapiens	ribosomal protein S6 kinase 3	424	81
667	930	G02355	Homo sapiens	Human secreted protein,	167	41
668	9304	gi8979743	Canis familiaris	Band4.1-like5 protein	1493	93
669	9346	gi2738989	Mus musculus	high mobility group protein homolog HMG4	384	89
670	9347	gi36613	Homo sapiens	serine/threonine protein kinase	199	91
671	935	gi5541870	Homo sapiens	QA79 membrane protein, allelic variant airm-1b	334	57
672	9350	gi3327124	Homo sapiens	KIAA0655 protein	757	87
673	9351	W57260	Homo sapiens	Human semaphorin Y.	573	95
674	9356	gi59977	Human endogenous retrovirus	tripartite fusion transcript PLA2L	127	59
675	9363	Y17834	Homo sapiens	Human PRO361 protein sequence.	968	92
676	9366	gi72431	Homo sapiens	KIAA1374	649	96

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		29		protein		
677	9369	G03793	Homo sapiens	Human secreted protein,	222	69
678	9378	gi4468311	Homo sapiens		163	39
679	9393	gi2738989	Mus musculus	high mobility group protein, homolog HMG4	384	89
680	9444	G01399	Homo sapiens	Human secreted protein,	157	93
681	9467	gi4454702	Homo sapiens	HSPC007	230	71
682	9486	gi10047243	Homo sapiens	KIAA1584 protein	605	93
683	949	Y30895	Homo sapiens	Human secreted protein fragment encoded from gene 25.	704	99
684	9499	W36002	Homo sapiens	Human Fchd531 gene product.	2173	96
685	9510	gi1665799	Homo sapiens		867	83
686	9523	Y53022	Homo sapiens	Human secreted protein clone qf116_2 protein sequence	1252	89
687	9534	Y66670	Homo sapiens	Membrane-bound protein PRO1180.	998	100
688	9539	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	633	100
689	954	G02490	Homo sapiens	Human secreted protein,	160	78
690	9546	gi181121	Homo sapiens	chorionic somatomammotropin	616	96
691	955	gi7243103	Homo sapiens	KIAA1361 protein	2042	100
692	9551	gi17723	Homo sapiens	ras-related	341	57

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		45		GTP-binding protein		
693	9558	W88403	Homo sapiens	Human adult testis secreted protein ga63_6.	2252	100
694	9561	gi6690017	Herpesvirus papio	NTR	100	30
695	957	Y86260	Homo sapiens	Human secreted protein HELHN47,	319	78
696	9572	gi972940	Mus musculus	Elf-1	806	92
697	9576	gi3249005	Homo sapiens	geminin	448	98
698	9586	gi2887288	Homo sapiens	mRNA cleavage factor I 25 kDa subunit	208	100
699	9587	G00995	Homo sapiens	Human secreted protein,	726	99
700	9592	gi495273	Rattus norvegicus	ribosomal protein S15a	202	78
701	9595	gi7799912	Homo sapiens	UBASH3A protein	453	47
702	9610	Y07875	Homo sapiens	Human secreted protein fragment encoded from gene 24.	574	100
703	9634	Y73325	Homo sapiens	HTRM clone 001106 protein sequence.	820	99
704	9639	G00805	Homo sapiens	Human secreted protein,	155	67
705	9647	G03786	Homo sapiens	Human secreted protein,	196	73
706	9653	gi3882341	Homo sapiens	KIAA0810 protein	523	100
707	9654	G01924	Homo sapiens	Human secreted protein,	469	100
708	9678	Y99376	Homo sapiens	Human PRO1244 (UNQ628) amino	474	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				acid sequence		
709	9709	Y11825	Homo sapiens	Human 5' EST secreted protein	657	100
710	9722	gi7677422	Mus musculus	GTPase Rab37	189	75
711	9731	Y12424	Homo sapiens	Human 5' EST secreted protein	207	100
712	9742	Y57954	Homo sapiens	Human transmembrane protein HTPMPN-78.	484	100
713	9749	gi3687829	Homo sapiens	hT41	386	65
714	9755	gi2055295	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	2583	100
715	9762	G03436	Homo sapiens	Human secreted protein,	176	61
716	9763	gi6180011	Homo sapiens	anaphase-promoting complex subunit 4	1016	100
717	9784	G03570	Homo sapiens	Human secreted protein,	401	96
718	9794	G00803	Homo sapiens	Human secreted protein,	333	69
719	9795	gi2516242	Mus musculus	Rab33B	669	94
720	9798	gi558599	Homo sapiens	ZID, zinc finger protein with interaction domain	605	96
721	9805	Y25881	Homo sapiens	Human secreted protein fragment encoded from gene 61.	566	96
722	9816	gi532056	Homo sapiens	protein-tyrosine-phosphatase	384	100
723	9830	G00857	Homo sapiens	Human	539	96

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				secreted protein,		
724	9836	G00914	Homo sapiens	Human secreted protein,	527	100
725	9837	gi2662099	Homo sapiens	KIAA0409	230	67
726	984	Y29517	Homo sapiens	Human lung tumour protein SAL-82 predicted amino acid sequence.	833	94
727	9849	gi7229305	Homo sapiens	ZNF264, partial cds	140	90
728	9851	gi5262560	Homo sapiens	hypothetical protein	369	64
729	9859	gi3881976	Homo sapiens	hypothetical protein	167	93
730	9863	gi7295707	Drosophila melanogaster	CG15433 gene product	837	78
731	9888	gi3319677	Homo sapiens		209	72
732	989	gi4557143	Rattus norvegicus	zinc finger protein RIN ZF	604	92
733	9919	G01843	Homo sapiens	Human secreted protein,	586	100
734	9922	W67869	Homo sapiens	Human secreted protein encoded by gene 63 clone HHGDB72.	551	93
735	9947	W78239	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	251	78
736	9956	Y36203	Homo sapiens	Human secreted protein #75.	273	77
737	9961	Y99357	Homo sapiens	Human PRO1190 (UNQ604) amino acid sequence	650	99
738	9972	Y12149	Homo sapiens	Human 5' EST secreted protein	284	100
739	9977	gi10039	Homo sapiens	osteoblast	822	98

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		439		differentiation promoting factor		

Table 3 - Amino Acids

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1	740	2	557	FVGRLLRLGELRLRPDPSSGGCRLQPALVGETEMSEKENNFPP LPKFI PVKPCFYQNFSDIPEVHQVLVKRIYRLWMFYCATLGV NLIACLAWWIGGGSGTNFGLAFVWLLLFTPCGYVCWFRPVYKA FRADSSFNMAFFFI FRSPVCPDRHPGDWLLRLGRVRLAVGNW ILPVQPGRCRGHA
2	741	305	838	FLGAGADIFCAYLRMSSKQATSPFACAADGEDAMTQDLTSREK EEGSDQHVASHLP LHPIMHNKPHSEELPTLVSTIQDADWDSDV LSSQQRMESENKLC SLYSFRNTSTSPHKPDEGSRDREIMTSV TFGTPERRKGS LADVDTLKQKKLEEMTRTEQEDSSCMEKLLS KDWKE
3	742	12	1315	EGYLTGRPTRPVAVRGKSTADLRMMGRSPGFAMQHI VGVPHVL VRRGLLGRDLFMTRTLCSPGPSQPGKEKRPEEVALGLHRLPAL GRALGHSIQQRATSTAKTWWDRYEEFVGLNEVREAQGVTEAE KVFMVARGLVREAREDLVHQAKLKEVRDRLDVRSREDSQYLE LATLEHRMLQEEKRLRTAYLRAEDSEREKFSLFSAAVRESHEK ERTRAERTKNWSLIGSVLGALIGVAGSTYVNRVRLQELKALLL EAQKGPVSLQEAIREQASSYSRQQRDLHNLMDLRLGLVHAAGP GQDSGSQAGSPPTRDRDVLVLSAALKEQLSHSRQVHSCLEGLR EQLDGLEKTCSQMAGVVQLVKSAHPGLVEPADGAMP SFLL EQ GSMILALSDTEQRLEAQVNRNTIYSTLVTCVTFVATLPVLYML FKAS
4	743	112	745	NLPPLTPQPGPRLAGSGPSHWFSPLSLPVASKAPGTMAQALGE DLVQPPELQDDSSSLGSDSELSPGPYRQADRYGFIGGSSAEP GPGHPPADLIRQEMKWVEMTSHWEKTMSRRYKKVKMQCRKGI PSALRARCWPLLCGAHVCQKNSPGTYQELAEAPGDPQWMETIG RDLHRQFPLHEMFVSPQGHGQQGLLQVLKAYTLRPEQG
5	744	99	265	LRGMAAAAAGPAASQRFFQSFS DALIDQDPQAALVGEFFLLP PLPADPPPSSTA

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6	745	210	758	WACFRSAHCSRHLNRNRI FMYLYWDKTRSPVCKGPALREERPQP RLKLEDYKDR LKSGEHLNPDQLEAVEKEYEEVLHNLEFAKELQK TFSGLSLDLLKAQKKAQRREHMLKLEAEKKLRITLQVQYVLQ NLTOEHVQKDFKGGGLNGAVYLP SKELDYLIKFSKLTCPERNES LRQTLEGSTV
7	746	48	450	XAGVQMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLD CFVI DNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYD YQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELVLFLEW SVWGSX*
8	747	1	469	CRGRLAQLEEA AAVATMSAGDAVCTGWL VKSPPERKLQRYAWR KRWFVLRGRMSGNPDVLEYR NKHSSKPIRVIDLSECAVWKH VGPSFVRKEFQNNFVFIVKTTSRTFYLVAKTEQEMQVWHSIS QVCNLGHLEDGAADSMESLSYTRSYLQ
9	748	242	409	IPAVPLTSCVTGVSYSLSVRDYPDPRQGD TVKH YKIRTL\DKRG FYISP\ RSTFSTLQ
10	749	1	1146	KDSVLN IARGKKYGEKTKRVSSRKKPALKC/TSQKQPALKATC DKEDSVNPTATEKKDEQISGTVSSQKQPALKATSDKKDSVSN I PTEIKDGQQSGTVSSQKQPAWKATSVKKDSVSN IATEIKDGQI \RGTVSSQRQPALKA\TGDEKDSVSN IAREIKDGEKSGTVSPQ KQSAQKVI FKKKVSLLNIATRITGGWKS GTEYPENLPTLKATI ENKNSVLNTATKMKDVQTSTPEQDLEMASEGEQKRLEEYENNQ POVKNQIHSRDDDDIIQSSQTVSEDDSLCCNCKNVILLIDQ HEMKCKDCVHLLKIKKTFCLCKRLTELKDNHCEQLRVKIRKLK NKASVLQKRLSEKEEIKSQLKHETLELEKELCSLRFAIQQ
11	750	3	892	SPLRYRAGQSGSTISSSSCAMWRCGGRQGLCVLRRLSGGHAHH RAWRWSNRACERALQYKLGDKIHGFTVNQVTSVPELFLTAVK LTHDDTGARYLHLAREDTNNLF SVQFRTTPMDSTGVPHILEHT VLCGSQKYPCRDPFFKMLNRSLS TFMNAFTASDYTLYPFSTQN PKDFQNL LSVYLDATFFPCLRELD FWQEGWRLEHENPSDPQTP LVFKGVVFNEMKGAFTDNERIFSQHLQNRLLPDHTYSVVS GGD PLCIPELTWEQLKQFHATHYHPSNARFFTYGNFPLDQH
12	751	367	856	RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPGTEATRPTAM SKSLKKKSHWTSKVHESVIGRNPEGQLGFELKGAENGQFPYL GEVKPGKVAYESGSKLVSEELLLEVNETPVAGLTIRDVLAVIK HCKDPLRLKCVKQGESSGLLSVLPGGGTARGAQ
13	752	144	442	SHRPQPDARWQGNAFQCVQKEKMQVSSAEVRIGPMRLTQDP IQ VLLIFAKEDSQSDGFWWACDRAGYRCNIARTPESALECF LDKH HEIIVIDHRQTQN
14	753	1	581	FRLAGCGHLLVSLGLL LLLARS GTRALVCLPCDESKCEEPRN CPGSI VQVCGCCYTCASQRNESCGGTFGIYGTCDRGLRCVIR PPLNGDSLTEYEAGVCE DENWTDQLLGFKPCNENLIAGCNII NGKCECNTIRTCSNPFEPFSDMCL SALKRIEEKPD CSKARC EVQFSRCPEDSVLIEGYAPP

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15	754	1	219	FRMAANVGSMFQYWKRFDLQQLQRELDATATVLANRQDESEQS RKRLIEQSREFKKNTPEVRRVTIVFALKGS
16	755	313	562	ETLSCRIMDHPSREKDERQRTTKPMAQRSAHCSRPSGSSSSSG VLMVGNFRVGGKIGCGNFGELRLGEGLPQVYFPGCGKY
17	756	273	574	GCCKD*HSGVIGRSWAMLFASGGFQVKLYDIEQQQIRNALENI RWASRRSPEGMEVGLFLSVGLVCHILKAMRICDVTFSDDGYCS ASELVKARPTVAGM
18	757	3	390	NSRVDDFVSARPKPRPLPRARGMVVVTGREPDSRRQDGAMSSS DAEDDFLEPATPTATQAGHAL/PPAAT/GSFLRLFPLTSEGLT SLHACPHCGATKTPCWQPCSVGGTTSPTTPRAGTSSTEMAHTL EMC
19	758	98	461	RALWVGCSGEACGIGMSGLLTDPEQRAQEPYPGFVLGLDVG SSVIRCHVYDRAARVCGSSVQKVENLYPQIGWVEIDPDVLWQ FVAVIKEAVKAAGIQMNQIVGLGISTQRATFITWN
20	759	100	731	GLAAEQSMQFVKLWCGCSGEFFTRLRRRTPLTEAMEGGPAVCC QDPRAELVERVAIDVTHLEEADGGPEPTRNGVDPPPRARAAS VIPGSTSRLLPARPSLSARKLSLQERPAGSYLEAQAGPYATGP ASHISPAWRRPTIESHHVAISDAEDCVQLNQYKLQSEIGKGA YGVVRLAYNESEDRHYAMKVLSSKKLLKQYGFPRRPPP
21	760	2	520	FVYGKPVTLWPTISSVVPSTFLGLGNYEVEVEAEPDVRGPEIV TMGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILS LLPLKFFPIIVIGIIALILALAIGLGIHFDCSGKYRCRSSFKC IELIARCDGVSDCKDGEDEYRCVRVGGQNAALQVFTAASRKT M
22	761	158	470	SLAMPFGCVTLGDKKNYNQPSSEVTDRLGQVIKTEEFCEIFR AKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIGILKMVKHPNIL QLVDVFVTRKEYFIFLEL
23	762	1	749	QRRRFRAGLWGGHGLTDGLRRNCGCGCSARVPRVGERLRGHR PDPLCLLLDMLFLSFHAGSWESWCCCCCLIPADRPWDRGQHWQ EMADTRSVHETRFEEAAVKVIQSLPKNGSFQPTNEMMLKFYSFY KQATEGPCKLSRPGFWDPIGRYKWDWSSSLGDMTKEEAMIAYV EEMKKIETMPMTEKVEELLRVIGPFYEIVEDKKSGRSSDITS DLGNVLTSTPNAKTVNGKAESSDSGAESSEEEAAC
24	763	3	558	SCFKGRTGGRSGSSGDSRRWARCGRHFSASTEPPPLSQPCSA LPRSGRRGCAVPSSVTKMLSFFRRTLGRSSMRKHAEKERLREAQ RAATHIPAAGDSKSIITCRVSLLDGTDVSDVLPKKAKGQELFD QIMYHLDLIESDYFGLRFMDSAQVAHWLDGTSIKKQVKIGSP YCLHLRVKFYSS
25	764	9	424	ESRERSGNRRGAEDRGTCGLQSPSAMLGAKPHWLPGLHSPGL PLVLVLLALGAGWAQEGSEPVLLGECLVVCEPGRAAAGGPGG AALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVN EGGGFDRAS

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26	765	2	507	EDVKSYYTVHLPQLENINSGETRTISHFHYTTWPDFGVPOSPA SFLNFLFKVRESGSLNPDHGPVVIHRSAGTGRSSTFSVVHTCL VLMEKGDDINIKQVLLNIRKFQMGIL\QTPDQLRFSYMAITEG AKCVKGDSSIQRWKELSKE/DLPPAFDHSPNKIMTEKYNR
27	766	84	852	LNRQRCGDQVLVPGTGLAAILRLTLPMPHDEEHARAGLS EDTL VLPPASRNQRILYTVLECQPLFDSSDMTIAEWVCLAQTIKRHY EQYHGFVVIHGTDMAFAASMLSFMLENLQKTVILTGAQVPIH ALWSDGRENLLGALLMAGQYVIEVCLFFQNLFRGNRATKVD ARRFAAFCSNLLPLATVGADITINRELVRKVDGKAGLVVHSS MEQDVGLLRLYPGIPAAALVRAFLQPPILKGVVMTFTGSGNG
28	767	992	210	LFRLAPGFLRSLARQGYHQIWAFFPLPSGATATWPAASRSRSL AARSLPRSPARPGPNDALLGEHDFRGQGVRAQRFRFSEEPGPG ADGAVLEVHPQIGAGVSLPGILAAKCGAEVILSDSSELPHCL EVCROSCQMNNLPHLQVVGLTWGHI SWDLLALPPQDI ILASDV FFEPEDFEDILATIYFLMHKNPKVQLWSTYQVRSADWSLEALL YKWD MKCVHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKD SL
29	768	23	624	SFIYKHTHRARFGPRAIVASPALTAGPHVSLTASCRVGMWVSC SPSPFLHPTNTLVAVLERDTLGIREVRLFNNAVVRWSEAEQORQ QLQVTPENRRKVLGKALGLIRFPLMTIEEFAAGNRARAQGLVW EGSGTQVGIW/CTEDSAPEFTAESLADAWHIQIGRN LACEDAS T/WAIC*PRPGSVPTVHTARPRLSCLSSCF
30	769	100	2	MASTQDAELAVSRXRAIALXPGXQSQXXPSQKKK
31	770	158	1957	LLKSCGVLLSGVCIPCEGKGPTVLVIQTAVPQDRPTKSSMRSA AKPWNPAIRAGGHGPDVRPLPAASSGMKSSKSSSTSLAFESRL SRLKRASSED TLNKP GSTAASGVVRLKKTATAGAI SELTESRL RSGTGAF TTTKRTGIPAPREFSVTVSRERSVPRGPSNPRKSVS SPTSSNTPTPTKHLRTPSTKPKQENEGGEK\VR LSPK/FRELL AEAKADSEINRLRSELK KYKEKRTLNAEGTDALGPNVDGTSV SPGDTEPMIRALEEKKNFQKELSDLEENRVLKEKLIYLEHS PNSEGAASHTGDSSCPTSITQESSFGSPTGNQLSSDIDEYKKN IHGNALRTSGSSSSDVTKASLSPDASDFEHITAETPSRPLSST SNPFKSSK CSTAGSSPNSVSEL SLASLTEKIQKMEENHSTAE ELQATLQELSDQQQMVQELTAENEKLVDEK TIL ETSFHQHRER AEQLSQENEKLMNLLQERVKNEEPTTQEGKIIIELEQKCTGILE QGRFEREKL LNIQQQLTCSLRKVEEENQGALEM IKRLKEENEK LNEFLELERHNNNMMAKTLEE CRVTLEGLKMENGSLKSHLQG
32	771	203	514	SQMHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRD ESNHLTDLYRDET IQVKGNGYVQSPRFPNSYPRNLLL TWRLLH SQENTRIQLVFDNQFGL

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33	772	59	713	PFKKMTDLLRSVVTVIDVFYKYTKQDGECSGLSKGELKELLEK ELHPVLKKNPDDPDVIMHMLDRDHRRDLDFTEFLLMIFKLT MACNKVLSKEYCKASGSKKHRRGHRHQEESETEDEEDTPGH KSGYRHSSWSEGEHGYSSGHSRGTVKCRHGSNSRRLGRQGNL SSSGNQEGSQKRYHRSSCGHSWSGGKDRHGSSSVELRERINKS HIK
34	773	209	601	VPKISGPDHIDFIPWDQLFMASSSSVTEFLVLGFSSSLGELQLV LFAVFLCLYLIILSGNIIIIISVIHLDSLHTPMYFFLGILSIS EIFYTTVILPKMLINLFSVVRTLSFVSCATQMFYEIVGPGTQE R
35	774	373	987	DHSTETPGIPAAEPVSHGTGKLERAPTLPGAELPAPAAVPCP TL*VC/LYPQLLGLSVATMTLTLYFGAHFAVIRRASLEKNPYQ AVHQWGTQORLIQHPESGSEGQSLLGPLRAFSAGLSLVGLLT L GAVLSAAATVREAQGLMAGGFLCFSLAFCAQVQVFWRLHSP T QVEDAMLDTYDLVYEQAMKGTSHVRRQELAAIQ
36	775	102	466	QPGYSEYDKNRGQGMMLNMMCGRQLSAISLCLAVTFAPLFNAQ ADEPEVIPGDSPPVAVSEQGEALPQAQATAIMAGIQPLPEGAAE KARTQIESQLPAGYKPVYLNQLQLLYAARGISCSV
37	776	2	430	RTRAADVVFSLTGKSRNVSSSTVRRSAVGGMSALALFDLLKP NYALATQVEFTDPEIVAETITPSPNGHGEVRGYLVKPAKMSG KTPAVVVHENRGLNPYIEDVARRVAKAGYIALAPDGLSSVGG YPGNDIKVVSAAA
38	777	106	556	VKQRHGNSLLTTETKICISRLGVPLSPQRRFQAIRIEEVKLW FAFILVLLAGCSSKHDTYNPPWNAKVPVQRAMQWMPISQKAGA AWGVDPQLITAI I AIESGGNPNVAVSKSNAIGLMQLKASTSGRD VYRRMGWSGEPTTSELKNSSR
39	778	3	892	HAAGIRHEAKPKRSFYAARDLYKYRHQYPNFKDIRYQNDLSNL RFYKNIKIPFKPDGVYIEEVL SKWKGDYEKLEHNHTYIQWLFPL REQGLNFYAKELTTYEIEEFKKTKEAIRRFLAYKMMLEFFGI KLTDKTGNVARAVNWQERFQHLNESQHNYLRITRILKSLGELG YESFKSPLVKFILHEALVENTIPNIKQSALEYFVYTIRDRER RKLLRFAQKHYPSENF IWGPPRKEQSEGSKAQKMSSPLASSH NSQTSMHKKAKDSKNSSSAVHLNSKTAEDKKVAPKEPV
40	779	123	395	ELQVFQPIGGMSDSGSQLGSMGSLTMKSQLOITVISAKLKENK KNWFGSPYPVEVTVDGQSKKTEKCNNTNSPKWKQPLTIVITPV SKLH
41	780	173	438	IETLSFVIRNWNTHAMSKPIVMERGKRYRDADKMALIPVKNVA TEREALLRKPEWMKIKLPADSTRIQGIKAAMRKNGLHSVCEE A SC
42	781	287	393	PRMVLGKPQTDPTLEWFLSHCHIHKYPSTLIPQ
43	782	119	556	GLRISVQERIKACFTESIQTQIAAAEALPDAISRAAMTLVQSL LNGNKILCCGNGTSAANAQHFASMINRFETERPSPALALNT DNVVLTAIANDRLHDEVYAKQVRALGHAGDVLLAISTRGNSRD IVKAVEAAVTRDITIV

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44	783	248	554	KQTQHAPGMMKKYLALALIAPLLISCSTTKKGDYNEAWVKDT NGFDIILMGQFAHNIENIWGFKEVVIAGPKDYVKYTDQYQTRSH INFDDGTITIEPIPGT
45	784	77	311	TDRTALNPGQESAMNRLFSGRSDMPFALLLLAPSLLLLGLLVA WPMVSNIEISFLRLPLNPNIESTFVGVSNYVRILS
46	785	184	627	KELVDEKSERGRAMDPVSQLASAGTFRVLKEPLAFRLALELLF AIFAFATCGGYSGGLRLSVDVCVNKTESNLSIDIAFAYPFRHLQ VTFEVPTECGKERQKLALIGDSSSSAEFFVTVAFAFLYSLAA TGRYIFFHNKNRENNGPL
47	786	3	742	LGTVSYGADTMDEIQSHVRDSYSQMQSQAGGNNTGSTPLRKAQ SSAPKVRKSVSSRIHEAVKAIIVLCHNVTPVYESRAGVTEETEF AEADQDFSDENRTYQASSPDEVALVQWTESVGLTLVSRDLTSM QLKTPSGQVLSFCILQLFPFTSESKRMGVIVRDESTAETTFYM KGADVAMSPIVQYNDWLEEECGNMAREGLRTLTVAKKALTEEQ YQDFEVSRLPGIPSSYDGAFLTLLKLVLPVVF
48	787	864	335	EGPHR\RLFQMVKA/LQEAPEDPNQILIGYSRGLVVIWDLQGS RVLYHFLSSQQLENIWWQDGRLLVSDGSGSYCQW\ PVSSEA QQPEPLRSLVPYGPFPCKAITRILWLTTTQGLPFTTFQGGMPR ASYGDRHCISVIHDGQQTAFTDFTSRVIGFTVLTEADPAASRRR SGVGAQG
49	788	410	951	KQGLEVRDLHFKEITSGRALLRVACKRPSMVPGGQLQRAGAGA QARITGLSPALWGARVHGWIPELPAGLPAGACLWPLIPACPSR HWGWVSAPVKG/WAQAILGLALCL/RGEHRGLGAGVSKVRSLK MDRKVWTETLIEVGMPLLATDTWGLPHSTAVVWSQPPPYLSDH STLELERDPL
50	789	1	437	LSCNSEQALLSLVPVQRELLRRRYQSSPAKPDSSFYKGLGTCF SQLRLSEPPPTPRHLSVASVSHHMFPSHRSLCPHLPDFFAAPF PSDNLPTLQSPFPSPPPATPSDHALILHH\DLNGGPDDPLQQ TGQLFGGLVRDIRRRYP
51	790	1	198	SPSSKLVGMWWAGRAGSSRTTSVSLCLP/SAPFGASNLLVNP LEPQNADKIKIKIADLGNACWVV
52	791	3	435	RVDPRVRAPRCGDKIKNHMY\KDCGSLKDCASDRCCETSCTL SLGSVCNTGLCCHKCKYAAPGVVCRDLGGICDLPEYCDGKKEE CPNDIYIQDGTPCSASVVCIRGNCSDRDMQCQALFGYQVKDGS PACYRKLNRIGNRFGT
53	792	1	728	PGRPTRPDASLAQ/DPRTTMFRIPEFKWSPMHQRLLTDLLFAL ETDVHVWRS\HSTKSVMDVFNSENENIIFVHNTIHLISQVMDNI IIACGGILPLLSAATSPTGSKTELENIEVTQGMSAETAVTFLS RLMAMVDVLVFASSLNFSEIEAEKNMSSGGLMRQCLKLVCCEVA VRNCLECRQRQDRGNKSSHGSSKQEVQSVTATAASKTPLE NVPGNLSPIKDPDRLLQDVIDNRLRAVVF

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54	793	2230	990	NSSGVKLLQALGLSPGNGKDHSILHSRNDLEEAFIHFMGKGAA AERFFSDKETFDHIAQVASEFPGAQHYVGGNAALIGQKFAANS DLKVLCCGPVGPKLHELDDNVFVPPELQEVDEFHLILEYQA GEEWGQLKAPHANRFIFSHDLSNGAMNMLEVFVSSLEEFQPD LGGSLGLHMMEGQSKELQKRKRLLEVVTISDIPTGIPV\HLELG \SMTNRELMSSIV\LOQVFPVAVTSLGLNEQELLEFLTQSASGPH SSLSSWNGVDPDGMVSDILFWILKEHGRSKSRASDLTRIHFHT LVYHILATVDGHWANQLAAVAAGARVAGTQACATETIDTSRVS LRAPQEFMTSHSEAGSRIVLNPKNPVVEWHREGISFHFTPVLV CKDPVRTVGLGDAISAEGLFYSEVHPHY
55	794	249	3	DDSSGWGLEQLVVRWSLALWPRLECSGMISAHCNLC/LGSSD SPASAPRVAGITDVCHHAWLVFVFLVVMGFPVGHVGLLELL
56	795	2	1176	LGEVLKCCQGVSSLAFALAFQRMMDKPLVVLGLPAPTAPSGC LSFWEAKAQLAKSCKVLVDALRHNAAAVPPFGGGSVLRAAEP APHASYGGIVSVETDLLQWCLESGSIPILCPIGETAARRSVLL DSLEVTASLAKALRPTKIIFLNNTGGLRDSHKLVSNNLPAD LDLVCNAEWVSTKERQQMRLIVDVLSRLPHHSSAVITAASTLL TELFSSNKGSGTLFKNAERMLRVRSLDKLDQGRVLDLVNASFGK KLRDDYLASLRPLHSIYVSEGYNAAAILTMEPVLGCTPYLDK FVVSRRQGGSGQMLWECLRRDLQTLFWRSRVTNPINPWYFK HSDGSFSNKQWIFFWGLADIRDSYELVNHAKGLPDSFHKPAS DPGS
57	796	755	374	YHAPALQPGQSKTLSQEKKNFFRPGAVAHTCNPSTLGGRGGR ITRSGDRDHPG*HGETPSLLKIQKKLAGRDGGRL*SQLLGRIR QENGVPNGGGGCSEPLRHCTPAW*QSETISRKKRKKERKY
58	797	2	476	FRPIGIIQALCSADGHQRRILTLRLGLLVIPFLPASNLFFRV GFVVPVSGCCVMLLFGFG/ALRKHTEKKLIAAVVLGILLS/N DAERLRCAVRGGGEWRSE/EAVFRGAVSVCPLSAEVRNIGRNL AAKGNQTGAIRYHREAVSLNPKTKSSTREFRPC
59	798	3	711	KIADFGFSNLTTPGQLLKTWCGSPPYAAPELFEGKEYDGPVKD IWSLGVLYVLVCGALPFDGSTLQNLRARVLSGKFRIPFFMST ECEHLIRHMLVLDPNKRLSMEQICKHKWMKLGADPNFDRLIA ECQQLKEERQVDPLNEDVLLAMEDMGLDKEQTLQSLRSDAYDH YSAIYSLLCDRHKRHKTLLRGLALPSMPRALGLSSTSQYP\AEQ AGTAMNISVPQVQLINPENQIV
60	799	2	344	AREFLGHRASITWS*ARVHHRFPKAEVA*P/SLLRDTLTDRT KCCHGDLLECADDRADLVEDIWENQDSISTILIECCEKPILEK SHCIAEVENDEMPADLPSLAADFVESKDV

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61	800	142	594	VPPKMKRGTSLSHRRGKPEAPKGSPPQINRKSGQEMTAVMQSGR PRSSSTTDAPTGSAMMEIACAAAAAAACLPGEEGTAERIERL EVSSLAQTSSAVASSTDGSIHTDSVDGTPDPQRTKAAIAHLQQ KILKLTEQIKIAQTARRNRRPGS*KDCTP*KCLRKSDEALNRV LQQI\RVPPKMKRGTSLSHRRGKPEAPKGSPPQINRKSGQEMTA VMQSGRPRSSSTTDAPTGSAMMEIACAAAAAAACLPGEEGTA ERIERLEVSSLAQTSSAVASSTDGSIHTDSVDGTPDPQRTKAA IAHLQQKILKLTEQIKIAQTARRNRRPG
62	801	232	1299	MQTIERLVKERDDLMSALVSVRSSLADTQOREASAYEQVKQVL QISEEANFEKTKALIQCDQLRKELERQAERLEKELASQQEKRA IEKDMMKKEITKEREYMGSKMLILSONIAQLEAQVEKVTEKI SAINQLEEIQSQSLASREMDVTKVCGEMRYQLNKTNMEKDEAEK EHREFRAKTNRDLEIKDQEIIEKLRIELDESKQHLEQQEQAAL AREECLRLTELLGESEHQLHLTRQEKDSIQQSFSKEAKAQAALQ AQOREQELTQKIQQMEAQHDKTENEQYLLLTSTQNTFLTCLKEE CCTLAKKLEQISQKTRSEIAQLSQEKRYTYDKLGLQRNEEL EEQCVQHGRST*
63	802	3	334	SYPVWWSNPLTAEVPPPELLAAAGFFHTGHQDKVRCFFCYGGLQ SWKRGDDPWTEHAKWFPSCQFLLRSGRDFVHSVQETHSQLLG SWDPWEEPEDAAPVAPSPASGYPELTPRREVQSESAQEPGG VSPAQAQRAWVLEPPGARDVEAQLRRLQEERTCKVCLDRAVS IVFVPCGHLVC\AECAPGLQLCPI\CRSPCGPLRPLWVP
64	803	70	456	MCSYREKKAEPQELLQLDGYTVDYTDPPQGLEGGRAFFNAVKE GDTVIFASDDEQDRILWVQAMYRATGQSHKVPPTQVQKLNK GGNVPLQDAPISQFYADRAQKHGMDEFISSNPCNFDHASLFEM *
65	804	2	1376	KQLIVLGNKVDLLPQDAPGYRQRLRERLWEDCARAGILLAPGH QGPQRPVKDEPDGENPNPPNWSRTVVRDVRLLISAKTGYGVVEE LISALQRSWRYRGDVYLVGATNAGKSTLFNTLLES DYCTAKGS EAIDRATISWP PGTTLLNLLKFPICNPTPYRMFKRHQRLLKDDST QAEEDLSEQEQNLNVLKKHGYVVGRTFLYSEEQKDNIPF EFDADSLAFDMENDPVMGTHKSTKQVELTAQDVKDAHWFYDTP GITKENCILNLLTEKEVNIVLPTQSIVPRTFVLKPGMVLFLGA IGRIDFLQGNQSAWFTVVASNILPVHITSLDRADALYQKHAGH TLLQIPMGKKERMAGFPPLVAEDIMLKEGLGASEAVADIKFSS AGWVSVTPNFKDRLHLRGYTPGTVLTVRPPLLYIVNIKQOR IKKSVAYKTKKPPSLMYNVRKKKGKINV
66	805	1	874	STVASMHRQETVECLRKFNARRKLKGAITLTMVSRNFSAAK SLLNKKSDGGVKPQSNKNLSVSPAQEPAPLQTAMEPQTTVVH NATDGIKSTESCN TTTTEDEDLKAAPLRTGNGSSVPEGRSSRD RTAPSAGMQPQPSLCSSAMRKQEI IKITEQLIEAINNGDFEAY TKICDPGLTSFEPEALGNLVEGMDFHKFYFENLLSKNSKPIHT TILNPHVHVIGEDAACIAYIRLTQYIDGQGRPSNPAKSEE\TR VWH\RR\DGKWLNVHYHCSGAPCPHRCSEL SHRGF

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67	806	3	1714	LPKNVVFVLDSSASMVGTKLRQTKDALFTILHDLRPQDRFSII GFSNRKIVWKDHLISVTPDSIRDGKVYIHMSPTGGTDINGAL QRAIRLLNKYVAHSGIGDRRVS LIVFLT DGKPTVGETHTLKIL NNTREAAARGQVCIFTIGIGNDVDFRLLLEKLSLENCGLTRRVHE EEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVQATKTLFPNY FNGSEII IAGKLVDRKLDHLHVEVTASNSKKFII LKTDVVPVRP QKAGKDV TGS PRPGDGEGDTNHIERLWSYLT TKE LSSWLQS DDEPEKERLRQRAQALAVSYRFLTPFTSMKLRGPVPRMDGLEE AHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPYQPRIKISKTSV DGDPHFVVD FPLSRLTVCFNIDGQPGDILRLVSDHRDSGVTVN GELIGAPAPPNGHKKQRTYLRTITILINKPERSYLEITPSRVI LDGGDRLVLP CNQSVVVG SWGLEVSVSANANVTVTIQGSIAFV ILIHLYKKPAPFQRHHLGFYIANSEGLSSNCRVFCESGILIQE LTQQSVAVAGR
68	807	2	841	FFLEQVSQYTFAMCSYREKKSEPQELMQLEGYTVDYTDPHPG LQGGCMFFNAVKEGDTVIFASDDEQDRILWVQAMYRATGQSYKP VPAIQTKLNP KGGTLHADAQLYADRFQKHGMDEFISANPCKL DHAFILFRILQRQTL DHRILNDSYSC LGWFS PGQVFLDEYCAR YGVRGCHRHL CYLAELMEHSENGAVIDPTLLHYSFAFCAS \HVH GNRPDGIGTVSVEEKERFEEIKERLSSLLENQISHFRYCFPF RPEGALKATLSLLERVLMKDIA
69	808	2	757	DGLLHEVLNGLDRPDWEEAVKMPV GILPCGSGNALAGAVNQ HGGFEPALGLDILLNCSLLL CRGGGHPLDLLSVTLASGSRCSF LSVANGFVSDVDIQSERFRALGSARFTLGTVLGLATLHTYRGR LSYLPATVEPASPTPAHSLPRAKSELTLTPDPAPPMASPLHR SVSDLPPLPQPALASPGSPEPLPILSLNNGGP ELAGDWGGAG DAPLSPDPQLSSPPGSPKAALHSPV*KKAPVIP PDM
70	809	3	530	KGVPTLLMAAGSFYDILAITGFNTCLGIAFSTGSTVFNVLRGV LEVVI G VATGSVLGFFIQYFPSRDQDKLVCKRTFLVLGLSVLA VFSSVHFGFP GSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW DIFQPLL FGLIG \AEVSI \SSLRPETVGLCVATVGI \AVLIRI FDYIF
71	810	228	541	LLKEVVVQASPVCKTCCSQLV RTPVTTFTEVQNV/CRCSAGYLI SVCSYTSSDHNQCYAGTASLALLWIGGILKGCLLWKQFRWTER SHWNFGYWALWSPGNNGC
72	811	173	404	ICTSTYLQIFPGKPSCFMCKGRLMCIYFILWYLGHYTSLHWNW CRYISDPNVD/ACPDPRNAEVSMHTV PALMELID
73	812	2	586	LES L PGFKEIVSRGVKVDYLTDPDFPSLSYPNYTLM TGRHCEV HQMIGNYMWDPTTNKSF DIGVNKDSL MPLWNGSEPLWVTLTK AKRKVYMYWP GCEVEILGVRPTYCLEYKNVPTDINFANAVSD ALDSFKSGRADLAAIYHERIDVEGHYGPASPQRKDALKA \VD TVLK YMTKWIQERGLQDRLNVI

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74	813	2	348	ARDFHPKQTLDFLRSDMANSKITEEVKRSIAQQYLDLTVA/LE QVDPDAEVDAA PSTTSSCGH*DSHAGS*RVLSLLGD*GPA*TG ANSMAGKLLLVAWLGFDPDPFWGKELSDPAFK
75	814	2	366	KQSGDVTNCNCTDGR LAPSC LTCVGHCI FGGYCTMNSKMMPECQ SPPHMTGPRCEEHVFSQHQP GHITS ILIPML*LLLLVLVAGVI FCHKRRVQGA KGFQHQ RMTNGAMNAQIANPTYKMY
76	815	420	681	TVENAGRWL*EEAEIQAE LERLERVRNLHIRELKRINNEDNSQ FKHPTLNERYLLLHLLGRGGFSEVYKVMYGLFWFFYTNVARI
77	816	37	428	MCEEFLVMGKGCSCVF*ILSNPQMWWLND SNPETDNRQESPS QENIDRVSD/MAFVPSAWTASGGVAWGNL GESGSR TGGVRAET LAPRLQV*PAHLRGHPRSNRGQGRPPWKAGLKGKQCEVLF RFA AF
78	817	1	358	FRAMFLAVQHDCRPM DKSAGSGHKSEEKREKMR TLLKDWKTR LSYFLQNSSTPGKPKTGKSKQQA FIK*VENPELANINS*LLN *KGEL**A*ANIQNLSCRPSPEEAQLWSEAFDE
79	818	1	169	GFFNFSSPKLKGWKINSSLVLEIRKNILRFLDAERDVS VVKSS FPSKDARHSSVHR*FTQLHWGPPSHTPARP*RGFFNFSSPKLK GWKINSSLVLEIRKNILRFLDAERDVS VVKSSFPSKDARHSSV HR
80	819	55	310	RIDDQQELKRV T*YSQKEYTKK KLHKKCNIIQADIKPDNILDN ESITILKLSDFGSASHVADNDITPSSSQTTSAASSPPRTLRR
81	820	1	134	SSKPWD*SLAPKHS G*TKNMDCYCIPTCIGRERCYGT CIGDT V
82	821	187	360	NSSKKLVMEHQWK KYLRNRYQRM LNRLITLIGSCGVL*LISTI PTSRLKFLKETGHGTPMEEIPEEELSEDVEQIDHADRELRRGQ NLRCKGIHRLPTHIQVGQN
83	822	208	723	KWMLLHSFKIFCLSLYPQL*CPFEFFSHSATIFHEL VYKQTKI ISSNQELIYEGRR LVLEPGRLAQHF PKTTEENPIFVVSREPLN TIGLIYEKISLPKVHPRYDL DGDASMAKAITGVVCYACRIAST LLLYQELMRKGIRWLI ELIKDDYNETVHKKTEVVITLGLFVSR
84	823	1	314	GTRKMGP TVSPICLP GTWGDYNLMDGDLGLISGWGRTEKRDRA DRLKAGRSPAAG*RKWEPGRGDPTWEESEEDVHKS KWTRCVD E KGA*C*TDNKRPLRCGVT
85	824	3	302	HELENLIKSAHSYSLY*G*YLHGA*TAEPEASFCPRRGWNRQA GAAGSRMNF RPGVLSSRQLGLPGPPDGPDYTVYYPFHRLAMVT AASRLEREHLTHL
86	825	87	422	PVPLPHPILEVCPGQ*EPQSAISLTA FQVQAGASRASPGPPAP SSSKPGRKAKVASPCPDRPAPPPT*PRPAAAPGSESSPRPPRP RTGRRQORAHARRAAARTAPWRPSC
87	826	3	289	HEGRRRGWASASQRF LRNWAFLTPSKVRRLKGQKAFGKLPSHS DTSLTSDLGFHHRFNP NASSSFKPSGTFKFAIQYGTGRVDGILS EDKLTVSGL
88	827	1	101	GRNIMHYPNNGHAICIAN GHCIIL*NSHNIKVVV

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89	828	1	535	INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQH LFAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFL DRLHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETP RTSDGEKTLIEKMFGGKLRTHIRCLNCTSTSQKVEAFTDLSLA FWPSSS
90	829	1	434	ARDDPRVRLSLSPNFF*LASKLGKQWTPLIILANSLSGTNMGE
91	830	3	782	MHRIKLNDRMTFPEELDMSTFIDVEDEKSPQTESCTDGAENE GSCSDQMSNDFSNDGVDGEGICLETNSGTEKISKSGLEKNSL IYELFSVMVHSGSAAGGHYYACIKSFSDEQWYSFNDQHVSRIT QEDIKKTGGSSGSRGYSSAFASSTNAYMLIYRLKDPARNAK FLEVDEYPEHIKNLVQKERELEEQEKQREIERNTCKIKLFLCL HPTKQVMMED*IEVHKDKTLKEAVEMAYKMDLEEVIPLDCCR L
92	831	2	604	SVMPVPALCLLWALAMVTRPASAAPMGGPPELAQHEELTLLFHG TLQLGQALNGVYRTTEGRLTKARNSLGLYGRTELLGQEVSRG RDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQKVL DSVQRLEVQLRSALWGPAYREFEVLKAHADKQSHILWALTGHV QRQRREMAQQHRLRQIERLHTAALPA
93	832	16	690	ITSVDPRVRGNASTGYGKIWLDDVSCDGEDSLWSCRNSGWGN NDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVG ILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMS NSGCAGGEASLWDCIRWEWKQTACHLNMEASLICSARHQPRLV GADMPGCSGRVEVKHAHTWRSVCDSDFSLHAANVLCRELNCGDA ISLSVGDHFG
94	833	108	727	SNYPSSRFRVAGITGVKLGMRSIPIATACTIYHKFFCETNLDA YDPYLIAMSSIYLAGKVEEQHLRTRDIINVSNRIFYNPSGEPL LDSRFWELRDSIVQCELLMLRVLRFQVSFQHPHKYLLHYLVSL QNWLNHRHSWQRTPVAVTAWALLRDSYHGALCLRFQAQHI LYLALQVYGVEVPAEVEA/DEAVGWQIYAMDTEIP
95	834	118	376	RGSRHAVHGWAFGLLFINKESVVMAYLFTTFNAFQGVFIFVH CALQKKVRSRRGPGSQPPLETTFPGYPGEGGEGGDSGAPSSPQ
96	835	3	333	ARKDDLPPNMRFHEEKRLDFEWTLKAG*EKG*PSK*NKGWEGQ E***TVRD*GIS**VKPQHLS*\ALQMALKRVYTLSSWNCLE DFDQIFWGQKSALAGQWFPEVSIIP
97	836	740	951	GKQORETLRRPSPTISVQRAGSPEHSSASH*HSPCPAPGQORVL PTALCTLMTSKHFHGCPLAGQGRAVTL

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98	837	81	1503	GVCGLPRFCGSIILCHYEMSSLGASFVQIKFDDLQFFENC GG SFGSVYRAKWISQDKEVAVKLLKIEKEAELSVLSHRNI IQF YGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMDHIMTWA TDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGA SRFHNTTHMSLVGTFFWMAPEVIQSLPVSETCDTYSYGVVLW EMLTREVPFKGLEGLQVAWLVEKNERLTIPSSCPRSFAELLH QCWEADAKKRPSFKQIIISILESMSNDTSLPDKCNSFLHNKAEW RCEIEATLERLKKLERDLSFKEQELKERERRLKMWEQKLT EQS NTPLLPLAARMSEESYFESKTEESNSAEMSCQITATSN GEGH GMNPSLQAMMLMGFGDIFSMNKAGAVMHSGMQINMQAKQNSSK TTSKRGRKKVNMALGFSDFDLSEGDDDDDDGEEBYNDMDNSE
99	838	185	328	MLWETGCSAACRVTVSPTVTFATFSTRGIDAMRPGPSFLWRQQ LSQG*
100	839	1	348	PTLGDQPDLSITRASRPKLCTRKNCNPLTITVHDPNSTQ*YY GMSWELRFYIPGFDVGTMTFIQKILVSWSPPKPIGPLTDLGDP MFQKPPNKVDLTVPPPFLVIKDTLQKFEKI
101	840	1	416	SLNNVTLPQAKTEKDFIQLCTPGVIKQEKLGTVYCQASSPGAN MIGNKMSAISVHGVSTSGGQMYHYDMNTASLSQQ*DQKPIFNV IPPIPVGSENWNRCQSGDDNLTSGLTLNFPGRVTSFSFEMES RSVAQAGVQ
102	841	105	354	RHTQECRCPTHITHTHSHTHSHTHSHSHSHTTPRCSHTQPP HAQAPALC*S*EDRGQPTWKLCARPRPKVKEGGWLGG
103	842	171	347	NYSLSVVLVRQLTAGTLLQKLRAKGIRNPDHSRALSE*HLSSL PHLIWIQVFLALQPS
104	843	2	690	ATYIVDFGFSTTFREGQMLTAFCGMYPYVAPERSLGQACQ*PA RDIQSLSVILYFRNTVGRRTLPFYS/ABASKLQEKILTGRY HAPPLALQLDSL/IKLLMLNARKCPSL*LMKNPWVKSSQKMP LIPYEEPL/RGPPQTIQLMVAMGFQAKNISVAIERKFNPMA TYLILEHTKQERKCSSTIRELSLPPGVPTSPSPSTELSTFPLSL MRAHREPAFNVQPPEESQ
105	844	2	777	AKQELAKLMRIEDPSLLNSRVLLHHAAGTIIARQGDQDVSLH FVLWGCLHVVYQRMIDKAEDVCLFVAQPGEVLGQLAVLTGEPLI FTLRAQRDCTFLRISKSDFYEMRAQPSVVLAAHTVAARMSP FVRQMDFAIDWTAVEAGRALYRCSSHRAAARPRGGDLGVVRP C*PPRPLRQGRSDCTYIVLNGRLRSVIQRGSGKKELVGEYGR GDIGVVSATPTH*PLAFSRPVPRQLTRIIIPGNPGSGEVFPGA
106	845	3	709	HASGWTPTGTTQTLGQGTAWDTVASTPGTSETTASAEGRRTPGA TRPAAPGTGSWAEGSVKAPAPIESPSPSKSRMSNTTEGVWEG TRSSVTNRARASKDRREMTTTKADRPREDIEGVRIALDAKKV LGTIGPPALVSETLAWELPQATPVSKQSQSGSIGETTPAAGM WTLGTPAADVWILGTPAADVWTSMEAASGECSAAGDLDAATGD RGPQATLSQTPAV*PWGPPG

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107	846	3	406	AGTSGTGDGTGPGNTAVSGTPVVS PGATPGAGSSSTPGEADIGN TSFGKSGTPTVSAASTTSSPVSKHTDAASATAVTISGSKPGTTP GTPGGATSGGKITPGIA*PTLDQKSPCFSGYGGYFPVNP HQNP CADSL
108	847	1	565	RAHRCCLPLPSLSCEIQIGFS*SSIFPGQ*ACPCSCCRSCRRN WPQSPRCPHPPAPCSLLSSCLPPPLSCSWRGTS GKPPSQSP AASRSMRPRCSPTSSSLRGASCRGPGGSAPAAASGPRCRGCSR SPRRCRSRSGCAAASPPRSQRRSPPLSPPPFPSTGTL LKTSRF GSATRE*SSPRPRRP
109	848	2	987	DDVPPPAPDLYDVPPGLRRPGPGTLYDVPRERVLPP EVADGGV VDSGVYAVPPPAEREAPAE GKRLSASSTGSTRSSQSASSLEVA GPGREPLELEVAVEALARLQQGVSATVAHL LLAGSAGATGSW RSPSEPQEPVQDLQAAVA AVQSAVHELLEFARS AVGNAAHTS DRALHAKLSRQLQKMEDVHQTLVAHQALDAGRGSGGATLEDL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPEGGG TLHPNPTDKTSSSIQSRPLSPPPKFTSQDSPDQYENSEGGWME DYDYVHLTGGRSF*KTQKELLGKRAA
110	849	84	372	MATDEENVVGLLENAQSRQESTRRLLILVGR TGAGKSATGNSIL GQRRFFSRLGATSVTRACTTGSRRWKCHVEVVDTPDIFSSQV SKTDPGCEERX*
111	850	2	47	TLGLRSLTKEGGGGDVAAFEVGTGAAASRALGQCGQLQKLIV IFIGSLCGLCTKCAVSNDLTQQEIQTPEIQORNA*CD SRVTFT NEGGRWWG
112	851	1192	1040	FFFLVETRHHIGQAGLELLTSLIK*SARLGLPKCWDRREPP YLAGFMI
113	852	791	362	RRSPPPAPPPPLPSPLSPPPRAPVSPASTMPILLFLIDTSASMN QRSHLGT'TYLDTAKGAVETFMKLRARDPASRGDRYMLVTFEEP PYAIKAGWKENHATFMNELKNLQAEGLTTLGQSLRTAFD LLLNL NRLVTGIDNYGQVG
114	853	812	348	NCRTYVFCFVLVFRLLFLHGSPLSPSLLSRAGLLCGSAENPTP FLCGITMAAGVSL LALVVRVILSTAILCPSGASRRQRSSEVEW GTDSGVYRLYCWRVGF LGGELRLGLSEARGGRVWGRGEKRC RVWAVRSLRKGFSGVAALRRGIWAG
115	854	93	170	VTPTPPQYYTCSCVLGFIACSI FLQMSLKPKVMLLTVALVACL VLFNLSQCWQRDCCSQGLGNLT EPGTNR*GPAAVSWASLPAP SSCR
116	855	1	183	GKAGGAAGLFAKQVQKKFSRAQEK*TRRFGKTCQPEERAREER QEGPEIEFGFSFFSLSLY

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117	856	53	2400	PKRLFLFQDVNTLQGGGQPVVTPSVQPSLQPAHPALPQMTSQA PQPSVTGLQAPSAALMQVSSLDHSAVSGNAQSFQPYAGMQAY AYPQASAVTSQLOPVRPLYPAPLSQPPHFQGSQDMASFLMTEA RQHNTTEIRMAVSKVADKMDHMTKVEELQKHSAGNSMLIPSMS VTMETSMIMSNIRIIQENERLKQEI LEKSNRIEQNDKISEL IERNQRYVEQSNLMMEKRNNSLQTATENTQARVLHAEQEKAKV TEELAAATAQVSHLQLKMTAHQKKETELQMQLTESLKETDLLR GQLTKVQAKLSELQETSEQAQSKFKSEKQNRKQLELKVTSLEE ELTDLRVEKESLEKNLSERKKSAQERSQAEEIDEIRKSYQE ELDKLRQLLKKTRVSTDQAAAEQLSLVQAELOQWEAKCEHLL ASAKDEHLQOYQEVCAQRDAYQQKLVLQLEKSVCFALCLALQA QITALTQKNEQHIKELEKNKSQMSGVEAAASDPSEKVKKIMNQ VFQSLRREFELEESYNGRTILGTIMNTIKMVTLLQLLNQEQEK EESSEEEEEKAERPRRPSQEQSASASSGQPQAPLNRERPE PMVPSEQVVEEAVPLPPQALTTSDGHRKGDSEAEALSEIKD GSLPPELSCIPSHRVLGPPTSIPPEPLGPVSMDECEESLAAS PMAAK\PDNPSGK\VCVQGK*APDGPTYKE\SSTRLFPGFQDP E\EGDPLALGLE\SPG\EPQPPQLQGVVDH*VPPVPHKGAFO EQEGRFPQFCRE
118	857	1	791	SETAQQIIDRLRVKLAKPEGANLFLMAVQDIRVGGGRQSNASYQ YTLLSDDLALREWEPKIRKKLATLPELADVNSDQDNGAEMN LVYDRDTMARLGIDVQAANSLNNAFGQRQISTYQPMNQYKV VMEVDPRYTQDISALEKMFVINNEGKAIPLSYFAKWQPANAPL SVNHQGLSAALTISFNLPTGKSLSDASAAIDRAMSQLGVPSTV RGSFAGPAQVFQETMNSQVILIIAAIATVYIVLGIPYERYVHP PTILL*RPGANLFLMAVQDIRVGGGRQSNASYQYTLLSDDLAL REWEPKIRKKLATLPELADVNSDQDNGAEMNLVYDRDTMARL GIDVQAANSLNNAFGQRQISTYQPMNQYKVMEVDPRYTQD ISALEKMFVINNEGKAIPLSYFAKWQPANAPLSVNHQGLSAAL TISFNLPTGKSLSDASAAIDRAMSQLGVPSTVRGSFAGPAQVF QETMNSQVILIIAAIATVYIVLGIPYERYVHPPTILL
119	858	3	417	IITPDAMGCQKDIAEKIQKGGDYLFVAVKGNQGRNLKAFEEKF PLKELNNPEHDSYAISEKSHGREEIRLHIVCDVPDELIDFTFE WKGLKKLCVAVSFRSIIAEQKKEPEMTVRYNIS*LGIAGDISV TAISGTDD
120	859	2	373	HYLKMLTQARREVI IANAYFFPGYRFLHALRKAARRGVRIKLI IQGEPDMPIVRVGARLLYNLVKGGVQVFYRRRPLHGKVALM DDHWATVGSNNLHPVS*SGNLQANVILHVLRVPTLNP
121	860	286	495	CWSKSAAFHSKLATTCIVPVCAAGHCSAW*SLRPTALAKEV RELK*HTR*LLNPATTRELTSLGRNLRLLKSERERYDKYRTT LTDLTHSLKTPLAVLQSTLSLRSEKMSVSDAEPVMLEQISRI SQQIGYYLHRASMRGGTLLSRELHPVAPLLDNLTSALIKGKPR KGGNVTVFPPTAMYRDGH

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122	861	2	725	GNTVMFQHLMQKRKHTQWTYGPLTSTLYDLTEIDSSGDEQSLLELIITTKKREARQILDQTPVKELVSLKWRYGRPYFCMLGAIYLLYIICFTMCCIIYRPLKPRNTNRTSPRDNLTLLQOKLLQEAYMTPKDDIRLVGELVTVIGAI IILLVEVPDIFRMGVTRFFGQTILG GPFHVLIIITYAFMVLVTMVMRLISASGEVVPMSFALVLGWCNV MYFARGFQMLGPFITIMIQKMIFGDL
123	862	1	135	EKAAAANIDEVQKSDVSTGQGVIDKDALGPMMLLEVAHLHFSAVF
124	863	2	364	LEVPSEVTPLGFAMQATKTLRLTCCLOEFNIMEKNKGWALLG GKDGHLLQGLFLLANALLERNQLLAQKVMYLLVPLLRGNDKHK LTSAGFFVELLRSPVAKRLPSIYSVARFKDWLQD
125	864	1	374	RPAPAPSAAPPEEAPSP\GVKGRGMAKRRVPAPVWGGAGGGTKSARRAAAAPDTERSEEGGRAVKEAYPSSRQPPPPSP*PLRCARRCHPNLAPSMPI SNREGKGRREEKIRPLSPASTHTSARA
126	865	3	364	LQGVHGSSSTFCSSLSSDFDPLEYCSPKGDPQRVDMQPSVTSR PRSLDSEVPTGETQVSSHVYHRHRHHYKKRFQRHGRKPGPETGVPPQSRPPIPRTPQPEPPSPDQVTRSNAA
127	866	2	250	MADPDPRYPRSSIEDDFNYGSSEASDTHIRMAFLRRVYSILSLQDLLATVTSTDNLAFEDGRTDWLQRPDCVSFKIHVLP
128	867	194	375	AGMSVVVVPPIGSSYLGLISQEHFPNEFTSGDGKKAHQDFGYFYGSSYVAASDSSRTPL
129	868	104	339	VAAALTFLFPQQLSPPGAWGLGLSACFCCAEGFSRLNQVLSSS LLLLSRTNCPCKYSFLDNLKLTTPRDVPTYPKVR
130	869	2	360	RDDACLYSPASAPVITVGATNAQDQPVTLGLTGNFGRVLDL FAPGEDIIIGASSDCSTCFVSQSGTSQAAAHVAGIAAMMLSAEP ELTLAELRQRLIHFSKDVINEAWFPEDQRVLT
131	870	2	105	LEIKFLEQVDQFYDDNFPMEIRHLLAQWIENQDW
132	871	2	466	EAGDADEDEADANSSDCEPEGPVEAEPPQEDSSSQSDSVEDR SEDEDEHSEEEETSGSSASEESESESESEDAQSQSQADEEEED DDFGVEYLLARDEEQSEADAGSGPPTPGPTTLGPKKEITDIAA AAESLQPKGYTLATTQVKTPILLL
133	872	1	354	LKNLRELLLEDNQLPQIPSGLPESLTELSTLIQTNINITKEGISRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEED
134	873	59	184	MRSQALGQSAPSLTASLKELSLPRRGSPFVCPNAGRTSPLG*
135	874	1	210	LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYSRTSPPLHSPSEIVFDFEPGPVFRGSWALLSWSTRP
136	875	131	254	QTPDKQNDQRNRKRAEPYETSQGSNNFVSTKVLNSNVLR
137	876	84	504	YFI IKGMVELVPASDTLRKIQVEYGVGTGSFKDKPLAEWLRYN PSEEEYEKASENFIYSCAGCCVATYVLGICDRHNDNIMLRSTG HMFHIDFGKFLGHAQMFGSFKRDRAPFVLTSDMAYVINGGEKPTIRFQLFVDL

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138	877	3	215	PSPLPSLSLPPPVAPGGQESPSPHATAEVESEASPPPARPLPGE ARLAPISEEGKPOLVGRF\QVTSSK\NRLSLFPCSQHPPLSLV LQNLQPLSSLQRAQIQRTV/PGGGPETREALAESDRAEGLGA GVEEEGDDGKEPQVGGSPQPLSHSPVWMNYSYSSLCLSSEES ESSGEDEEFWAELOSLRQKHLSEVETLQTLQKKEIEDLYSRIG KQPPPGIVAPAAMLSSRQRLSKGSFPTSRNSLQSEPPGPG ETA/GHPASIFSLRPLSVDCFSPPGPGGLPRGNRPPLTSPFLT *CSPSPHTAEVESEASPPPARPLPGEARLAPISEEGKPOLVGR FPSDFIQGTG
139	878	1	337	RRFVSQETGNLYIAKVEKSDVGNVTCVVTNTVTNHKVLGPPTP LILRNDGVMGEYEPKIEVQFPETVPTAKGATVKLECFALGNPV PTIIWRRADGKPIARKARRHKS RVGK
140	879	72	917	MLRTCIVLCSQAGPRSRGWQSLSFDGGAFHLKGTGELTRALLV LRLCAWPPPLVTHGLLLQAWSRRLLSRLSGAFLRASVYGQFVA GETAEVKGCVQQLRTLRLPLLA VPTEEEPDSA AKSGEAWYE GNLGAMLRCDLSRGLLEPPSLAEASLMQLKV TALTSTRLCCKE LASWVRRPGASLELSPERLA EAMDSGQNLQV SCLNAEQNH LR ASLSRLHRVAQYARAQHVRLLVDAEYTS LNPALSLLVAA LA VR WNSPGE GGPWWNTYQACLKDTF*
141	880	219	308	PHHRIAGDTAIDKNIHQSVSEQIKKNFAK
142	881	182	317	QMTNPFPLCFTTMISNCNFFKGP GPPGEGKDRGPTGESGPRG FP
143	882	177	341	NGIIASFRLRTFIFCFIHIQGCQAGQTIKVQVSFDLLSLMFTF VSPCTNDLIH
144	883	3	1441	KLSVNHRRTLTKLMHTVEQATLRISQS FQKTTEFD TNSTDIA LKVFFFDSYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVA V AFLYYKSIGPLSSSDN FLLKPQNYDNSEEEERVISVISVM SSNPPTLYELEKITFTLSHRKVTDRYRSLCAFWNYSPTMNGS WSSEGCELTYSNETHTSRCNHLTHFAILMSSGPSIGIKDYN I LTRITQLGIIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCS LFLAELVFLVGINTNTNKLFC SIIAGLLHYFFLA AFAWMCIEG IHLVLI VVGVIYKNGFLHKNFYIFGYLSPAVVVGFS AALGYRY YGTTKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFR HTAGLKPEVSCFENIRSCARGALALLFLLGTTWIFGV LHVHVA SVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYRLFKNVPC CFGCLR
145	884	1	429	GTREAA PSRFMFLFLLTCELA AEVA AEVEKSSDGP GAAQEPT WLTDPVPAAMEFIAATEVAVIGFFQDLEIPAVPILHSMVQKFP G VSGISTDSEVLTHYNITGNTICL FRLVDNEQLNLEDEDIESI DATKLSRFIEINSL
146	885	1	156	DETSGLIVREVSIEISRQQVEELFGPEDYWCQCVAWSSAGTTK SRKAYVRIA
147	886	1	121	GTRSIHVKLDVVGKLTQPKLAAQLRMVDDGSGKVEGLPGI

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148	887	128	652	XCGEDGSFTQVQCHTYTGYCWCVTPDGKPISGSSVQNKTPVCS GSVTDKPLSQGNSGRKDDGSKPTPTMETQPVFDGDEITAPTLW IKHLVIKDSKLNNTNIRNSEKVYSCDQERQSALEEAQONPREG IVIPECAPGGLYKPVQCHQSTGYCWCVLVDTRPLPGTSTRYV MPX*
149	888	128	273	VLQLIKSQKFLNKLVLVETEKEKILRKEYVFADSKVSDSKLL KWA VR
150	889	1	948	RRSLDLQLGPLGRDPPQECSTFSPDTSGEPEGQLSPGVQFQ RRQNQRRFSMEDVSKRLSLPMDIRLPQEFLOKLQMESPDLPKP LSRMSRRASLSDIGFGKLETYVKLDKLGEGTYATVFKGRSKLT ENLVALKEIRLEHEEGAPCTAIREVSLKLNKXANIVTLHDLI HTDRSLTLVFEYLDSDLKQYLDHCGNLSMHNKVRPRGQGGP ILAAATCEAQCQDPLSPPGIRLLRWLKP SHVGKRERAMPSTSP GTGLSALPQEQTHTVCHCLAVGIKPTLNSEHQFPLSNGSVSY LPKCREASGEARGYE
151	890	3	108	HERHEPSPTALAFGDHPVQPKQLSFKIIQVNDN
152	891	2	208	ARGPSLLSEFHGSDRPGQERRTSYEPHHPGSPVDHDSLESKR PRLEQASDSHYQGHTGESLPGRVH
153	892	1	116	GTRKEEFSAEENFLILTEMATNHVQVLVEFTKLPGLIF
154	893	74	661	HTHKLVAAPRPLPPTSQWPRDAGRQASGGLPSLSTGPPKGRPD GLARGHPAEWLAGSPGNNSTQGSLLPQLDLYAGALFVHICLG WNFYLTILTLGITALYTIAGMVPAAGRSTQGTCKGVRPPPP TGPREQPRKWPQEPQKFLPVSLLPGARAPSSNLASTGRGPGC CNLHGRPADAHGGGGCHPDNQR
155	894	55	312	MVNHSLOETSEQNVLQHTLQQQQQMLQOETIRNGELEDTQTK LEKQVSKLEQELQKQRESSAEKLRKMEEKCESAAHEADLKRQK *
156	895	38	185	VCPKWCRLTMLGHCCYFWHVWPAS*ALSAGPTPTSRSPSP LRSIST
157	896	37	462	MRGPPVLLLQAAPMECPVPQGI PAGSSPEPAPDPGPHFLRQE RSFECRMCGKAFKRSSTLSTHLLIHS DTRPYPCQFCGRFHQK SDMKKHTYIHTGEKPHKCQTQREPTMVLS PADKTNVKAAX*
158	897	3	175	HEQLTNTATAPSATPVFGQVAASTAPSLFGQQTGITASTAVA TPQVISSRFINLDF
159	898	187	677	VSVFKNCPMY*ICIFLTkmfcvlii*NKF*VHKPLQEVEIA AITHGALQGLAYLHSHMTMIHRDIKAGNILLTEPGQVKLADFGS ASMASPANSFVGTPYWMapevILAMDEGQYDGKVDVWSLGITC IELAERKPPLFNMNAMSALYHIAQNESPTLQSNW

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160	899	2	1060	RHARPGGGGHSNQRKMSLEQEEETQPGRLLGRRDAVPAFIEPN VRFWITERQSFIRRFLOWTELLDPTNVFISVESIENSROLLCT NEDVSSPASADQRIQEAWKRSLATVHPDSSNLIPKLFPAFL PFMATVFLSMTPLKGIKSVILPQVFLCAYMAAFNSINGNRSY TCKPLERSLLMAGAVASSTFLGVIPQFVQMKYGLTGPIKRLP PVIPLVQASGMNVMSRSLESIKGIAVMDKEGNVLGHSRIAGT KAVRETLASRIVLFGTSALIPVFTYFFKRTQYFRKNPGLSWI LKLSCTVLAMGLMVPFSFSIFPQIGQIQYCSLEEKIQSPTEET EIFYHRGV
161	900	3	564	HASGRLEVFYNGTWGSGVGRNITTATAGIVCRQLGCGENGVS LAPLSKGTSGFMWVDDIQCPKTHISIWQCLSAPWERRISSPAE ETWITCEDRIRVRGGDTECSGRVEIWHAGSWGTVCDSDWDLAE AEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNESFL WDCHAKPWGQSDCG
162	901	1099	2	LGDFPQPQRORRPGASDLPPHLAGARQWEVRFRRHLPARTLPF SLRMEGPELHLASQFVNEACRALVFGGCVEKSSVSRNPEVPP ESSAYRISASARGKELRLILSPLPGAQPQOEPLALVFRFGMSG SFQLVPREELPRHAHLRFYTAPPGPRLALCFVDIRRFRGWDLG GKWQPGRGPCVLQEQYQFRENVLRLNLADKAFDRPICEALLDQR FFNGIGNYLRAEILYRLKIPPFKARSVLEALQQHRPSPELTL SQKIRTKLQNPDLLELCHSVKPEVVQLGGRGYGSESGEEDFAA FRAWLRICYGMPGMSLQDRHGRTIWFQGDPGPLAPKGRKSRKK KSKATQLSPEDRVEDALPPSK
163	902	3	335	LTWSACYWRDILRIQLWIAADILLRMLEKALLYSEHQNTSNTG LSSQGLLIFAEILIPAIRTLARLLVIIASLDYGIEKPHLGTGM HRVIGLMLLYLIFANAESVIRVIG
164	903	2	135	FFFEMESRSAAQAGVQWCNLSLQALPPRFTPFSCLSLPSSWD Y
165	904	74	645	YECEELAKKLENSQRDGISRNKLALAELYEDEVKCKSSKSNRP KATVFKSPRTPPQRFYSSEHEYSGLNIVRPSTGKIVNELFKEA REHGAVPLNEATRSGDDKSKSFTGGGYRLGSSFCKRSEYIYG ENQLQDVQILLKLWSNGFSLDDGELRPYNEPTNAQFLESVKRG VTLIACMPEIQQLMLEIF
166	905	14	1257	WPCGAAPGLTHASERMFTLTMTIQLAPVMGWRKPLKMFSS EEMRGLHHHHKCLTKILKVEGQVPDLPSCLPLTDNTRMLASIL INMLYDDLRCDDPERDHFRIKICEEYITGKFDPOQMDKNLAIQT VSGILQGFDFLGNQLLGLKGVMMEMVALCGSERETDQLVAVEA LIHASTKLSRATFIITNGVSLLKQIYKTTKNEKIKIRTLVGLC KLSAGGTDYGLRQFAEGSTEKLAKQCRKWLGNMSIDTRTRRW AVEGLAYLTLDADVKDDFVQDVPALQAMFELAKTSKDTILYSV ATTLVNCTNSYDVKEVIPELVQLAKFSKQHVPEEHPKDKKDFI DMRVKRLKAGVISALACMVKADSAILTDQTKELLARVFLALC DNPKDRGTIVAQGGGKALIPLALEGTD

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167	906	3	894	VDSVGGGSESRLDSPSTSSPGAGTRQLVKASSTGTSSDDFEE RDPDLGDGLNGLGSPFGKWTLSAAQTHQLRRLRGPACREC EAFMVSGTECEECFLTCHKRCLETLLILCGHRRLPARTPLFGV DFLQLPRDFPEEVFVVTCTAEIEHRALDVQGIYRVSGSRVR VERLCQAFENGRLVELSGNSPHDVSSVLKRFLQELTEPVIPIF HLYDAFISLAKTLHADPGDDPGTPSPSPSPEVIRSLKTLVLQPLD SNYNTLRHLVAHLFRVAARFMENKMSANNLGIVFGPTL
168	907	1	394	GLHVISLHSDGRHWEDPLSELDSEVSFAFLVTETLVFYLFCL LADETVVPPDVPSYLSQGTLSDRQETVVRTEGGPQANGHIES NGKASVTVKQSSAVTVSLGAGGGLQVFTGQVPGIRWGKLGAEH AS
169	908	179	551	KIKHRPEEEPRWAAAGASAGPGAEEVAPPRPGTVAPGANGMT DSATANGDDRDP EIELFVKAGIDGESIGNCPFSQRLFMILWLK GVVFNVTTVDLKRKPADLRNLAPGTHPPFLAFNWYVKT
170	909	1	335	LGFSDGQEARPEEIGWLNNGYNETTGERGDFPGTYVEYIGRKKI SPPTPKPRPPRPLPVAPGSSKTEADVEQVLYKYRKKPSSSHR PQTPHNGKSKNLFHKQGLKKKKASL
171	910	1	895	RTRGVMELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKE VWDYVTVRKDAYMFWWLYYATNSCKNFSELPLVMWLQGGPGGS STGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPGVTGFSY VNGSGAYAKDLAMVASDMMGLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLELYKAIQRTIKCNFAGVALGDSWISPVDSVL SWGPLYLYSMSLLEDKGLAEVSKVAEQVLNAVNGKLYREATLW GKAEMIEEQVKGNTQRRACLAFFSGGYRAHWCCQTWSLH
172	911	553	194	PGWSRSPDLVIRLPPPKVLGLQYYHFFFLRWSL/DSVAQAE VQWHDLRSLQAPPPGFTPFSCSLPGSWDYRCPPPRPANFLYF **RRGFTVLARMVSI*PRDPPASASQSAGITVLSLFFFEME SCSVAQAGVQWRYLGSQALPPGFTPFSCSLSPSSWDYRRPPP RPANFFVFLVETGVSPC*PGWSRSPDLVIRLPQPPKVLGLQV
173	912	1761	1	PSMKTGELEKETAPLRKADASSISVLEIHSQKAQIEEPDPPPM ETSLDSEMAKDLSSKTALSTESCTMKGEKSPKTKDKRPP ILECLEKLEKSKKTFDKDAQRLSPIPEEVPKSTLESEKPGSP EAAETSPPSNIIDHCEKLASEKEVVECQSTSTVGGQSVKQVDL ETLKEDSEFTKVEMDNLDNAQTSGIEEPSETKGSQKSKFKYK LVPEEETASENTEITSERQKEGIKLTIRISSRKKKPDSPPKV LEPENKQEKTEKEEEKTNVGRTLRRSPRISRPTAKVAEIRDQK ADKKRGEGEDEVEEESTALQKTDKKEILKKSEKDTNSKVSQV PKGKVRWTGSRTRGRWKYSSNDESEGSGSEKSSAEEEEEE SEEAIALADDDEPCKKCGLPNHPHLLCDSCDSCDGYHTALPFAP PLMIHPQMGGW\F\CPTFCPTLNLLLLLEKLEDQF\QDL\VAL KKERALPERRK\ERLVYVGI\SIENIIPPQ\EPDFSEDQEEKK KDSKSKKANLL\ERRSTRTRKCISYRFDEFDEAIDEAIEDDIK EADGGGVGRGKDISTITGHRGKDISTILDEER

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174	913	3	539	KRRGSFKMAELDQLPDESSAKALVSLKEGSLSNWNEKYSSL QKTPVWVKGRNTSSAVEMPFRNSKRSRLFSDEDDRQINTRSPKR NQRVAMVPQKFTATMSTPDKKASQKIGFRLRLNLLKLPKAHKWC IYEFYSNIDKPLFEGDNDFCVCLKESFPNLKTRKLTRVEWGK IRRLMG
175	914	166	635	MPEYLRKRFGGIRIPIILAVLYLFTIYIFTKISVDMYAGAIFIQ QSLHLDLYLAIVGLLAITAVYTVAGGLAAVIYTDALQTLIMLI GALTLMGYSFAAVGGMEGLKEKYFLALASNRSENSSCGLPRED AFHIFRDPLTSDLPPWPGVLFMSIPSLX*
176	915	673	1025	XSASATSLTLSHCVDVVKGLLDFKKRRGHSIGGAPEQRYQIIP VMCCSLLATGGADRLIHLWNVVGSRLEANQTLEGAGGSITSVD FDPSTGYQVLAATYNQVAQFWK*
177	916	3	139	QKRFPNSNCRDGLFLWGQALHI IAKLLGKWRLGMVFFSLLL SY
178	917	1	541	VHVCSSKMGALSTERLQYYTQELGVRERSGHSVSLIDLWGLLV EYLLYQENPAKLSDQAEAVRQGNPYPIYTSVNVRTNLSGED FAEWCEFTPYEVGFPGYKAYVPTLFGSELFGRLQLQPEPR ICYLQGMWGSASFATSLDEIFLKTAGSGLSFLEWYRGSVNITDD CQKPQLHN
179	918	1	628	EFLGRPTRPAKDEGNDEGKDEGKDEGKDEGKDEGKDERK DEGKDEGKDERKDEGKDEGKDEGKDEGKDEGKDEGKDEG NDEGKDEGKDEGKDEGKDEGKDEGKDERKDEGKDEGKDERKDE GKDDEGKDEGKDEGKDEGKDEGKDEGKDEGNDEGKDEGKDEGKD EGKDEGKDEGKDEGNDEGNDEGNDEGKDEGKDERNDEGKDEGK DEGKDEGKDERNDEGKDERKDEGKDEGKDEGKDEGKDEGKDEG NDEGKDERKDEGKDEGKDEGKDK
180	919	27	471	PSLRPAWHEGEDFSYGLQPYCGYSFQVVGEMIRNREVLPCPDD CPAWAYALMIEGWNEFPSSRRARFKDIHSRLRAWGNLSNYSSE QTSGGRTNTQTSSLSTSPLCNVSNAPYVGPKQKVPFPQTQVI PMKGQIRPMVPPPQLYVP
181	920	2	454	RNSGRHPRVRWILEERKRVMEACAKYRASSRRRAVTPRHVSR IFVEDRHRVLYCEVPKAGCSNWKRVLMVLAGLASSTADIQHNT VHYGSALKRLDTFDRQILHRLSTYTKMLFVREPFERLVSAFR DKFEHPNSYYHPVFCMAILAR
182	921	2	378	IMYSISPANSEEGQELYVCTVKDDVNLDTVLLLPFLKEIAVSQ LDQLSPPEQLLVKCAAIIGHSPHIDLQLHLLPGWDKNKLLQVL RALVDIHVLCWSDKSQELPAEPILMPSSIDIIDGTKEKK
183	922	181	513	GPHVVLVLRRCFLLSYFKGVEKAKAMPSRILKTHLSTQLLPP SFWENNCKVRYQQLPVTEGKVSQPKRVLQPTQSI RDHLCLST VSDAYQORENIKFYIQDIHLNSFK
184	923	32	239	FYYICRLSKEDKAFLWEKRYCYFKHPNCLPKILASAPNWKWVN LAKTYSLLHQWPALYPLIALELLDSK

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185	924	3	361	KMMI*GLFEIQQCPIGKHCNQLQVLRN/PNRDL/WLVSSFSGKS SKGRERMGGHDEYYRLRGR/HNPSPDHSYKRNSESERKRKSH *HMSKSQERHNSPSRGRNSDRSGGRCSRSDNGRSRYR
186	925	443	1412	PLSLFARVAGSRVEMPEPPGLGDEGRPLLHPGRREAVGSWVSA FAGDSTPCPGDLSVPRREPRLTAL*PHRSPVVRTSLIGLLL GFSVKEELRGVGVAAARTPLGIR
187	926	2	917	FDKRQHEARTIQMENEIHYLQENLKSMEEIQGLTDLQLQEADE EKERILAQLRELEKKKKLEDAKSQEQVFGDLKELKKLKKAVAT SDKLATAELTIAKDQLKSLHGTVMKINQERAEELQEAERFSRK AAQAARDLTRAEEIEELLQNLRLQKGEQFRLEMEKTGVGTGAN SQVLEIEKLNEMERQRTIARLQNVLYLTGSDNKGGFENVLE EIAELRREGSYQNDYISSMADPFKRRGYWYFMPPPSSSKVSSH SSQATKDSGVGLKYSASTPVRKPRPGQDQGEKSQPPASGYW VYSP
188	927	171	1082	SDASSFKTRVIVPRPRVFPLGSAITENSLESDSQIQGFVGVF YSAFLVADKVIVTSKHNNDTQHIWESDSNEFSVIADPRGNTLG RGTITITLVLKEEASDYLELDTIKNLVKKYSQFINFPIYVWSSK TETVEEPMEEEEAAKEEKEESDDEAAVEEEEEKKPKTKKVEK TVWDWELMNDIKPIWQRPSKEVEEDEYKAFYKSFSKESDDPMA YIHFTAEGEVTFKSIILFVPTSAPRGLFDEYGSKKSDYIKLYVR RVFITDDFHDMPKYLNFVKGVDSDDLPLNVSRETLOQHKLL KV
189	928	718	275	CGSWMRRALIPPCRGGPSASDRCCSCSPSGFSAGRGRCVPQGC LRPHRVQLLRRWGPSPAGQRLSKGFQLLRWGPSPAPEPRK GPFPPDPWPVTAVTVMAGSVPSAQSVDALESPPGLALEGPS SPRNLLWREMSIFLPGIF
190	929	1	550	PGPTPPPRHGSPPHRLIRVETPGPPAPPADERISGPPASSDRL AILEDYADPFVDQETGEGSAGASGAPEKVPENDGYMEPYEAQK MMAEIRGSKETATQPLPLYDTPYEPEEDGATPEGEGAPWPRES RLPEDDERPPEEYDQPWEWKKERISKAFVADIKVIKDLPPPPP VGQLDSSPSLP
191	930	1	562	QFFSLFLRYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVG YSTHMVGKWHLGFYRKECMPTRRGFDTFGSLGSGDYTHYK CDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQILASHN PTKPIFLYIAYQAVHSPLQAPGRYFEHYRSIININRRRYAAML SCLDEAINNVTLALK
192	931	3	580	RVRKGRGGERLQSPLRVPOKPERPPLPPKPQFLNSGAYPOKPL RNQGVVRTLSSSAQEDIIRWFKEEQPLRAGYQKTSDTIAPWF HGILTLLKANELLSTGMPGSFLIRVSEIRIKGYALSYLESDGC KHFLIDASADAYSFLGVDQLQHATLADLVEYHKEEPITSLGKE LLLYPCGQDQLPDYLELFE

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193	932	3	1641	GSLEKALFQLLKVGWQWAEQTRRLQRLDVSLSVARVRSAGPSC QNKGDLVMEALLEGIQNRGHGGGFLTSCEAELQELMKQIDIMV AHKKSEWEGRTHALETCLKIREQELKSLRSQLDVTHKEVGMLH QQVEEHEKIKQEMTMEYKQELKKLHEELCILKRSYEKLQKKQM REFRGNTKNHREDRSEIERLTAKIEEFQKSLDWEKQRLIYQQ QVSSLEAQRKALAEQSEIIQAQLVNRKQKLESVELSSQSEIQH LSSKLERANDTICANELEIERLTMRVNDLVGTSMTVLQEQQK EEKLRSEKLLLEALQEEKRELKAALQSQENLIHEARIQKEKLQ EKVKATNTQHAVEAISLESVSATCKQLSQELMEKYEELKRMEA HNNEYKAEIKKLKEQILQGEQSYSSALEGMKMEISHLTQELHQ RDITIASTKGSSSDMEKRLRAEMQKAEDKAVEHKEILDQLES LKLENRHLSEMVMKLELGLHECSLPVSPSGSIATRFLEEEELRS HHILERLDAHIEELKRESEKTVRQFTALK
194	933	159	1053	TGFLGWSQGPSLTPTSLSALYPSQVEETGVVLSLEQTEQHSRR PIQRGAPSQKDTTPNPGDSLDTPGPRILAFILHPPSLSEAALAD PRRFCSPDLRRLGPILDGASVAATPSTPLATRHQPSPSLADL PDELPVGTENVHRLFTSGKDTEAVETDLDAQDADALDLEMLA PYISMDDDFQLNASEQLPRAYHRPLGAVPRPRARSFHGLSPPA LEPSLLPRWGSDPRLSCSSPSRGDPSASSPMAGARKRTLAQSS KDEDEGVELLGVRPPKRSPSPEHENFLLFPLSLSFLLTG
195	934	3	425	ELQDCFDVHDASWEEQIFWGWHDVHIFDTKTQTWFOPEIKGG VPPQPRAAHTCAVLGNKGYIFGGRVLQTRMNDLHYLNLDWTW SGRITINGESPKHRSWHTLTPIADDKLFLCGGLNAYNMPLSDG WIHNVTTCHWK
196	935	2	295	FFFLRTRSHSVTPRWECSDDITAHWQPQWGSDDPLTFS/RPQ VVVPFRHTTLCPI\ANFFVFCIFCRNRISPCWPGWSRTPWAQLI RLPRPPKVLGLQV
197	936	2	737	PREGQVKQGLLGDCWFLCACAALQKSRHLLDQVIPPQPSWAD QEYRGSFTCRIWQFGRWVEVTDDRLPCLAGRLCFSRCQREDV FWLPLLEKVYAKVHGSYHLWAGQVADALVDLTGGLAERWNLK GVAGSGGQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGE ARGQHGRAAASVPPTARPOAHCSFLCDWLHSPVRTKWEEVSLF SRVSSVCDLPLLSSSRGTWPFSPLTSPFH
198	937	3	638	AECLEASIARYAHRVANSRYTFDGETVTLSPSQGVNQLHGGPE GFDKRRWQIVNQNDROVLFALSSDDGDQGFPGNLGATVQYRLT DDNRISITYRATVDKPCPVNMTNHVYFNLDGEQSDVRNHLQI LADEYLPVDEGGIPHDGLKSVAGTSFDFRSAKIIASEFLADDD QRKVKGYDHAFLQAKGDGKKVAHVWSADEKLQLKVYT
199	938	69	425	PLSRFLSKESQEDWGMERQSRVMSEKDEYQFQHQGAVELLVFN FLLILTILTIWLFKNHRFRFLHETGGAMVYDKPPKFAMSREQM SQSCSHTAHNASLLTDAGPLSCGESRASCLFL

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200	939	3	435	DSKEPRLQQLGLLEEEQLRGLGFRQTRGYKSLAGCLGHGPLVL QLLSFTLLAGLLVQVSKVPSSISQEQSRQDAIYQNLTLQKAAV GELSEKSKLQEIYQELTQLKAAVGELPEKSKLQEIYQELTWLK AAVGELPEKSKMQE
201	940	657	469	MQSIAGHRRDRGESPLGWGQSEASPSALTEAPKAAHTTRLG FLAANNPNGHSQPQDSFLL*
202	941	1	714	FETLSMRGIPHMLALGPQQLLAQDEEGDTLLHLFAARGLRWAA YAAAEVLQVYRRLDIREHKGKTPLLVAAAANQPLIVEDLLNLG AEPNAADHQGRSVLHVAATYGLPGVLLAVLNSGVQVDLEARDF EGLTPLHTAILALNVAMRPSDLCPRVLSTQARDRLDCVHMLLQ MGANHTIQVSGDVGQTLGDCVEWGHLDVRELQANADFASSLL RALEHVTSLLCALRVFCLFLCQL
203	942	3	479	DAWADAWVGTKMADLDSPPKLSGVQQPSEGVGGGRCSEISAEL IRSLTELQELEAVYERLCGEEKVVERELDALLEQONTIESKMV TLHRMGPNLQLIEGDAKQLAGMITFTCNLAENVSSKVRQLDLA KNRLYQAIQRADDILDLKFCMDGVQTALR
204	943	1	706	AVEFRVPRSGSAYLYSYVTVGELWAFITGWNILSYVIGTASV ARAWSSAFDNLIGNHISKTLQGSIALHVPVLAEPDFFALGL VLLLTGLLALGASESALVTKVFTGVNLLVLGFVMSGFVKGDV HNWKLTEEDYELAMAEINDTYSGLPLGSGGFVPPGFEGILRGA ATCFYAFVGFDCIATTGEEAQNQRSIPMGIGISLSVCFLADF AVSSALTLMPPYYQLQPESP
205	944	1	852	GFHPNTTHYRARAARAGAGSFVGEVSAVDKDFGPNGEVRYSF EMVQPDFELHAISGEITNTHQFDRESLMRRRTAVFSFTVIAT DQGIPQPLKDQATVHVYMKDINDNAPKFLKDFYQATISESAAN LTQVLRVSASDVDEGNGLIHYSIIKGNEERQFAIDSTSGQVT LIGKLDYEATPAYSLVIQAVDSGTIPLNSTCTLNIDILDENDN TPFF/LLNQHFFVDVLENMRIGELGASGTATDS\DSGDIADLY YKFTGTHKPPGTFSISPKHLGVFFLAQK
206	945	3	363	GDCYDLYGGEKFATLAELVQYYMEHHGQLKEKNGDVIELKNPL NCADPTSQRWFHGHLSGKEAEKLLTEKGKHSFLVRESQSHPG DFVLSVCTGDDKGESNDGKSKVTHVMIHCOELK
207	946	218	717	IDSGNQNGGNDKTKNAERNYLNVLPGEFYITRHSNLSEIHVA FHLCVDDHVKSGNITARDPAIMGLRNILKVCCTHDITTIPIPL LLVHDMSEEMTIPWCLRRRAELVFKCVKGFMEMASWDGGISRT VQFLVPQSISEEMFYQLSNMLPQIFRVSSTLTLSKH
208	947	3	368	SILPALLVTILIFMDQQITAVIVNRKENLKKAGVHLDLFWV GILMALCSFMGLPWYVAATVISIAHIDSLKMETETSAPGEQPQ FLGVREQRVTGIIIVFILTGISVFLAPILKCIPLPV
209	948	2	575	GASRVEAGSANGMLIDGGSQIVKVQGHADGTTINKSGSQDVVQ GSLATNTTINGGRQYVEQSTVETTTIKNGGEQRVYESRALDIT IEGGTQSLNSKSTAKNTHIYSGGTQIVDNTSTSDVIEVYSGGV LDVRGGTATNVTQHDGAILKTNNTNGTTVSGTNSEGAFSIHNHV ADNVLLENGGHLDINAYGS

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210	949	1	296	FFSSIQLTDDQGPVLMTTVAMPVFVSKQNETRSKGILLGVVGTDPVKELLKTI PKYKVMNDLIPEIKATEMPRALFSQSSGFKLYFGAMFLLTTITAC
211	950	3	594	SCSGTGTNACYMEDMSNIDLVEGDEGRMCINTEWGAFGDDGAL EDIRTEFDRELDLGS LNPGKQLFEKMISGLYL GELVRLILLKM AKAGLLFGGEKSSALHTKGKIETRHVAAMEKYKEGLANTREIL VDLGLEPSEADCI AVQHVCTIVSFRSANLCAAALAAI LTRLE NKKVERLRTTVGMDGTLYKIHPOY
212	951	2	2167	FVAIATNGVVPAGGSYYMISRSLGPEFGGAVGLCFYLGTTTFAG AMYILGTIEILLAYLFPAMAIFKAEDASGEAAAMNNMRVYGT CVLTCMATVVFVGKYNKFALVFLGCVILSILAIYAGVIKSA FDPNFPICLLGNRTLSRHGF DVCAKLAWEGNETVTTRLWGLF CSSRFLNATCDEYFTRNNVTEIQGIPGAASGLIKENLWSSYLT KGVIVERSGMTSVGLADGTPIDMDHPYVFSDMTSYFTLLVGIY FPSVTGIMAGSNRSGDLRDAQSIPTGTILAIATTSAVYISSV VLFGACIEGVVLRDKFGEAVNGNLVVGTLAWPSPWVIVIGSFF STCGAGLQSLTGAPRLLQAISR DGI VPFLOVFGHGKANGEPTW ALLLTACICEIGILIASLDEVAPILSMFFLMCYMFVNLA CAVQ TLLRTPNWRPRFRYYHWTL SFLGMSLCLALMFICSWYALVAM LIAGLIYKYIEYRGAKKEWGDGIRGLSLSAARYALLRLEEGPP HTKNWRPQLLVLRVDQDQNVVHPQLLSLTSQKAGKGLTIVG SVLEGTFLNHPQAQRAEESIRRLMEAEKVKGFCQVVISSNLR DGVSHLIQSGGLGGLQHNTVLVGWPRNWRQKEDHOTWRNFIEL VRETTAGHLALLVTKNVSMFPGNPERFSEGSIDRWGIGHDGGM LMLVPFLLRHHKVWRCKM RIFTVAQMVDMMHAM
213	952	1	128	FYLRLLSFFCFQEHEKRCWSVDFNLMDPKLLASGSDDAKGTV
214	953	3	244	RNSKAMHRSSCDGP LLSLPVGRSATHALVQAQLICSGARRGM HAFIVPIRSLQDHTPLPGKPIMLPQGTLP GGEP RPPP
215	954	2	609	CGTLILQARAYVGPVHLAVVTRTGFTAKGGLVSSILHPRPIN FKFKYKSMKFVAALSVLALLGTIYSIFILYRNRPVPLNEIVIRA LDLVTVVPPALPAAMTVCTLYAQSR LRQGFICIHPLRINLG GKQLQVCFDKTGTLTEDGLDVMGVVPLKGQAFPLPVPEPRRLP VGPLLRALATCHALSRLQDTPVGDPMDLKM
216	955	292	855	QIEYFRSLDEHHISYVIDEDVKSGRYMELEQRYMDLAENARF EREQLLGVOQHLSNLTLMKAEQDNKEAQEMIGALKERSHHMERI IESEQKGKAALAAATLEEKATVASDQIEMNRLKAQLENEKQKV AELYSIHNSGDKSDIQDLLESVRLDKEKAETLASSLQEDLAHT RNDANRLQDAIAKGRG
217	956	2	400	ARYRFTLSARTQVGSGEAVTEESPAPPNEATPTAAPPTLPPTT VGATGAVSSDATAIAATTEATTVP I IPTVAPTMTATTTT VAT TTTTAAATTTTESPPTTSGTKIHESAPDEQSIWNVTVL PNS KWA

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218	957	1	662	LKSTQDEINQARSKLSQLHESRQEAHRSLEQYDQVLDGAHGAS LTDLANLSEGVSLAERGSFGAMDDPFKNKALLFSNNTQELHPD PFQTEDPFKSDPFKGADPFKGDPPFQNDPFAEQQTSTDPFGGD PFKESDPFRGSATDDFFKKQTKNDPFTSDPFTKNPSLPSKLDP FESSDPFSSSSVSSKGSDFGTLDPFSGSGSFNSAEGFADFSTI EGRRG
219	958	1	752	RTRGGSGNSSQPSLREGHDKPVFNAGAGKPHSSTSSPSVPKTS SRTQKSAVEHKAKKLSLHPSHSRPGMVTPHNKAKSPGVRQPG SSSSSAPGQPSGTVARPTVSSGPVPRRQNGSSSSGPERSISGS KKPTNDSNPSRRTVSGTCGPGQPASSSSGGPGRPIGSGVSSARP LGSSRGPGRPVSSPHELRRPVSGLGPPGRSVSGPGRSISGSI AGRTVSNSVPGRPVSSSLGPGQTVSSSGPTIKPKCT
220	959	439	582	RGKGITPRYHLCISDPHNLKICCRVNGEVVQSSNTNQMVFKTE DLIAW
221	960	230	420	VVAVTRWLCENGVSYLKRCVCSACRHGTRCAGEVAAAANNSHC TVGIAFNAKIGGMGNQLTWM
222	961	311	490	GAPPPFVPTLKSDDDTSNFDEPKKNSWSSSPCQLSPSGFSGE ELPFVGFYSYKALGIL
223	962	2	422	FVERLAHLHAACAPRRKVALLLEVC RDVYAGLARGENQDPLGA DAFLPALTEELIWSPDIGDTQLDVEFLMELLDPDELGEAGYY LTTWFGALHHIAHYQPETDRAPRGLSSEARASLHQWHRRTLH RKDHPRAQQLD
224	963	385	844	FWMDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHT LLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVKKRVTFLEE VTEYYISGDEDRKGPWEEFARDGCRFQKRIQETEDAIGYCLTF EHRERMFNRLQGTCFKGLNVLKQC
225	964	3	166	AASTAYSFFGTVENMAPKVVRNPGHTQSADWGSFGGLMGRFEF GIFLKGEIVK
226	965	1	118	GFVFLPGPMSVGLDFSLPGMEHVYGIPEHADNLRLLKVT
227	966	1	390	GSECQGTDLDRNCTSDLCVHTASGPEDVALVGLIAVAVCLV LLLLVLILVYCRKKEGLSDVDADSSILTSGFQPVSIKPSKADN PHLLTIQPDLSSTTTTTYQGSGLCPRQDGPSPKFQLTNGHLLSPL G
228	967	1	777	LIYNEDMICWIESRESSNQLKCIQITKAGGLTDEWTINILQSF HNVQQMAIDWLTRNLYFVDHVGDRIFVCNSNGSVCVTLIDLEL HNPKAIAVDPIAGKLFFTDYGNVAKVERCDMDGMNRTRIIDSK TEQPAALALDLVNKL VYVVDLYLDYVGVDYQGNRHAVIQGR QVRHLYGITVFEDYLYATNSDSYNIVRISRFGNTDIHSLIKIE NAWGIRIYQKRTQPTVRSHACEVDYPYGMGGCSHICLLSSSYT K
229	968	3	488	SSGNPQPGDSSGGGAGGGLPSPGEQELSRRLQRLYPVAVNQOET PLPRSWSPKDKYNYIGLSQGNLRVHYKGHGKHNKDAASVRATH PIPAACGIYYFEVKIVSKGRDGYMGIGLSAQGVNMNRLPGWDK HSYGYHGDDGHSFCSSGTGQPYGPTFTTGdVI

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230	969	1	228	FFFFKMGSRSVTQAGVQWCDVSSLOAPPPRFTLFCLSLPSSWDYRCVPPCPANFFVFLVETGFHRVSQYGLDLTSLTS
231	970	2	119	QLSLARGKVFLCALSFVYFAKALAEGLKSTITQIERRVDIPS SLVGVIDGSFEIGNLLVITFVSYFGAKLHRPKIIGAGCVIMGV GTLIIAMPQOFFMEQYKYERYSPSSNSTLSISPCLLSSSSQLPV SVMESKSKISKISNECEVDTSSSMWIYVFLGNLLRGIGETPIQPL GIAYLDDFASEDNAAFYIGCVQTVAIIGPIFGFLLGSLCAKLY VDIGFVNL/DHF*VSAQLGTRKGVLCVLFCLLCQSIGRRLSE EHHHSDREKG
232	971	221	1068	QPAGRVEAFCKFHMWAEGMTSLMKAALDLTYPITSMFSGAGFN SSIFSVEFKDQQIEDLWIPYFAITTDITASAMRVHTDGLWRYV RASMSLSGYMPPLCDPKDGHLLMDGGYINNLPADVARSMGAKV VIAIDVGSRDDETDLTNYGDALSGWLLWKRWNPLATKVVLNM AEIQTRLAYVCCVRQLEVVKSSDYCEYL RPPIDSYSTLDFGKF NEICEVGYQHGRITVFDIWRSGVLEKMLRDQQGPSKKPASAVL TCPNASFTDLAEIVSRIEPAKPAM
233	972	133	635	LWVIMFVSYLILTLHLVQTAVLARPGGESIGCDDYLGSDDKVV KCGVCCGDNATGCVVSGVFKHALTSLGYHRVVEIPEGATKINI TEMYKSNNYLALRSRSGRSIINGNWAIDRPGKYEGGGTMTFTYK RPNEISSTAGESFLAEGPTNEILDVYVSLDVSGLFFGF
234	973	1	420	ISGSTRSAGPLRRNYNFIAAVVEKVAPSVVHVQLWGRNQOWIE VVLQNGARYEAVVKDIDLKLDLAVIKIESNAELPVLMLGRSSD LRAGEFVVALGSPFSLQNTATAGIVSTKQGGKELGMKDSMD YVQIDATINYG
235	974	2	860	PRVRELKEILDRKGHFSENETRWIIQSLASAIAYLHNNDIVHR DLKLENIMVKSSSLIDNNEINLNKIVTDFGLAVKKQSRSEAML QATCGTPIYMAPEVISAHDYSQQCDIWSIGVVMYMLLRGEPPF LASSEKLFELIRKGEHFENAVWNSISDCAKSVLKQMLKVPDP AHRITAKELLDNQWLTGNKLSSVRPTNVLEMMEKWKNNPESVE ENTTEKNKPSTEEKLKSYPWGNVPETNYTSDEEEKQVGR IAAFLPVSVKYPHHTWNIFLQICLFVVS
236	975	1	467	LSISVSDVSLSDDEGQYTCSLFTMPVKTSKAYLTVLGVPEKPQI SGFSSPVMEGDLMQLTCKTSGSKPAADIRWFKNDKEIKDVKYL KEEDANRKTFTVSSTLDFRVDSDDGVAVICRVDHESLNATPQ VAMQVLEMHYTPSVKIIIPSTPFPQEG
237	976	3	417	YNQKVDLFLSLGIFFEMSYHPMTASERIFVLNQLRDPSTPKF PEDFDDGEHAKQKSVISWLLNHDPAKRPTATELLKSELLPPQ MEESELHEVLHHTLTINVDGKAYRTIDGPRSFRQRISPAIA\YT YD\SDILKGN

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238	977	2	740	DQDYKYDSTSDSDSNFLNPPRGWDHTAPGHRTFETKDQPEYDST DGEGLWSLWSVCSVTCGNGNQKRTSCGYACTATESRTCDRPN CPGIEDTFRTAATEVSLLAGSEEFNATKLFVDTDCSERWMSC KSEFLKKYMHKVMNDLPSCPCSYPTVEVAYSTADIFDRIKKDF RWKDASGPKEKLEIYKPTARYCIRSMLSLESTTLAAQHCCYGD NMQLITRGKGAGTPNLISTEFSAEHLHYKVDV
239	978	2	612	ESEENGESAMDSVTAKEGTNVPLVAAGPCDDEGIVTSTGAKEE DEEGEDVVTSTGRGNEIGHASTCTGLGEESEGLICESAEGDS QIGTVVEHVEAEAGAAIMNANENNVDMSGTEKGSKDTDICSS AKGIVESSVTSVSGKDEVTPVPGGCEGPMTSAASDQSDSQLE KVEDTTISTGLVGGSYDVLVSGEVPECEVAH
240	979	79	361	VCIICLIFSYYFDSALQSAKSSLGNDLSATFLEMKGHFYM YAGSLLLKMGQHGNNVQWRALSELALCYLIAFQVSLPLGAID ISRSLDVF
241	980	2	681	QHPSQEKPVLTSPRQKLNRYRSHHDQMICKCLSLSLISYS ATIGGLTTIIGTSTSLIFLEHFNQYPASEVNVFGTWFLFSFP ISLIMLVSWFWMHWLFLGCNFKETCSLSKSKKKTREQLSEKR IQEYEKLGDISYPEMVTGFFFILMTVLWFTREPFGVPGWDSF FEKKGYRTDATVSVFLGLFLFLIPAKKPCFGKKNDDGENQEHSL GTEPIITWKDF
242	981	1	491	LEREGDKGTPVLRGFSVSGSWSRMPFFLLLTCLFITGTSVS PVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWH FTGMAGDAMPTFCIPENHCGTHAPVWLNHSHPLEGDGIVQRQA CASFNGNCCLWNTTVEVKACPGGYVYRLTKPSV
243	982	1	983	CGRTMSDIRHSLRRDALSAKEVLYHLDIYFSSQLQSAPLPI VDKGPVELLEEFVQVPKERSAQPRLNSLQELQLEIMCNYF QEQTKDSVRQIIFSSLFSPQGNKADDSRMSLLGKLVSMAVAVC RIPVLECAASWLQRTPVVYCVRLAKALVDDYCCCLVPGSIQTLK QIFSASPRFCCQFITSVTALYDLSSDDLIPMDLLEMIVTWIF EDPRLILITFLNTPIAANLPIGFLELTPLVGLIRWCVKAPLAY KRKKKPLSNHVSNNKVTKDPGVGMDRDSSLYSKLHLSVLQV LMTLQLHLTEKNLYGPPGADPLRPHG
244	983	32	362	SACSTGPELPGRATRSLTRPANQKGCDDRLYYDGCAMIAMNG SVFAQGSQFSLDDVEVLTATLDLEDVRSYRAEISSRNLAVSAP VDTVCVCSSKTWKVAPFVRAWWRP
245	984	158	398	APLSRLCFPQVLVNEGGGFDRASGSFVAPVRGVYSFRFHVVKV YNRQTVQVTSALAPIPGSGGWGGRRGAQLTSGWTLH
246	985	2	707	PHIIGAEDDDFGTEHEQINGQCSCFQSIELLSRPAHLAVFLR HVVSQFDPATLLCYLYSDLYKHTNSKETRRIFLEFHQFFLDRS AHLKVSVPDEMSADLEKRRPELIPEDLHRHYIQTMQERVHPEV QRHLEDFRQKRSMGLTLAESELTCLDAERDKDRLTLEKERTCA EQIVAKIEEVLMTAQAVEEDKSSTMQYVILMYMKHLGVKVKEP RNLEHKRGRIGFLPKIKQSM

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247	986	18	441	SPGTGRGPGPPTS FVCLPTPQCPFIDDFILALHRKIKNEPVVFP EGPEISEELKDLILKMLDKNPETRIGVPDIKLHPVWTKNGEEP LPSEEEHCSVVEVTEEEVKNSVRLIPSWTTVILVKSMLRKRSF GNPFEPQARMA
248	987	3	732	HASGIKIDKTS DGP KLF LTEDDQKKLHDFEEQCVEMYFNEKDD KFHSGSEERIRVT FERVEQMC IQI KEVGDRVNIKRSLQSLDS QIGHLQDLSALTVDTLKTLTAQKASEASKVHNEITRELSISKH LAQNLIDDG PVRPSVWKKHGVNTLSSSLPQGDLESNNPFHCN ILMKDDKDPQCNI FGQDLPAVPQRKEFNFP EAGSSSGALFP SA VSPPELRQRLHGV ELLKIFNKKQKKRA
249	988	3	468	CCRWIDCFALYDQQEELVRHIEKVHIDQRKGEDFTCFWAGCPR RYKPFNARYKLLIHMRVHSGEKPKNCTFEGCEKAFSRLENLKI HLRSHTGEKPYLCQHGPCQKAFSNSSDRAKHQORTHLDTKPYAC QIPGCTKRYTDPSSLRKHVKAHSSK
250	989	356	553	LPLLWTLSDFGGTMDQSGMEIPVTLLIKAPNQKYSQDTISCFL NWTVGKLKTHLSNVYPSKPVSV
251	990	1	895	AGTRMCVVA AAEELVCGA\RGLWMRRTRRPRFVLMNMDDLNL HYRFLNWRRRRIREIREVRAFRYQERFKHILVDGDTLSYHGNSG EVGCYVASRPLTKDSNYFEVSIVDSGVRGTIAVGLVPQYYS LD HQPGLPDSVAYHADDGKLYNGRAKGRQFGSKCNSGDRIGCGI EPVSFDVQTAQIFFTKNGKRVGSTIMPMSPDGLFPAVGMHSLG EEVRLHLNAELGREDDSVMMVDSYEDWGRLDVRVCGTLLEY LGKKGKSIDVGLAQARHPLSTRSHYFEVEIVDPGEKCYIA
252	991	51	674	QQAEEHLAAYSVS DSDSGKDP SMECCRRATPGTLLLLFLAFLLL SSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYS LRRLCLSSK SCEGRNIRYRTC SNVDCPPEAGDFRAQQCSAHNDVKHHGQFYE WLPVSNPDNPNCSLKCQAKGTTLVVELAPKVLDTGTRCYTESLD MCISGLCQVSADLFSFNLSRGFQCCLCVNGLHSLTL
253	992	2	554	RLLRQELVVLCHLHHPSLISLLAAGIRPRMLVMELASKGSLDR LLQQDKASLTRTLQHRIALHVADGLRYLHSAMI IYRDLKPHNV LLFTLYPNAAI IAKIADYGIAQYCCRMGIKTSEGTGPFRAPEV ARGNVIYNQQADVVSFGLLLYDILTTGGRIVEGLKFPNEFDEL EIQGLPDPVKE
254	993	3	437	KASNSTHEFRIGLPEGWESEKKAVIPLGIGPPLTLICLGLVGG ILIIYGRKGFTAHFYLDSPSPKVI STPPPIFPI SKEVGPPI IKHFPKHVANLHASRGFTEKFETLKKFYQEGQSC T VDLGITAN SSNHPDNRHRNRS LI
255	994	3	445	SFPDRTASLVLLSVFVGQAGMQORGLAIVALAVCAALHASPAI LPIASSCCTEVSHHISRLLERVNMCRIQRADGDCDLAAVILH VKRRRI CVSPHNHTVKQWMKVQA AKKNGKGNVCHRKHHGKRN SNRAHQGHETYGHKTPY

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256	995	2	737	FEQPGNPGDPRVRTPPPWGPHFFALIPSSPKEVPATPSSRRDP IAPTATLLSKKTPATLAPKEALIPPAMTVPSPKKTPAIPTPKE APATPSSKEASSPPAVTPSTYKGAPSPKELLIPPAVTSPPSPE APTPPAVTPPSPEKGPATPAPKGTPTSPPVTPSSLKDSPTSPA SVTCKMGATVPQASKGLPAKKGPTALKEVLVAPAPESTPIITA PTRKGPQTKKSSATSPPICPDPSAKNGSKG
257	996	79	3	FFLKIQGLGWARWLTPVIPVLWEAE
258	997	307	475	AGFGYGLPISRLYAKYFQGDNLNLYSLSGYGTDAIYLVKSLEF NSKILFLKPLLLL
259	998	26	622	WMRAPMLQKQAPRMDTPPPEERLEKQNEKLNQEEETEFKEL DGLREALANLRGLSEERSEKAMLRSRIEEQSOLICILKRRSD EALERCQILELLNAELEEKMMQEAELKAQGEYSRKLEERFMT LAANHEMLRFRKDEYKSENIKLRENEKLRLENNSLFSQALKD EEAKVLQLTVRCEALTGELETLKERC
260	999	2	241	DPGASHASVQVQVLKEQLFAGRMPSPPFRSCALMGMCGRSADN LSCPSPLNVMEPVSFPLKSLGKGMIIQFHRHIVSLV
261	1000	1	620	VTTHTHSVGRGHELQLLNEELRNIELECONIMQAHRLQKVTDO YGDITWTLHDGGFRNYNTSIDMQRGKLDIMEHPEKSDKDSSSA YNTAESCRSTPLTVDRSPDSSLPRVINLTNKNLRSTMAATQS SSGQSSKESTSTKAKTTEQGCSAESKEKVLGSKLPDQEKAVS EHIPYLSYPYHSSRYANIPAHARHYQSYMQLIQ
262	1001	3	420	VWGCLATVSTHKKIQGLPFGNCLPVSDFNNSTGIPFFYMTA KDPVVADLMKNPMASLMLPESEGEFCRKNIVDPEDPRCVQLTL TGQMIAVSPEEVEFAKQAMFSRHPGMRKWPRQYEWFFMKMRIE HIWLQKWYG
263	1002	43	441	QAANMAVARVDAALPPGEGSVVNWSGQLQKLGPNLPCEADIH TLILDKNQIIKLENLEKCKRLIQLSVANNRLVRMMGVAKLTLL RVLNLPNHSIGCVEGLKELVHLEWLNLAGNNLIAMEQINSCTA LQHL
264	1003	3	834	FRAAVGAVPEGAWKDTAQLHKSEEAQRVLRYYLFQGGQRYIWIE TQQAFYQVSLLDHGRSCDDVHRSRHGLSLQDQMERKAIYGPV ISIPVKSYPQLLVDEAFSIALWLADHYWYALCIFLISSISIC LSLYKTRKQSQTLRDMVKLSMRVCVCRPGGEEEWVDSSELVPG DCLVLSQEGGLMPCDAALVAGECMVNDSSLTGESIPLVLTALP EGLGPYCAETHRRHTLFCGTLILHARAYVGPHVLAVVTRTGMS REAGLERDPSAPLKRWS
265	1004	2	670	FVGGGLHLHLCLLLCFMLPEDAAMAVLTASNHVSNVTVNYNIT VERMNRMQGLRVSTVPAVLSPNATLALTAGVLVDSAVEVAFLW TFGDGEQALHQFQPPYNESFPVPDPSVAQVLVEHNVHTHTYAAP GEYVLTVLASNAFENRTQQVLIRSGRVPISLECVSCKAQAVY EVSRSYVYLEGRCLNCSSGSKRGRWAARTFSNKTTLVDETTT STGSASM

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266	1005	2	1093	PEFLGRLFRGKAATLHVHSDQKPLHDGALGSQQNLVRMKEALR ASTMDVTVLVLPSPGLEKRSVLNGSHAMMDLLVELCLQNHLP SHALEIRSETQOPLSFKPNTLIGTLNVHTVFLKEKVPPEEKVKP GPPKVPEKSVRLVVNYLRTQKAVVRVSPEVPLQNILPVICAKC EVSPEHVVLLRDNIAGEELELSKSLNELGIKELYAWDNRRETF RKSSSLGNDETDEKKEKKFLGFFKVNKRNSKGLTTPNSPSMHS RSLTLGPSLSLGSISGSVSKSEMKRRAPPPPGSGPPVQDKAS EKVSLGSQIDLQKKRRAPAPPPPPQPPPPSPLIPNRTEDEKEN RKSTMVYCCASFPTQAKRF
267	1006	686	400	VQWHNLHSLQPLPAGFK*FLCFSLPSSWDYRCAPPLP/APFFF YFLEFLVELGFHHIG*AGLELTSTDLPASAS/ESAGITGMSHRA RPMDFLLKIL
268	1007	1	453	GRRFRPPSDEEREPEWEPWTQLRLSGHLKPLHYNMLTAFMENF TFSGEVNVEIACRNATRYVVLHASRVAVEKVQLAEDRAFGAVP VAGFFLYPQTQVLVVVLNRTLDAQRNVLKIIYNALIEENLLG FFRSSYVLHGERRFLGVTQFSP
269	1008	333	526	KELDPFYNS*RKIKYLRIYLTKEVKDLYKENYKTLLEITDDT N/KKHIPSSWTGRINTVKMTIL
270	1009	699	882	VPHPLQAIHEQMNCKEYQEDLALRAQNDAAARRPSEMFKVRLA QGRGLASLSSGIQSGVG
271	1010	16	148	RWNSLTVCVLTFLGHRLLKRFLVPKLRRFLKPOGHPRLLLWFK R
272	1011	1	659	YGEFVTYQGVAVTRSRKEGIAHNYKNETEWANIDTVMWFTE EDLDLVTLYFGPEPDSTGHRYGPESPERREMVRQVDRTVGYLRE SIARNHLTDRNLIIITSDHGMTTVDKRAGDLVEFHKFPNFTFR DIEFELLDYGPNGMLLPKEGRLEKVYDALKDAHPKLHVYKKEA FPEAFHYANNPRVTPLLMYSDLGVIHGVSRLLLEAPPPGAPSP GSGS
273	1012	146	413	RIPLRLRLRSSTYRSKGFDTVKSHSGSWTGPFGGEDLATIPKGL NTYFLVNIATIFESKNFFLPGIKWNGILGLSYATLAKPSSSLE TFF
274	1013	3	251	IKSYSGPNGRSCQIWQRLRWGSRELLLGWKLSSHSTFCPFQFP DIVEFCEAMANAGKTVIVAALDGTQKVRRLIQVWSWD
275	1014	326	651	YCFCDLLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPPELPVGDTOY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPCKS/DMLDQLYLIRK
276	1015	224	435	RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL
277	1016	2	429	GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPCEGKPYNQKSDI WALGCVLYELASLKRAF EAANLPALVLKIM

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278	1017	1	262	VQCGGIHQVSGAVVVSGLLQGMMLGSPGHVFPHCGPLVLAP SLVVAGLSAHREVAQFCFTHWGLALLYVSPERRGMVPSGGVWG D
279	1018	1	480	PRMTGSTHASAPSYGGSCRNNLFYREETYTPKAETDEMNEVET APIPEENHVWLQPRVMRPTKPKKTSAVNYMTQVVRCDTKMKDR CIGSTCNRYQCPAGCLNHKAKIFGSLFYESFASICRAAIHYGI LDDKGGGLVDITRNGKVPFFVKSERHGVQSLR
280	1019	271	792	VPQNIICAFFCVPCRFASITPFWGLTLHLQHLGNVFLQTLF GAVTLLANCVAPWALNHMSRRLSQMLLMFLLATCLLAIIFVPQ EMQTLRVVLATLGVGAASLGITCSTAQENELIPSIIRGRATGI TGNFANIGGALASLVMILSIYSRPLPWIIYGVFAILSGLVLL LP
281	1020	2	679	VLVSRDHMSAQQFFQLVGGSAECDTIPGRQCMASCFLLKQ FDDVLIYLSNFKSHFYNDIIFNFNYAQAKAATGNTSEGEAEFL LIQSEKMKNDYIYLSWLARGYIMNKKPRLAWELYLKMETSSES FSLQLLIANDCYKMGQFYYSAKAFDVLRLDPNPEYWEKRGGA CVGIFQMI IAGREPKETLREVLHLLRSTGNTQVEYIMIRIMKKW AKENRVSILK
282	1021	3	359	LKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVREITVHQRTVDFVALHIVTLL LPQLSHFFCLRIERVIIYLEKPIFARLRWLM
283	1022	3	538	GVPRNLPSLSLEYLLSYNRIVKLAPEDLANLTALRVLDVGGNC RRCDHAPNPMCPCPRHFPQLHPDTFSLSRLEGLVLKDSLSW LNASWFRGLGNLRVLDLSENFYKCI TKTKAFQGLTQLRKLN SFNYQKRVSFAHLVSGPPFLRGS LGRPLKGAGTWHGNLSFPLH FEWGKT
284	1023	3	442	ILFAALIWSSFDENIEASAGGGGGSSIDAVMVD SGAVVEQYKR MQSQESSAKRSDEQRKMKEQQAEEELREKQAAEQERLQLEKE RLAAQEQKKQAEAAKQAE LKQKQAEAAAKAAADAKAKAEAD AKAAEEAAKKAADAKK
285	1024	1	119	AMEIVHEPRDLERYMREAVKVSNDSPVLLDRFLNDAIEC
286	1025	67	227	MLSPGYDYGVCVEFSLLEDAIGCMEANQVALYFGQMMLEGYI FLYMGREGFK
287	1026	2	1101	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRV IARPVGSSVRL KCVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRP EDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPVLTGTHPVNT TVDFGGTTSFQCKVRSVDPKPIQWLKRVEYGAEGRHNSTIDVG GQKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGAN TMGYSFRSAFLTIVLPDPKPPGPPVASSSSATSLPWPVVIGIPA GAVFILGTLLLWLCAQKKPCTPAPAPPLPGHRPPGTARDRSG DKOLPSLAALSAGPGVGLCEEHGS PAAPQHLLGPGPVAGPKLY PKLYT\ DIPHHTHTHTPHPPAN
288	1027	3	96	NFHFTGKCLFMSGLSEVQLTHMDDHTLPGY

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289	1028	95	407	SPRKRKTRHSTNPPLECHVGWVMDSRDHGPGTSSVSTSNASPS EGAPLAGSYGCTPHSFQHPHPSHELLKENGFTQQVYHKYRRR CLSERKRLGIGSQEMNT
290	1029	1	359	PGSGGSAGGRDGSAYQGALLPREQFAAPLGRPVGTSYSATYPA YVSPDVAQSWTAGPFDGSLHGLPGRRPTFVSDFLFEFPGEGR ECVNCALSTPLWRRDGTGHYLCNACGLYHKMN
291	1030	2	513	PDHRHGALWWWYSCGVLPTVSRNEGDERNQVLTLYLWIRQEW TDAYLRWDPNAYGGLDAIRIPSSLVWRPDIVLYNKYCLS/AAP PLSYPSLDLPLAVGV**SPLPTT*PGCHAALEAFPQDPSKLP TQPLHGTPTLGYPRPAQAERLLGTTCVVGRCINHKLSRAHF
292	1031	1	595	YALTGALVIVTGMVMGNIADYFNLFPVSSMSNTFTFLNAGILIS IFLNAWLMEIVPLKTQLRFGFLMLVAVAGLMFSLALFSAA MFI LGVVSIGITMSIGTFLVTQMYEGRQGRSRLLETFDSFFSMAG MIFPMIAAFLARSIEWYWVYACIGLVYVAIFILTFGCEFPAL CSHATKLGTASSYPSLDVVQLRTLNA
293	1032	71	479	MAKVGLKTEHYDRYPHMFSGGQRQRIATARGMLDPDVVIAD PVSALDVSVRAQVLNLMDLQQLGLSYVFIHDLVSVEHIAD EVMVMYLGRCVEKGTQDQIFNNPRHPYTQALLSATPRLNPD RERIKLSX*
294	1033	2	427	SATLERVLNHPDETQARRLMTLEDIVSGYSNVLISLADSQGKT VYHSPGAPDIREFTDAIPDKDAQGGEVYLLSGPTMMMPGHGH GHMEHSNWRMINLPVGPLVDGKPIYTLIALSIDFHLHYINDL MNKLIMTASVII
295	1034	3	342	VLAYPGIKVSTAEARAILPAQYRRQDCIAHGRHLAGFIHACYS RQPELAALKMKDVIAEPYRERLLPGFRQARQVAEIGAVASGI SGSGPTLFALCDKPEAQRVADWLK
296	1035	2	279	GQQQRVALARALILKPKVLLFDEPLSNLDANLRRSMRDKIREL QKQFDITSLYVTHDQSEAFVSDTVLVMNKGHIMQIGSPQDLR VRLINW
297	1036	3	157	AVHYLERVRIAHAHKFPGQISGGQQQRVAIARSLCMKPKIML FDEPTSAL
298	1037	1	217	APYDAENYFDYDNLNNGPSLQHWFGVDSLGRDIFSRVLVGAQI SLAAGVFAVFAGIAIGTLLGLLAGYYEGW
299	1038	3	570	VFCLIAIDLDPIDELVDFPIVYASALNGIAGLDHEDMAEDMTPL YQAIVDHVPAPDVLDGPFQMQISQLDYSYVGVIGIGRIKRG KVKPNQQVTIIDSEGKTRNAKVGKVLGHLGLERIEITDLAAGD IVAITGLGELNISDTVCDTQNVLEALPALSVDIPTVSMFFCVNT SPFCGKEGKFVTSRQI
300	1039	1	366	QGTAEASQSSKDKTRLAFAAGLKFQDYGSDYGRNYGVAYDIG AWTDVLPFEGGDTWTQTDVFMTRATGVATYRNNDFFGLVDGL NFAAQYQGNDRSDFDNYTEGNHGFSGFSATYEG
301	1040	3	201	DTYSVSIPLGATINMAGAAITITVLTAAVNTLIGIPVDLPTAL LLSVVASLACAGSGVAGGSLL

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302	1041	1	140	ANAQQGLPSGITLKLNNLVDKGLVDRLYAASSSGVPVNNLLVRG TCS
303	1042	2	442	ARMTLIPGTHLLENIHNIWNGVGTNSAPFWRMLLNSFVMAFS ITLGKITVSMLSAFAIVWFRFPLRNLFFWMIFITLMLPVEVRI FPTVEVIANLQMLDSYAGLTPLMASATATFLERKLNMSGPDK VVPAARISGYGPRVRKQ
304	1043	2	403	CAKCLRDADECPSGAFERIGRDISLDALEREVMKDDIFFRTSG GGVTLSSGGEVLQAEFATRFLQRLRLWGVSCAIETAGDAPASK LLPLAKLCDEVFLDKIMDATQARDVVKMNLPRVLENLRLLLVS EGVN
305	1044	1	346	YLLLFVCFLVMSLLVGLVYKFTAERAGKQSLDDLMNSSLYLMR SELREIPPHDWGKTLKEMDLNLSFDLRVEPLSKYHLDDISMHR LRGGEIVALDDQYTFQRIPRSHYVLAVG
306	1045	1	207	VELFLSDEGDDVVIEVADQGCQVPESLRDKIFEQGVSTRADEP GEHGIGLYLIASVYVTRCGGVITLEDN
307	1046	3	213	DAIIAPDANALPAAQAENLKNKVAIVGFSTPNVMRPYVER GTVKEFGLWDVVQQGKISVYVADALQ
308	1047	1	129	YIVVTGKTHCGTPLTTVTGDATQSGYLTNLNPEMWEVSGYNRV
309	1048	271	46	XEGVEPDINASKTRQQLNDVAGKMKIIEARLSALTNNQTKSLK LNPVALPKVASQLLDELGYSLARRADLQSAHX*
310	1049	16	253	ENIAEEYATKRYRSNVINWGMLPLQMAEVPTFEVGDYIYIPGI KAALDNPGETTFKGYVIHEDAPVTEITLYMESQEART
311	1050	2	299	LQTEIGSMVYAVKPGDGSAREQAASCQRVIGGLANIAEEYATK RYRSNVINWGMLPLQMAEVPTFEVGDYIYILGFKAAYSPGTA FTVYAISGYGPRI
312	1051	1	344	TLEDLLMALDGEQHLQQQVSEKVLADNVLIAPGSVKPDATFWS ALIQDRYNVMTICIEKDACVLVEQDLNSDQGAERILFAFNDDRIV YVGFDSDRKEWDALDMSLLPNEITKEK
313	1052	2	630	ESNSRCRKMPGERCRGGPARLSLLLDLPTRPLPHPRQVIDFGS ASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCV MDELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAACKAHH FFKRNPHPDAAANPWQLKSSADYLAETKVRPLERRKYMLKSLDQ IETVNGGSAVSRITFPDREALAEHADLKSMMVEL/MKRL
314	1053	1	302	RLVKKRVECRQCGKAGRNQSTLKTMRSHTEGKPYECDHCGKA FSIGSNLNVHRRHTGEKPYECLVCGEAFSDHSSLRSHVKTHER GEKLFVSSVWKRLQ
315	1054	1318	730	CGPGFSLSFFFLRWSF\ALVAQAGVQWHDLGSLQPPAPGFKRF SSLSLLSRWDYRHAHARLI FVFLVEMGFLHVQAGLELPTSGD PPTSASQSARITGVTTPLGTFFFFLRFWSFALVAQAGGCQLDLG SLQLPPPFGKRLVCHFQTPQKHRCSCQAPGDCLOESFVMTGCV LRTVSESQVRANAGAGAETVQGL

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316	1055	2486	1429	MGNAAAANKGSEQESVKEFLAKAKEDFLKKWESPAQNTAHLDDQ FERIKTLGTGSPGRVMLVKHKETGNHYAMKILD*QKVGKLGQI EHTLNEKRILQAVNFPFLVKLEFSFKDNSNLYMVMEYVPGGEM FSLRRIIRGFSEPHARFYAAQIVLTFEYLHSLDLIYRDLKPEN LLIDQQGYIQVTDGFAKRVKGRWTWLCGTPEYLAPEIILSKG YNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRP PSHFSSDLKDLLRNLLQVDLTKRFGNLKNGVNDIKNHKWFATT DWIAIYQKVEAPFIPKFKGPGDTS\NFDDYEEEEIRV\SINE KFG\KEFSEF
317	1056	867	461	SSSRSSHGDSPPHSQTPCDTNRGLDTKH*/DSQSIEEKDSSQS E*NRIERRKEVERILQTNSDYM*HWSN*PENILPKKFFSKHQK CTATLSMRNTSIM/KKEGLF*AQFPSLLLSHLPAVGLGIYTG HLTTSTSTF
318	1057	544	784	TFHSSLEKNILQPCR*RR\ICLPLLL*PSVPLLAPQYFSDLR NSIVNSQPPEKQAMHLCFENLMEGIERNLLTKNRDR
319	1058	1606	228	GTSGVQQEISRLTNENLDLKELEKNERKLKQLKRIYMKK AQDLEAAQALAQSERKHELNROVTQORKEKDFQGMLEYHKED EALLIRNLVTDLPQMLSGTVPCLPAYILYMCIRHA\DYTNDD LKVHSLLTSTINGIKVLKKNDDFEMTSFWLSNTC\RLHLCL KOYSGDEGFMTQNTAKQ\EHCLKNFDLTYRQV\L\SDLSIQ IYQQLIKIAEGLVQPMIVSAMLEN*SIQGLSGVKPTGSQKHSS SMADEDNSYRLEAIIROMNAFHTVMCDQGLDPEIILQVFKQLF YMINAVTLNDLLLRKDVCSWSTGMQLRYNISQLEEWLGRNLH QSGAVQTMELIQAQALLQLKKKTQEDAEAI CSLCTSLSTQOI VKILNLYTPLNEFEERVTVAFIRTIQAQLQERNDPQQLLLDAK HMFVPLFPFNPSSLTMDSIHIPACLNLEFLNEV
320	1059	3	250	HEENTILKAAEVQVPPK*VVTPEAKAFI*RCLAYQKEDCIDAQ QLACDP\YLLHYIQKLVFVSSPAGAAIASTFGVSNSSCN
321	1060	1332	500	GTTDEIMTRWARVSTTYNKRPLPATSWEDMKKGSFEGTSQNL KRKQLEANRLSLKNDAPQAKHKKNKKKEYLNEDVNGFMEYLR QNSQMVHNGQIIATDSEEVREEIAVALKKDSRREGRRLLKQAA KKNAMVCFHCRKPGHGIADCPAALENQDMGTGICYRCGSTHE ITKCKAKVDPALGEFPFAKCFVCGEMGHLSRSCPDNPGLYAD GGGCKLCGSVEHLKKDCPESQNSERMVTVGRWAKGMSADYEEI LDVFPKPKPKTKIPKVVNF
322	1061	384	102	DHVRKSLKNAENIVNIFKCNVVSLEPNLPAFGQAQWLTPVIP ALWEAEVGG*GQEIETILANAVK/SPFLKIQKKKISRWW AP/VSPRYSGG

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323	1062	1	777	SDAWADAWARSLSVSPSSYPELHTEVPLSVLILGLLVVFILSV CFGAGLFVFLKRRKGVPSPRNTNNLDVSSFQLOQGSYNTET HDKTDGHVYNYIPPPVQMCQNPIYMAGREGRPSSLLPKPGKE FQLLGNLEEKKEEPATPAYTISATELLEKQATPREPELLYQNI AE/PSQGS/TAQA*STITFVPYLKGQFAPSYESRRQNQDRIN KTVLYGTPRKCFVGQSKPNHPLLQAKPQSEPDYLEVLEKQTAI SQL
324	1063	1	1496	ALCHIAVGQQMNLHLHKLGLVVLASTVAVMSAVAQLWEDEW EVLILISLQGTAPFLHVGAVAAVTMLSWIVAGQFARAERTSSQV TILCTFFTTFVVALYLAPLTISSPCIMEKKDLGPKPALIGHRGA PMLAPEHTLMSFRKALEQKLYGLQADITISLDGVPFLMHDTTL RRTTNVEEEFPELARRPASMLNWTTLQRLNAGQWFLKTDPFWT ASSLSPSDHREAQNSICSLAELELAKGNATLLNLNRDPPRE HPYRSSFINVTLEAVLHSGFPQHQMVLPSRQRPLVRKVAPGF QQTSGSKEAVASLRGHIQRLNLRYTQVSRQELRDYASWNLSV NLYTTNAPWLFSLWCAGVPSVTSNSHTLSQVPSPLWIMPPD EYCLMWVTADLVSTTLIVGIFVLQKWLGGIRSYNPEQIMLSA AVRRTSRDVSIMKEKLIFSEISDGVEVSDVLSVCSDNSYDTYA NSTATPVGPRGGGSHTKTLIERSGR
325	1064	1899	776	NSADYGDGPDSSDADPDSGTEGVLDPSDPFSTEVKPRILLMG LRRSGKSSIQKVVFHKMSPNETLFLESTNKICREDVSNSSFVN FQIWFDPGQIDFFDPTFDYEMIFRGTGALIFVIDSQDDYMEAL ARLHLTVTRAYKVNTDINFEVF IHKVDGLSDDHK IETQORDIHQ RANDDLADAGLEKIHLSFYLTISIYDHSIFEAFSKVVQKLIPQL PTLENLLNIFISNSGIEKAFLFDVVSKIYIATDSTPVDQMOTYE LCCDMIDVVIDISCIYGLKEDGAGTPYDKESTAIKLNNTTVL YLKEVTKFLALVCFVREESFERKGLIDYNFHCFRKAIHEVFV RMKVVKSRKVQNRLQKKKRATPNGTPRVLL
326	1065	1181	346	RTRGRDPGAGFRRTANKRCCRRRFLIGCGWLPLRSDWPLVSKM LSKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPVAVASS LFDLSVLKLHHSLOQSEPDLRHLVLVNTLRRIQASMAPAAAL PPVPSPPAAPSVADNLLASSDAALSASMASLLEDLSHIEGLSQ APQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGL FEDIDTSMYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELD YLMDVLVGTQALERPPGPGR

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327	1066	1844	337	LQEVKARRNTLHKEKDHLVNDYEQNMKLLQTKYDADINLLKQEHALSASKASSMIEELEQNVQQLKQQLQESLQKQQLRDQENKFQMEKSHLKHIEYKKAHDLQSELDKGKEDTQKKIHKFEEALKWKKWRQI*LDPN/LLREKQSKFELWQLEDIRQRYEQQIVELKLEHEQEKTHLLQQHNAEKDSLVRDHEREIENLEKQLRAANMEHENQIQEFKKRDAQVIADMEAQVHKLREELINVNSQRKQQLVELGLLREEEKQRATREHEIVVNKLKAESEKMKIELKKTAAETEMTLEKANSKLKQIEKEYTQKLAKSSQIIAELQTTISSLKEENSQQQLAAERRLQDVRQKFEDEKKQLIRDNDQAIKVLQDELENRSNOVRCAEKKLQHKELSESQEQITYIRQYETKLKGLMPASLRQLEDTISSLSKQVNFLOKRASILQEE/RDYISRQKVQPISR*LHERMQRMRIISRLCCGTSSSRFEDLDIVNCEISGIF
328	1067	1149	238	VINLVYLISPRPELKPVDKESEVVMKFPDGFKEKFSPPILQLDEVDFYDPKHVIFSRLSVSADLESRICVVGENGAGKSTMLKLLLGDLAPVRGIRHAHRNLKIGYFSQHHV/EQL/DLNVQCLWELAGHASFPGRPEEEY\RHQLGFGMGISGEL\AMRPLCQPVLGARKKPKWPFAQMDYCPAPTFYIL\DEPTN\HLGHGRAIEALGPCLQTISGVGVILVSHESALSRLVCRE\LWVC*G\GGVTRVERKDFDQYRALLQGTVSAREGFPLGPPRLKDSPRDMGLVSQTPWGGHHVGYPLPGRG
329	1068	26	674	CSAVEVKMAARTAFGAVCRRLWQGLGNFSVNTSKGNTAKNGGLLLSTNMKWVQFSNLHVDVPKDLTKPVVTISDEPDILYKRLSVLVKGDHKAVIDSYEYFAVLA AKELGISIKVHEPPRKIERFTLLQSVHIYKKHRVQYEMRTLRYRCLELEHLTGSTADVLEYIQRNLP EGVAMEVTKFCFFIFL\TQLEQLPEHIKEPIWETLSEEKEESKS
330	1069	2105	1283	DFWDTAGQERFQSMHASYYHKTHACIMVFDVQRKVTHRNLSWYTELREFRPEIPCI VVANKIDGGAIPAPGC*QFTGDLPSYISSIPRAGNLQ*LVLPP TIRYNPWL VACILPTL*RSQLSRPALFPRHRSLLTELFLGPVSQSSLP IPLSGMKASSGPPLQTFPPSLDRQTNVLP SLY\ADINVTQKS FNF AKKFSLPLYFVSAADGTNVVKLFNDAILRAVSYKQNSQDFMDEIFQEL ENFSLEQEEEDVPDQE QSSSIETPSEEVASPHS
331	1070	1	1109	GATPLGSVGGRTGKMDAATLT YDTLRF AEFEDFPETSEP VWILGRKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGCMLRCGQMIFAQALVCRHLGRDWRWTQRKRQPD SYF SVLNAFIDRKDSYYSIHQIAQMGVGEKSGIQWYGPNTVAQVLKKLAVFDTWSSSLAVHIAMDN TVMEEIRRLCRTSVPCAGATAFPASDRHCNGFPAGAEVTNRPS PWRPLVLLIPLRLGLTDINEAYVETLKHCFM\MPQSLGVIGGKPNSAH\YFIG*VG\EELIYLDPHTTQPAVEPTDGC FIPDES FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAFGAECCLGMTRKTFGLRFFFSMLG
332	1071	39	284	ALCVVPFNFTFHN\DFLLLDKEGTLDPVMSFSSTHWT TIGPADMFFS\FRQHYKNFKSHGTNPSKSVWAHATCQSCAFFNLLGW

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333	1072	2	1484	TRLAIEFGTRDPCAQAPCEQQCEPGGPGQYSCHCRLGFRPAEDD PHRCVDTDECQIAGVCQCMCVNYVGGFECYCSEGHLEADGIS CSPAGAMGAQASQDLGDELLDDGEDEDEDEAWKAFNGGWTEM PGILWMEPTQPPDFALAYRPSFPEDREPQIPYPEPTWPPPLSA PRVPYHSSVLSVTRPVVVSATHPTLPSAHQPPVIPATHPALSR DHQIPVIAANYPDLP SAYQPGILSVSHSAQPPAHQPPMISTKY PELFPAHQSPMPDTRVAGTQTTTHLPGIPPNHAPLVTTLGAQ LPPQAPDALVLRQTATQLPIIPTAQPSLTTSRSPVSPAQHS VPAATQPAALPTLLPSQSPTNQTSPISPTHPHSKAPQIPREDG PSPKLALWLPSAPTAAPTALGEAGLAHSQRDDRWLLVALLV PTCVFLVLLALGIVYCTRCGPHAPNKRITDCYRWVIHAGSKS PTEPMPPRGS LTGVQTCRTSV
334	1073	1	1406	LRVRRRPHLPAPPALRARRSDRRSSRAPAAFPPRPPHASPAPG PAMAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTDSPA TTGAVVTISASLVAKDNGSLALPADAHLYRFHWIHTPLVLTGK MEKGLSSTIRVVGHVPGEFPVS VWVTAADCWMCQP VARGFVVL PITEFLVGD LVVTQNTSLPWSSYLTKTVLKVS FLLHDP SNFL KTALFLYSWDFDGTQMVTEDSVYYNYSIIGTFTVKLKVVAE WEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVLGPTLIQTF QKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAY NLTHTRDPGDYCF SIRAENIISKTHQYHKIQVWPSRIQPAVF AFP CATLITVMLAFIMYMTLRNATQQKDMVENPEPPSGVRCCC QMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV
335	1074	1	866	VVEFAFQLSSVSCLTVSFGWQLGTVSSCLSRDWFLKGNLLII IVSVLIIILPLALMKHLGYLGYTSGLSLTCMLFFLVSVIYKKFQ LGCAIGHNETAMESEALVGLPSQGLNSSCEAQMFTVDSQMSYT VPIMAFVCHPEVLP IYTELCRPSKRRMQAVANVSIGAMFCM YGLTATFGYLT FYSSVKAEMLMYSQKDPLILCVRLAVLLA\ V TLTVPVVLFP IRRALQQLLFP GKAFSWPRHVAIALILLVLVNV LVICVPTIIRDIFGVIGSTSAPSLIFILPSCI
336	1075	3	825	GAGSKSSMMQLMHLESFYEK\ PPPGLIKEDDTKPEDCIPDVP NEHAREFLAHTPTKGLWMPLEKEVKVKH/CTFHWIAS*FLGDG KFIPKATRLKDVVWSN*FTCLFWDLTRFIHDCIFF*NWSLMNK NFNIIY*FFISLR*NTLILQKYFPFSLLLGWHCKWYGHRTGYK ECPFFIKDNQKLQQFRVAHEDFMYDIIRDNKQHEKNVRIQQLK QLLEDSTSGEDRSSSSSEGEKHKHKKKKKKEKHKRKKKEKHKK KKRKHKSSKSNEGSDSE

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337	1076	3	2451	<p>ETAGAAAENMLGSLCLPGSGSVLLDPCTGSTTSETTSEAWSV EVLPSDSEAPDLKQEERLQELESCSGLGSTSDDTDVREVSSRP STPGLSVVSGISATSEDI PNKIEDLRSECSDFGGKDSVTSPD MDEITHDFLYILQPKQHFQHIEAEADMRIQLSSSAHQLTSPPS QSESLAMFDPLSSHEGASAVVRPKVHYARPSHPDPPILEG AVGGNEARLPNFGSPMF*LPAMEAFKQRHS/YTPERLVRSR S\DIVSSVRRPMSDPSWNRPP\GNEERELPPAAIGATSLVAA PHSSSSSPSKDSSRGETEERKSDDEKSDRNRPWWRKRFVSAM PKAPIPRKKEKQEKDKDDLGPDRFSTLTDDPSRPLSAQAQVA EDILDKYRNAIKRTSPSDGAMANYESTEVMDGESAHDSRDE ALQNISADDLPDSASQAHPQDSAFSYRDAKKLRLLALCSADS VAFPVLT\HSTRNGLEPDHTDPEDNEIVCFKLVQIAEAINLQDK NLMAQLQETMRCVCRFDNRTRCKLLASIAEDYRKRAPYIAYLT RCRQGLQTTQAHLERLLRVLRDKEVANRYFTTVCVRLLESK EKKIREFIQDFQKLTAAADKTAQVEDFLQFLYGAMAQDVIWQN ASEEQLQDAQLAIERSVMNRIFKLAFYPNQDGDILRDQVLHEH IQRLSKVVTANHRALQIPEVYLREAPWPSAQSEIRTISAYKTP RDKVQCILRMCSITMNLISLANEDSVPGADDFVPVLVFLIKA NPPCLLSTVQYISSFYASCLSGEESYWWMQFTA AVEFIKTIDD RK</p>
338	1077	536	1305	<p>WPMSLARGHGDTAASTAAPLSEEGEVTSGQLALAVEDTGGPSA SAGKAEDEGEGERETEREGSGGEEAQGEVPSAGGEEPAEDS EDWCVPSCDEEVELPADGQPPMPPSEIQRLYELLAHGTLEL QAEILPRRPPTPEAQSEERSDEEPEAKEEEEEKPHMPTEFDF DDEPVT PKDSLIDRRRTPGSSARSQKREARLDKVLSDMKRHKK LEEQILRTGRDLFSLDSEDPSPASPPLRSSGSSLFPRQRKY</p>
339	1078	2	1771	<p>LGRGTFGQVV*CWKRGTNEIVA KILKNHPSYARQQIEVSI ARLSTESADDYNFVAYECFQHKNHTCLVFEMLEQNLDFLKQ NKFSPLPLKYIRPVLQQVATAMKLSLGLIHADLKPENIMLV DPSRQPYRVKVIDFGSASHVSKAVCSTYLSRYRAPEIILGL PFCEAIDMWSLGCVIAELFLGWPLYPGASEYDQI/RYSISQTQ LPAEYLLSAGTKTRFFNRDTPSPYPLWRLKTPDDHEAETGIK SKEARKYIFNCLDDMAQVMNTTDLEGSMDLVEKAVRREFIDLL KKMLSIDSVKRFSVPGSLNHPFVTMSLFLDFPHSTHVSKCFQ MEICKRRVNMIDTVNQSKTPFITHVAPSTSTNLTMTFNNQLTT VHNQPSAASMAVAQRSMPLQTGTAIICARPDFFQALIVCPP GFQGLQASPSKHAGYSVRMENAVPIVTPAQGAQPLQIQGLLA QQAWPSTQQLILLPPAQQLTGVAHTSVQHAAPVETMAGTQ QLADWRNTHAGSHYNPIMQPPALLTGHTVLPAAQPLNVGV VMRQQPTSTTSSRSKQHLVYCGRRARVSKIASR</p>

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340	1079	2	2721	EFAICRYPLGMSGGQIPDEDITASSQWSESTAACYGRLDSEEG DGAWCPEIPVEPDDLKEFLQIDLHTLHFITLVGTQGRHAGGHG IEFAPMYKINYSRDGTRWISWRNRHGKQVLDGNSNPYDIFLKD LEPPIVARFVRFIPTDHSMNVMCMRVELYGCVWLDGLVSYNAP AGQQFVLPGGSIILNDSVYDGA VGYSMTEGLGQLTDGVSGLD DFTQTHEYHVWPGYDYVGNRESATNGYIEIMFEFDRIRNFTT MKVHCNNMFAKGVKIFKEVQCYFRSEASEWEPNAISFPLVDD VNPSARFVTVPLHHRMASAIKCQYHFADTWMMFSEITFQSDAA MYNNSEALPTSPMAPTTYDPMLKVDDSNTRILIGCLVAIIFIL LAIIVIIILWRQFWQKMLEKASRRMLDDEMTVSLSLPSDSSMFN NNRSSSPSEQGSNSTYDRIFFLRPDYQEPSRLIRKLPEFAPGE EESGCSGVVKPVQPSGPEGVPHYAEADIVNLQGVTTGNTYSVP AVTMDLLSGKRCGCGREFPPGKLLTFKEKLGEQGFGEVHLCEV EGMEKFKDKDFALDVSANQPVLVAVKMLRADANKNARNDFLKE IKIMSRCLKDPNIIHLLSVCITDDPLCMITEYMENGDLNQFLSR HEPPNSSSSDVRTVSYTNLKFMTQIASGMKYLSSLNFVHRDL ATRNCLVGKNYTIKIADFGMSRNLYSGDYRIQGRAVLPIRWM SWESILLGKFTTASDVWAFG\VTLWE\TFTFCQRKG PYS\QLS \DETGY*RNTGEFFPRPKGGQTYLPSTSPFVPDSCVIKMLSC WRRDTKNRPSFQEIHLLLLQQGDERCCQCLAMFLRLRSSLODL PLTHAYATPSGHLMKLRDRGLFALPSFPGHPHSLPLTHIYFFF FTLKN
341	1080	916	3	CSASPLRPGLLAPDLLYLPAGQPRRPEAEPGQKPVVPTLYVT EAEAHSPALPGLSGPQPKWVEVEETIEVRVKMGPGQVSPTE VPRSSSGHLFTLPGATPGGDPNSNNSNNKLLAQEAWAQGTAMV GVREPLVFRVDARGSDWAASGMGSLEEETMEEAGEEEGEDG DAFVTEESQDTHSLGDRDPKILTHNGRMLTLADLEDYVPGEGE TFHCGGPGPGAPDDPPCEVSVIQREIGEPTVG\SLCCSAWGMH WVPEALSASLGLSPMGR\HHRDPRSVALRAPPSSCGRPRLGLW AVLPG
342	1081	862	444	QGLAAEFLOVPAVTRAYTAACVLTAAVQLELLSPFQLYFNPH LVFRKFQAPFLPWALMGFSLLLGNSILVDLLGIAGVGHIIYFFLE DVFPNQPGGKRLLTQTPGFLGLQSSKAPAGSSLTITWTQSQGGP GTAGELAAPS

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343	1082	3658	337	EKNALEPTVYFGMGV*APQVPRFQQRITGYQYYLQLRKDIWEE GIPCTLEQPIHLAAGLAVQAI FGD F D Q Y E S Q D F L Q K F A L F P V G W LQDEKVL E E A T Q K V A L L H Q K Y R G L T A P D A E M L Y M Q E V E R M D G Y GEESYPAKDSQGS D I S I G A C L E G I F V K H K N G R H P V V F R W H D I A N M S H N K S F F A L E L A N K E E T I Q F Q T E D M E T A K Y I W R L C V A R H K F Y R L N Q C N L Q T Q T V T V N P I R R R S S R M S L P K P Q P Y V M P P P P \ Q L H Y N G H Y T E P Y A S S Q D N L F V P N Q E G \ Y Y G Q F Q T S L N R A Q I D F N G R I R \ N A S V Y S A H S T N S I N N P Q P Y L Q P S P M S S N P S I T G S D V M R P D Y L P S H R H S A V I P P S Y R P T P D Y E T V M K Q L N R G L V H A E R Q S H S L R N L N I G S S Y A Y S R P A A L V Y S Q P E I R E H A Q L P S P A A A H C P F S L S Y S F H S P S P Y P A E R R P V V G A V S V P E L T N A Q L Q A Q D Y P S P N I M R T Q V Y R P P P P Y P P R P A N S T P D L S R H L Y I S S S N P D L I T R R V H H S V Q T F Q E D S L P V A H S L Q E V S E P L T A A R H A Q L H K R N S I E V A G L S H G L E G L R L K E R T L S A S A A E V \ A P R A V S V G S Q P \ S V F T E R T Q R E G P E E A E G L R Y G H K K S L S D A T M L I H S E E E E D E D F E E S G A R A P P A R A R E P R P G L A Q D P P G C P R V L L A G P L H I L E P K A H V P D A E K R M M D S S P V R T T A E A Q R P W R D G L L M P S M S E S D L T T S G R Y R A R R D S L K K R P V S D L L S G K K N I V E G L P P L G M K K T R V D A K K I G P L K L A A L N G L S L S R V P L P D E G K E V A T R A T N D E R C K I L E Q R L E Q G M V F T E Y E R I L K K R L V D G E C S T A R L P E N A E R N R F Q D V L P Y D D V R V E L V P T K E N N T G Y I N A S H I K V S V S G I E W D Y I A T Q G P L Q N T C Q D F W Q M V W E Q G I A I I A M V T A E E E G G R E K S F R Y W P R L G S R H N T V T Y G R F K I T T R F R T D S G C Y A T T G L K M K H L L T G Q E R T V W H L Q Y T D W P E H G C P E D L K G F L S Y L E E I Q S V R R H T N S T S D P Q S P N P L L V H C S A G V G R T G V V I L S E I M I A C L E H N E V L D I P R V L D M L R \ Q Q R M M L V Q T L C Q Y T F V Y R V L I Q V P E K A P R L I L S S P Q F P Y G A Q S C E A F T A
344	1083	6	304	RKKQKLAEE*VELSKLADLKDAEAVQKFFLEET*L\GEEILAK GVDHLTNPSAVCGQPQWLLQVLQQTLPPLPVIQMLLTkPLPVNQ RLVSAG/SLAKDDVE
345	1084	1255	635	SFCLHEFGWLGS SPQSDHPVPALLGLGAFVHHSLLQVHSSPGA GPVSF L F L G E S C P V D E P R C V P S C A F G L S C F P L L N S A A L E R G L F F F V V F F F L E S G S C Q V A R A G V R D / R D R G S L Q P P P P G L K Q F C L S L P S R W D H R H P P L R V P * F V F V F L V E L G F H H V A Q A G L K L L T L S D P P A P A S H S A G I T G V S Q R D Q P V L F L R W A S C S E L V G
346	1085	116	415	EGFPGRSLSGGLCCRLRRRFPIDGYRPRRRRRWSCCPSGVRPV RRMSQKSWIESTLTKRECVYIIPSSKDPHRCPLPGCQICQQLVR RGFTVLARMVISIS
347	1086	918	760	QNSTCLTAQTHSL L Q H Q P L Q L T T L L D Q Y I R E Q R E K D S V M S A N G K P D P D T V P D S

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348	1087	1	750	LNPWKNALQDFCLPFLRITSLLQHHLFGEDLPSCQEEEEFSVL ASCLGLLPTFYQTEHPFISASCLDWPVPAFDIITHWCFEIKSF TERHAEQKALLIQESKWKLPHLLQLPENYNITFYHYHRKTCS VCTKVPKDPVAVCLVCGTFVCLKGLCKQSQSYCECVLHSQNCGA GTGIFLLINASVIIIRGHRFCLWGSVYLDHAGEEDRDLRRGK PLYICKERYKVLEQQWISHTFDHINKRWGPHYNGL
349	1088	3	1374	KGQLVNLLPPENFPWCGGSQGPRMLRTCIVLCSQAGPRSRGWQ SLSFDGGAFHLKGTGELTRALLVLRCAWPPLVTHGLLLQAWS RRLGSRSLSGAFLRASVYGQFVAGETAEEVKGCVQQLRTLRLR PLLAVPTEEEPDSAAKSGEAWYEGNLGAMLRCDLSRGLLEPP SLAEASLMQLKVTALTSTRLCKELASWVRRPGASLELSPERLA EAMDSGQNLQVSCINAEQNQHILRASLSRLHRVAQYARAQHVRL LVDAEYTSNPALSLVAALAVRWNSPGEAGPWWNTYQACLK DTFERLGRDAEAAHRAGLAFGVKLVRGAYLDERAVAQL\HG\ MEDPPTQADYEATS\QSYS\RCELEMLTHVARHGPMCHLMVAS HNEESVRQATK\GQAGYVVYKSIPIYGSLEEVIPIYLIRRAQENR SVLQGARREQELLSQKLWRRLLPGCRRIPH
350	1089	1036	306	VVEFGEMSTARAPEGLRWFLYVHPDLQLNKQLIQRVESLGFK ALVITLDTPVCGNRRHDIRNQLRRNLTLTLQSPKKGNAIPYF QMTPISTSLCWNDSWFQSITRLPIILKGILTKEDAELAVKH VQGIIVSNHGGRLDEVLASIDALTEVGAAE*GNMKYYLDAGV RTGNDVQKALALGAKCIFLGRPIILWGLACKGEHGVKEVLNILT NEFHTSMA\LTGCRSVAEINRNLVQFSRL
351	1090	1229	957	FFLRWSFTL\LPRLE/CQWLNLGSLQPPPPGFK*SSCLRLSS WGLQVPTSMLG*FFCIFSREGISPCWPGWSQTFKVIHLPRPPR VLRLOA
352	1091	1145	365	LLCFVHTALQSFQGELYEPHVVIATVFLVKLGICK*RASWRK KVTILVVK*S/LKICFTKYGSCYHPGEKSSWLEN*RMVNDCLA TSCSNRSFVIQIPSSNLFMVVDSSCLCESVAPITMAPIEIR YILLCAGPLTTTETSQGYQW*GNLGEKY*RRKITSFPLLERES S*ESCHCQILTSEMQRKKQSLETCLNYSQHNSLK CERLKAQ KIRRRPESCHGFHPEENARECGGAPSLQAQTVLLLLPLLLMLF SR
353	1092	1140	790	VPSPTHDPKPAEAPMPA*PAPPGPASPGGALEPPAAARAGGSP TAVRSILTKERRPEGGYKAVWFGEDIGTEADVVLNAPTLDVD GASDSGSGDEGEGAGRGGGPPYDAPGGDDSYI

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354	1093	3	2293	LISLAGPTDDIQSTGPGVHALNLRALFRDTRLGENIIPYVAD GAKAAILGFTSPVWAVRNSSTLLFSALITRIFGVKRAKDEHSK TNRMTGREFFSRFPPELYPFLKQLETVANVTSDMGEPNRHPS MFLLLLVLRLYASPMGTSSALSMGPFVFPFIMRCGHSPPVYHS REMAARALVPFVMIDHI PNTIRTLTLLSTLPSCTDQCFRQNHIG TLLQVFHLVQAYSDSKHGTNSDFQHELTDTITVCTKAKLWLAKR QNPCLVTRAVYIDILFLLTCCLNRSADNQPVLSESLGFWEVEVR GIISGSELITGFPWAFKVPGLPQYLQSLTRLAIAAVWAAAAS GERETNPVPI SFSQ LLESAPFEVRS LLEALLEKFLAAASGLGE KGVPPLLCNMGEKFLLLAMKENHPECFCCKILKILHCMDPGEWL PQTEHCVHLTPKEFLIWTMDIASNERSEIQSVALRLASKVISH HMQTCVENRELIAAELKQWVQLVILSCEDHLPTESRLAVVEVL TSTTPLFLTNPPILELQDTLALWKCVLTLQSEEQAVRDAAT ETVTTAMSQENTCQSTEFACQVDASIALALALAVLCDLLQW DQLAPGLPILLGWLLGESDDL VACVESMHQVEEDYLFKAENV FWAETLIFVKYLCKHLFCLLSKSGWRPPSPPEMLCHLQRMVSEQ C\HLLSQFFRELPPAAEFVKTVEFTRLRIQEERTLACLRLAF LEGKEGEDTLVLSVWDSYAESRQLTLPRTEAAC
355	1094	25	1265	HAFRPIALQRGVSFRGCSNQYAESRRLOGESGSRFAHLMESL LQHLDRFSELLAVSSTTYVSTWDPATVRRALQWARYLRHIHRR FGRHGPIRTALERRLHNQWRQEGGFGRGPVPGLANFQALGHCD VLLSLRLLENRALGDAARYHLVQQLFPFGPVRDADEETLQESL ARLARRRSVAHMLRFNGYRENPNLQEDSLMKTQAEILLERLQE VGKAEAEERPARFLSSLWERLPQNNFLKVI AVALLOPPLSRRPQ EELEPGIHKSPGEGSQVLVHWLLGNSEVFAAFCRALPAGLLTL VTSRHPALSPVYLGLLTDWGQRLHYDLQKGIWVGTESQDVPWE ELHNRFSQSLCQAPPPLKDKVLTALCTCKAQDGDFFEPGLSIWT DLLLALRSGAFRKRQVLGLSAGLSSV
356	1095	3	1027	SHLIQHQRHT*E*AHECNECGKAFSQTSCLIQHMKMRKEKS YECNEYEGSFSSHSDLILOQEVLTROKAFDCDVWEKNSSQRAH LVQHQSHTKE/K/PHECNEDGKIF/NQIQ/ LIQHRLRVHTRE K\YVCTACGKAFSSHSAIAQHQIIHTREKPSCEDE*RGKISVK LLIDSC/RIYTSEKSYKCI ECGKFFMLLVFSYLSHIWRIHMI KFHCCNECEKAISQRNYLV*YQIHAMQKDYCN/EACMCVRRF SHNPTLIQHQRHT*ENLFGCSK/C/GRSFNRSLSLCHIRIS I/RRQEFDVTQMEKLDTTFQA/STQHRNNGEKIVDYLFMKLLI HSPNLFHCTKI
357	1096	2638	2867	AVTLTAKICSFTPEPSETMSPPAGTNNSRHAALRAVTLPVKVC SFTPEPARSRTHQKEETPNTSEHQKEQTPEAPP

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358	1097	4747	4550	<p>MAYSWQTDPNPNESHEKQYEHQEFLEFVNQPHSSSQVSLGFDQI VDEISGKIPHYESEIDENTFFVPTAPKWDSTGHSLNEAHQISL NEFTSKSRELSWHQVSKAPAIGFSPSVLPKPQNTNKECSWGSP IGKHHGADDSRFSILAPSFTSLDKINLEKELENENHNHYHIGFE SSIPPTNSSSFSSDFMPKEENKRSGHVNIVEPSLMLLKGSLOPG MWESTWQKNIESIGCSIQLEVPQSSNTSLASFCNKVKKIRER YHAADVNFNSGKIWSTTTAFPPYQLFSKTKFNIHIFIDNSTQPL HFMPCANLYVKDLIAEILHFCTNDQLLPKDHILSVWGSEEFLO NDHCLGSHKMFQKDKSVIQLHLQKSREAPGKLSRKHEEDHSQF YLNQLLEFMHIWKVSRQCLLTIRKYDFHLKYLKLTQENVYNI IEEVKKICSVLGCVETKQITDAVNELSLILQRKGENFYQSSSET SAKGLIEKVTTTELSTSIYQLINVCNSFYADFQPVNVPRCTSY LNPGLPSHLSFTVYAAHNI PETWVHRINFPLEIKSLPRESMLT VKLFGIACATNNANLLAWTCLPLFPKEKSILGSMFLSMTLQSE PPVEMITPGVWDVSQSPVTLQIDFPATGWEYMKPDSEENRSN LEEPLKECIKHIALRSQKQTPLLLSEEKKRYLWFYRFYCNNEN CSLPLVLGSAPGWDERTVSEMHTILRRWTF SQPLEALGLLTSS FPDQEIRKVAVQQLDNLLNDELLEYLPQLVQAVKFEWNLESPL VQLLLHRSLSIQVAHRLYWLLKNAENEAYFKSWYQKLLAALQ FCAGKALNDEFSKEQKLIKILGDIGERVKSASDHQRQEVKKE IGRLEEFFQDVNTCHLPLNPALCIKIDHDACSFTSNALPLK ITFINANLMGKNISIIIFKAGDDLQDMLVLQLIQVMDNIWLQE GLDMQMIYRCLSTGKDQRLVQMPDAVTLAKIHRHSGLIGPL KENTIKKWFSQHNHLKADYEKALRNFFYSCAGWCVVTFILGVC DRHNDNIMLTSGHMFHIDFGKFLGHAQTGGIKRDRAPFIFT SEM\ EYFITEGG\ KNPQHFQDFV\ ELCCRAYNIIRKHSQLLL\ NLL\ EMMLYAG\ LPELSGI\ QDLKYVYNNLRPQDTDLEATSHF TKKIKESLECFPVKLNLIHTLAQMSAISPAKSTSQTFFQESC LLSTTRSIERATILGFSKKSSNLYLIQVTHSNNETSLTEKSFE QFSKLHSQLQKQFASLTLPFPHWWHL PFTNSDHRRFRDLNHY MEQILNVSHEVTNSDCVLSFFLSEAGQQTVEESSPVYLGEKFP DKPKVQLVISYEDVKLTILVKHMKNIHLPDGSAPS AHVEFY LPYPSEVRRRKTKSVPKCTDPTYNEIVVYDEVTELQGHVLMLI VKSKTVFVGAINIRLCSVPLDKEKWYPLGNSII* PLLLLFYTSN FMQSVLH</p>
359	1098	679	346	<p>FFLRWSLDSVTQAGVQSHDLSSLQPPPPGFKQSSLFGLPSSWE *RWVPPCPANFFVFLVETGFRHVGQAGLELLTSNDLPVSACQS AGITGVTTVPQRKSMILYEVTICYP</p>

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360	1099	2	1601	FVREIRGPAVPRLTSAEDRHRHGPHAHSPELQRTGRDYSLDYL PFRLWVGIVVATFCLVLVATEASVLVRYFTRFTEEGFCALISL IFIYDAVGKMLNLTHTYPIQKPGSSAYGCLCQYPGPGGNEQW IRTRPKDRDDIVSMDLGLINASLLPPECTROGGHPRGPGCHT VPDIAFFSLLLFLTSFFFAMALKCVKTSRFFPSVVRKGLSDFS SVLAILLGCGLDAFLGLATPKLMVPREFKPTLPGRGWLVSFPG ANPWWWVAAALPALLLSILIFMDQQITAVILNRMEYRLQKGA GFHLDLFWVAVLMLLTSALGLPWYVSATVISLAHMDSLRRRESR ACAPGERPNFLGIREQRLTGLVVFIITGASIFLAPVLKFIPMP VLYGIFLYMGVAALSSIQFTNRVKLL\MPAKHQPDLLLLRHV PLTRVHLFTAISFA\CLGLLW\IIKSTPAATIFPLMLLGLVGV RKALERVFSPOELLWLDELMPPEERSIPEKGLEPEHSFSGSDS EDSELMYQPKAPEINISVN*LE*EFVREIRGPAVPRLTSAEDR HRHGPHAHSPELQRTGRDYSLDYLPFRLWVGIVVATFCLVLVA TEASVLVRYFTRFTEEGFCALISLIFIYDAVGKMLNLTHTYPI QKPGSSAYGCLCQYPGPGGNEQWIRTRPKDRDDIVSMDLGLI NASLLPPECTROGGHPRGPGCHTVPDIAFFSLLLFLTSFFFA MALKCVKTSRFFPSVVRKGLSDFS SVLAILLGCGLDAFLGLAT PKLMVPREFKPTLPGRGWLVSFPGANPWWWVAAALPALLLSI LIFMDQQITAVILNRMEYRLQKGA GFHLDLFCVAVLMLLTSAL GLPWYVSATVISLAHMDSLRRRESRACAPGERPNFLGIREQRLT GLVVFIITGASIFLAPVLKFIPMPVLYGIFLYMGVAALSSIQF TNRVKLLDASKTPARPATLAACASDQGPPLHSHQLCPVWGCF GIIKSTPAATIFPLMLLGLVGVRKALERVFSPOELLWLDELMP EEERSIPEKGLEPEHSFSGSDSEDSSELMYQPKAPEINISVN

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361	1100	1	2636	MGLKARRAAGAAGGGGDGGGGGGAANPAGGDAAGDEERKV GLAPGDVEQVTLALGAGADKDGTLLLEGGGRDEGQRTPQGIG LLAKTPLSRPVKRNNAKYRRIQTLYDALERPRGWALLYH\AL VFLIVLG\CLILAVL\TTFKEYETVSGDWLLLLETFAIFIGA EFALRIWAAGCCCRYKGWRGRLKFARKPLCMLDIFVLIASVPV VAVGNQGNVLATSLRSLRFLQILRMLRDGPGEGETWKLLG\SA ICAH\$KELITAWYIGFTLILSSFLVYLVEKDVPEVDAQGEEM KEEFETYADALWGLITLATIGYGDKTPKTWEGRLIAATFSLI GVSFFALPAGILGSGLALKVQEQHRQKHFEKRRKPAELIQAA WRYATNPNRIDLVAWRFYESVVSFFFRKEQLEAASSQKLG LLDRVRLSNPRGSNTKGKLFPLNVDAIEESPSKEPKPVGLNN KERFRTAFRMKAYAFWQSSDAGTGDPMAEDRGYGNDFPIEDM IPTLKAAIRAVRILQFRLYKKKFKETLRPYDVKDVIEQYSAGH LDMLSRIKYLOTRIDMIFTGPPSTPKHKKSQKGSFTFPSQQ SPRNEPYV\ARPST\SEI\EDQRH*WGKFVKSLLKGQV\QGLGR KLDFLVDMHMQHMERLQVQVTEYYPTKGTSSPAEAEKKEDNRY SDLKTIICNYSETGPPEPPYSFHQVTIDKVSPYGGFFAHPVNL PRGGPSSGKVQATPPSSATTYVERPTVLPILTLLDSRVSCHSQ ADLQGPYSDRISPRQRRSITRSDTPLSLMSVNHEELERSPSG FSISQDRDDYVFGPNGGSSWMREKRYLAEGETDTDTPFTPSG SMP\LSSTGDGSDSVWTPSNKPI

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362	1101	1	5433	<p>RTRGITIEFDPKYTA FEVEEDVGLIMIPVRLHGTGYGVTA DFISSSSASFGG</p> <p>VDYLHGSTVTFQHQNLSPFINISI IDNNESEFEFPIEILLTGATGGAVLGRH</p> <p>LVSRIITAKSDSPFGVIRFLNQSKISIANPNSTMILSLVLERGTGGLLGEIQVN</p> <p>WETVGPNSQEALLPQNRDIADPVSGLFYFGE GEGGVRTIILTIYPHEEIEVEE</p> <p>TFI IKLHLVKGEAKLDSRAKDVTLTIQEF GDNPGVQFAPETLSKKTYSSEPLA</p> <p>LEGPLLITFFVRRVKGTFGEIMVYVWELSSSEFDITEDFLSTSGFPTIADGESEA</p> <p>SFDVHLLPDEVPEIEEDYVIQLVSVEGGAELDEKSITWFSVYANDDPHG VFA</p> <p>LYSDRQSIILIGQNLIRSIQINITRLAGTFGDVAVGLRISSDHKEQRIVTENAE</p> <p>RQLVVKDGATYKVDVVP IKNQVFLSLGSNFTLQLVTVMLVGGFRFGMPTILQE</p> <p>AKSAVLPVSEKAANSQVGFESTAFQLMNITAGTSHVMSRRGTYGALSVAWTT</p> <p>GYAPGLEIPEFIVGNMPTTLGSLSFSGHGEQRKGVFLWTFPSPGWPEAFVLHL</p> <p>SGVQSSAPGGAQLRSGFIVAEIEPMGVFQFSTSSRNIIVSEDQMIRLHVQRL</p> <p>FGFHSDLIKVSYQT TAGSAKPLEDFEPVQNGELFFQKFQTEVD FEITIIINDQL</p> <p>SEIEEFFYINLT SVEIRGLQKFDVWNSPRLNLD FSVAVITILDNDLAGMDIS</p> <p>FPETTVA VAVDTTLIPVETESTYLTSTSKTTTILQPTNVVAIVTEATGVS AIP</p> <p>EKLVT LHGT PAVSEKPDVATVTANVSIHGTFSLGPSIVYIEEMKNGTFNTAE</p> <p>VLIRRTGGFTGNVSI VTKTFGERC AQMEPNALPFRGIYGISNLTWAVEEEDFE</p> <p>EQTLTLIFLDGERERKVSQIILDDDEPEGQEFYVFLTNPQGGAQIVEGKDDT</p> <p>GFAAFAMVITGSDLHNGIIGFSEESQSGLELREGAVMRRHLIVTRQPNRAF</p> <p>EDKVFWRVTLNKT VVVLQKDG VNLMEELQSVSGTTCTMGQTKCFISIELKP</p> <p>EKVPQVEVYFFVELYEATAGAAINNSARFAQIKILESDSQSLVYFVSGSRLA</p> <p>VAHKKATLISLQVARDSGTGLMMSVNFSTQELRSARTIGRTIISP AISGKDFV</p> <p>ITEGTLVFE PGQRSTVLDVILT PETGSLNSFPKRQFQVLFDPKGGARIDKYG</p> <p>TANITLVSDADSQAIWGLADQLHQPVNDDILNRVLHTISMKVATENTDEQLSA</p> <p>MMHLIEKITTEGKIQA FSVASRTLFYEILCSLINPKRKDTRGFSHFAELTENF</p> <p>AFSLLTNVTCGSPGEKSKTILDCPYLSILALHWYPQINGHKGFEKGGDYIR</p> <p>I PERLLDVQDAEIMAGKSTCKLVQFTEYSSQWFISGNNLPTLKNKVLSSLVK</p> <p>QSSQQLTNDNEVLYRIYAAEPRIIPQTS LCLLNQAAASWLSDSQFCVKVIEE</p> <p>TADYVEACALHMSVYAVYARTDNLSYNEAFTSGFICISGLCLAVLSHIFCA</p> <p>RYSMFAAKLLTHMMAASLGQILFLASAYASPQLAEESCSAMA AVTHYLYCQ</p> <p>FSWMLIQSVNFVYVLMNDEHTERRYLFLFLLSWGLPAFVVILLIVILKGIYH</p> <p>QSMSQIYGLIHGDLCFIPNVYAALFTAALVPLTCLVVFVVFVFIHAYQVKPWK</p> <p>AYDDVFRGRTNAAEIPILILYLFALISVTWLGGLHMA YRHFVWLVLVFI NSL</p> <p>QLL\YPLFYFLLL* DQSSSSAPGGVDYILHGSTVTFQHQNLSPFINISI IDN</p> <p>NESEFEFPIEILLTGATGGAVLGRHLVSRITAKSDSPFGVIRFLNQSKISIAN</p> <p>PNSTMILSLVLERGTGGLLGEIQVNWETVGPNSQEALLPQNRDIADPVSGLFYF</p> <p>GEGEGGVRTIILTIYPHEEIEVEETFI IKLHLVKGEAKLDSRAKDVTLTIQEF</p> <p>GDPNGVVQFAPETLSKKTYSSEPLALEGPLLITFFVRRVKGTFGEIMVYVWELSS</p> <p>EPDITEDFLSTSGFPTIADGESEASFDVHLLPDEVPEIEEDYVIQLVSVEGGA</p> <p>ELDEKSITWFSVYANDDPHG VFALYSDRQSIILIGQNLIRSIQINITRLAGTF</p> <p>GDVAVGLRISSDHKEQPIVTENAE RQLVVKDGATYKVDVVP IKNQVFLSLGSN</p> <p>FTLQLVTVMLVGGFRFGMPTILQEA KSAVLPVSEKAANSQVGFESTAFQLMNI</p> <p>TAGTSHVMSRRGTYGALSVAWTTGYAPGLEIPEFIVGNMPTTLGSLSFSGH</p> <p>EQRKGVFLWTFPSPGWPEAFVLHLSGVQSSAPGGAQLRSGFIVAEIEPMGVFQ</p> <p>FSTSSRNIIVSEDQMIRLHVQRLFGFHSDLIKVSYQT TAGSAKPLEDFEPVQ</p> <p>NGELFFQKFQTEVD FEITIIINDQLSEIEEFFYINLT SVEIRGLQKFDVWNSPRL</p> <p>NLD FSVAVITILDNDLAGMDISFPETTVA VAVDTTLIPVETESTYLTSTSK</p> <p>TTTTLQPTNVVAIVTEATGVS AIP EKLVT LHGT PAVSEKPDVATVTANVSIHG</p> <p>TFSLGPSIVYIEEMKNGTFNTAEVLIRRTGGFTGNVSI VTKTFGERC AQMEP</p> <p>NALPFRGIYGISNLTWAVEEEDFE EQTLTLIFLDGERERKVSQIILDDDEPEG</p> <p>QEFFYVFLTNPQGGAQIVEGKDDTGFAAFAMVITGSDLHNGIIGFSEESQSG</p> <p>LELREGAVMRRHLIVTRQPNRAFEDKVFWRVTLNKT VVVLQKDG VNLMEEL</p> <p>QSVSGTTCTMGQTKCFISIELKPEKVPQVEVYFFVELYEATAGAAINNSARF</p> <p>AQIKILESDSQSLVYFVSGSRLAVAHKKATLISLQVARDSGTGLMMSVNFST</p> <p>QELRSARTIGRTIISP AISGKDFVITEGTLVFE PGQRSTVLDVILT PETGSLN</p> <p>SFPKRQFQVLFDPKGGARIDKYGTANITLVSDADSQAIWGLADQLHQPVNDD</p> <p>ILNRVLHTISMKVATENTDEQLSAMMHLIEKITTEGKIQA FSVASRTLFYEIL</p> <p>CSLINPKRKDTRGFSHFAELTENFAPSLLTNVTCGSPGEKSKTILDCPYLSI</p> <p>LALHWYPQINGHKGFEKGGDYIRI PERLLDVQDAEIMAGKSTCKLVQFTEYS</p> <p>SQQWFISGNNLPTLKNKVLSSLVKQSSQQLTNDNEVLYRIYAAEPRIIPQTS</p> <p>LCLLNQAAASWLSDSQFCVKVIEETADYVEACALHMSVYAVYARTDNLSYNE</p> <p>AFTSGFICISGLCLAVLSHIFCARYSMFAAKLLTHMMAASLGQILFLASAY</p> <p>ASPQLAEESCSAMA AVTHYLYCQFSWMLIQSVNFVYVLMNDEHTERRYLFL</p> <p>FLLSWGLPAFVVILLIVILKGIYH QSMSQIYGLIHGDLCFIPNVYAALFTAAL</p> <p>VPLTCLVVFVVFVFIHAYQVKPWKAYDDVFRGRTNAAEIPILILYLFALISVTW</p> <p>LWGLHMA YRHFVWLVLVFI NSLQLLVPSVLLFTSMRSTFFSFHTGTLTSRE</p> <p>KKSTFVLTCLLSPDSKGLGVLCFLTEWAFQVH</p>

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363	1102	2	2855	AAGATMERDGCAGGSGRGEGGRAPREGPAGNGRDRGRSHAAE APGDPQAAASLLAPMDVGEEPLEKAARARTAKDPNTYKVL LSVCVLTTILGCI FGLKPSCAKEVKSCKGRCFERTFG\NCRCD AACVELG\NCCGLPGGTCI\EP\EHIW\TCNKFRCG\EKRLT RSLCACSDCKD\RGDCLP SNLQFLCVQGE\KSWGRKNPCESH LMPE\QCP\AGFETPSLPLLI F/SLDGFRAYLHTWGGLLPVI SKLKKCGTYTKNMRPVYPTKTFPNHYSIVTGLYPESHGIINN MYDPKMNASFSLKSKEKFNPEWYKGEP I WVTAKYQGLKSGTFF WPGSDVEINGIFPDIYKMYNGSVPFEEILAVLQWLQLPKDER PHFYTTYLEEDSSGHSYGPVSSEVIKALQVRDGMVGMMDGL KELNLHRCNLNLILISDHGMEQGSCKKIYLNKYLGDVKNIKVI YGPAAARLPSPDPKYYSFNYEGIARNLS CREPNQHFKPYLKH FLPKRLHFAKSDRIEPLTFYLDPPQWLALNPSEKCYGSGFHG SDNVFSNMQALFVGYPGPFKHGIEADTFENIEVYNLMCDLLNL TPAPNNGTHGSLNHLLKNPVYTPKHPKEVHPLVQCFTRNPRD NLGCSCNPSILPIEDFQTQFNLTVAEEKI IKHETLPYGRPRVL QKENTICLLSQHQFMSGYSQDILMPLWTSYTVDRNDSFSTEDF SNCLYQDFRIPLSPVHKCSFYKNNTKVSYGFLSPPQLNKNSSG IYSEALLTTNIVPMYQSFQVIWRYFHDTLRLKYAEERGNVNV SGPVDFDFDYDGRCDL\ENLRQKRRVHPVTQENFWIPNSTSF Y/VVLTSC\KDTSQTPLHC\ENL\DTLGFPFCLHRDWINSETC \VHG\KHDSSW\VEEFVKCLHRA\RITGC*GTSGLGSFYQQRK EPVSDILKLKTHLPTFSQED
364	1103	657	1	TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERLPGRKASCSTA GSGSRGLPPL\SPMVSSAHNPNAEIPERRKDSTSTPNLPPS MMTRNTYVCTERPGAERP SLLPNGKENS SGT PRVPPASPSH SLAPPSGERSRLARGSTIRSTFHGGQVRDRAGGWGWFNKH LQRAPRNAGAPSLMPGHRTVLIN YGGGQDLKNWETCLAAPPNK HRR
365	1104	1	1313	HTLHSSPTSEAEFVSRLSTQNYFRSLPRGTSNMTYGT FNFL GGRLMIPNTGISLLIPDAIPRGKIYEIYLT LHKPEDVRLPLA GCQTLLSPIVSCGPPG\VLLTRPVILG\MDHCG\EPSPDW\S LRLKKQSCGSEWEDVLHLGEEAPSHLYCQLEASACVFTSQL SRYALVGEALSVA AAKRLKLLLFAPVACTSLEYN I LVYCLHDT HDALNVVVQLEKQLQGQLIQEPLVLHFKDSYHNLRLSIHDVPS SLWKSLLVSYQEI PFYHIWNGTQRYLHCTFTLERVSPSTSDL ACKLWWVQVEGDGQSFS INFNITKDT RFAELLALESEAGVPAL VGPSAFKIPFLIRQKI ISSLDPPCRRGADWRTLAQKLHLD SHL SFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGTGPA GRW LLSQCSEAEAC
366	1105	1	343	GSAAGQVQQQQQRRHQQKVTVKYDRKELRKRLVLEEWIVEQL GQLYGCEEEMPEVEIDIDDLFDAYSDEQRASKLQEALVDCYK PTEEFIKELLSRIRGMRKLSP\POKKS

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367	1106	2	1398	IMLDGRVRWLTPVISALWEAEMEDVIARMQDEKNGIPRTVKS FLSKIPSVFSGSDIVQWLIKNLTIEDPVEALHLGTLMAAHGYF FPISDHVLTCLKDDGTFYRFQTPYFWPSNCWEPENTDYAVYLCK RTMQNKARLELADYEASLARLQRAFARKWEFIFMQAEAAQAKV DKKRDKIERKILDSQERAFWDVHRPVPVCVNTTEVDIKKSSRM RNPHKTRKSVYGLQNDIRSHSPHTPTPETKPPTEDELQQQIK YWQIQDLRHRCLKMSKVADSLLSYTEQYLEYDFFLLFPDPSNPW LSDDTTFWEELEASKEPSQQRVKRWGFGMDEALKDPVGREQFLK FLESEFSSSENLRFWLAVEDLKKRPIKEVPSRVQEIWQEFAPG APSAINLDSKSYDKTTQNVKEPGRYTFEDAQEHYKLMKSDSY PRFIRSSAYQELLQAKK\KGKSLTSKRLTSLAQSY
368	1107	1	461	GTRDYPRIVNHLDHTYVTAPQAFMMFQYFVKVVPVVMKVDGE VLTNNQIYVTRHEKAAYVLMGDDQGLPGVFILYELSPMMVNLTE IHTFFSLFLTIVGA\TIGGMFFEHFVINYLTHKWGLGFYFKNE NSLQGGHRTLYGVNFFMYWSLRGGS
369	1108	2	1522	SVWWSQRQFVVRWAGCAGPCGRAVFLAFGLGLGLEEKQAES RRAVSACQEIQAIFTQKSKPGPDPLDTRRLQGRLEEYLIGQS IGKGCSSAAVYEATMPTLPQNLEVTGSTGLLPGRGPSTSAPGEG QERAPGAPAFPLAIKMMWNISAGSSSEAILNTMSQELVPASRV ALAGEYGAVTYRKS KRGPQLAPHPNIIIRVLRAFTSSVPLLPG ALVDYDPDVLPSRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNT PSPRLAAMMLLQLLLEGVDHLVQQGIAHRDLKSDNILELDPDG CPWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVS TARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFGQGAHLE SRSYQEAQLPALPESVPPDVRQLVRALLQREASKRPSARVAAN VLHLSLWGEHILALKNLKLDKMGWLLQQSAATLLANRLTEKC CVETKMKMLFLANLECETLCQAALLLCSWRAAL
370	1109	105	1252	RPLRLRLAELPDHCYRMNSSPAGTPSPQPSRANGNINLGPSANP NAQPTDFDFLKVIGKNGYKVLAKRKSDGAFYAVKVLQKKS I LKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPPEKLYFVLD YVNGGELFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIY RDLKPENILLDCQGHVVLTDGFLCKEGVEPEDTTSTFCGTPEY LAPEVL\RKEPYDRAVDWWCLGAVLYEMLHGLPPFYSQDVSQM YENILHQPLQIPGGRTVAACDLLQSLLHKDQORQLGSKADDFLE IKNHVFFSPINWDDLHYHKLTPPFNPNVTGPADLKHFDPEFTQ EAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDDILD

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371	1110	3	1608	RPQTLKGHQEKIRQRQSILPPPQGPAPIPFQHRGGDSPEAKNR VGPQVPLSEPGFRRRESQEEPRVLAQKIEKETQILNCALDDI EWFVARLQKAAEAFKQLNQRKKKKKKKAPAEGLTLRARPP \SEGEFIDCFQKIKLAINLLAKLQKHIONPSAAELVHFLFGPL DLIVNTCSGPDIAHSVSCPLLSDAVDFLRGHLVPKEMSLWES LGESWMRPRSEWPREPQVPLYVPKFHSGWEPPVDVLQEAPWEV EGLASAPIEEVSPVSRQSIKNSQKHSPTSEPTPPGDALPPVSS PHTHRGYQPTPAMAKYVKILYDFTARNANELSVLKDEVLEVLE DGRQWWKLRSRSGQAGYVPCNILGEARPEAGAPFEQAGQKYW GPASPTHKLPPSPFGNKDELMQHMDEVNDELIRKISNIRAQPO RHFRVERSQPVSQLTYESGPDVRAWLEAKAFSPRIVENLGI LTGPQLFSLNKEELKKVCGEGRVRYSQLTMQKAFLEKQQSGS ELEELMNKPFHSMNQRRGDS
372	1111	3	1046	AWHEGLVSSPAIGAYLSASYGDSLVLVATVVALLDICFILVA VPESLPEKMRPVSWGAQISWKQADPFASLKKVGKDVLL\IC ITVCLSYLPEAG\QYSSFF\LYLR\QVIGFG\SVKIAAFIAMV GILSIVAQTAFSLILMRSLGNKNTVLLGLGFQMLQLAWYFGS QAWMMWAAGTVAAMSSITFPAISALVSRNAESDQQGVAQGIIT GIRGLCNGLPALYGFIFYMFHVELTELGPKLNSNNVPLQAV IPGPPFLFGACIVLMSFLAALFIPEYSKASGVQKHSNSSSGSL TNTPERGSDIEDIEPLLQDSSIWELSSFEEPGNQCTEL*TRQKV GFCIRHL
373	1112	1	1950	MAAGLATWLPFARAAAVGWLPLAQQPLPPAPGVKASRGDEVLV VNVSGRRFETWKNLTDRYPTDLGSSSEKEFFYDADSGEYFFDR DPDMFRHVLNFYRTGRHLCPQECIQAFDEELAFYGLVPELVG DCCLEEYRDRKKENAEERLADEEAEQAGDGPALPAGSSLRQRL WRAFENPHTSTAALVFYVVTGFFIAVSVIANVVETIPCRGSAR RSSREQPCGERFPQAFFCMDTACVLIFTGEYLLRLFAAPSRCR FLRSVMSLIDVVAILPYYIGLLVPKNDVSGAFVTLRVFRVFR IFKFSRHSQGLRILGYTLKSCASELGFLFLSLTMAIIIFATVM FYAEKGTNKTNFTSIPAAFWYTIVTMTLGYGDMVPSTIAGKI FGSICSLSGVLVIALPVPVIVSNFSRIYHQNRADKRRQQKV RLARIRLAKSGTTNAFLQYKQNGGLEDSSGSGEEQAVCVRNRS FEQQHHLLHLCLEKTTCHFTDELTFSEALGAVSPGGRTSRST SVSSQPVGPGSLLSSCCPRRAKRRIRLANSTASVSRG\SMQE LDMLAGL\RRSHAP\QSRSSL\NAKPHDSLNLNCDG\DFVAA IISIPTPANTPDSESPSSPGGGGRAGSTLRNSSLGTPCLFPE TVKISSL
374	1113	4	664	GWGKPFKDWTTGGQDTGGEPALLVGAGEGRAPRLNCPGQIRS PGPGDLSIYDNWIRYFNRSSPVYGLVP/RSKTSARIYPTYHTA FDTFDYVDKFLDPGEEGDKGHPETRTGEAED*ALALSPCR\F SSHQAVARTAGSVILRLSDSFFLPLKVDYSETLRSFLQAAQ DLGALLEQHSISLGPLVTAVEKFEAEAAALGORISTLQKGS PLQVRML

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375	1114	1	1147	GIRGGGSLASGGPGPGHASLSQRLRLYLADSWNQCDLVALTCF LLGVGCRLTPGLYHLGRTVLCIDFMVFTVRLLIHFTVKNQLGP KIVIVSKMMKDVFFFLFFLGVWLVA YGVATEGLLRPRDSDFPS ILRRVFYRPYLQIFGQIPQEDMDVALMEHSNCSSEPGFWAHP GAQAGTCVSQYANWLVLVLLVI FLLVANILLVNLLIAMFSYTF GKVQGNSDLYWKAQRYRLIREFH SRPALAPPFIVISHLRLLLR QLCRRPRSPQPSSPALEHFRVYLSKEAERKLLTWESVHKENFL LARARDKRES DSERLKRTSQKVDLALKQLGHIREYEQRLKVLE REVQQCSRVLGWVAEALSRSALLPPGGPPPPDLPGSKD
376	1115	3	329	LIKLCCKSAKSCENDLEMGM LNSKFKKTRYQAGMRNSENLTAN NTLSKPTRY/QGELKEIKQDISSLRYELLEESQATGELADLI QQLSEKFGKNLNDHLRVNKGKDI
377	1116	1	2043	LPLLHAGFNRRFMENSSIIACYNELIQIEHGEVRSQFKLRACN SVFTALDHCHEAIEITSDDHVIQYVNP AFERMGMGYHKGELLGK ELADLPKSDKNRADLLDTINTCIKKGKEWQGVYYARRKSGDSI QQHVKITPVIQGGKIRHFVSLKKLCTTDNNKQIHKIHRDSG DNSQTEPHSFYKNNRRKESIDVKS ISSRGSDAPSLQNNRYPSM ARIHSMTIEAPITKVINI INAAQENS PVTVAEALDRVLEILRT TELYSPQLGTDKEDPHTSDLVGGLMTDGLRRLSGNEYVFTKNV HQSHSLAMPITINDVPPCISQLLDNEESWDFNIFELEAITHK RPLVYLGLKVFSRFGVCEFLNCSETTLRAWFQVIEANYHSSNA YHNSTHAADV LHATAFFLGKERVKGS LDQLDEVAALIAATVHD VDHPGRTNSFL/CNAGSELAVLYNDT\AV\LESHHTALAFQ\L TVKDTK\CNIFKNID/RGNHYRTL RQAIIDMVLATEMTKHFEH VNKFVNSINKPMAABIEGSDCECNPA GKNFPENQILIKRMMIK CADVANPCRPLDLCIEWAGRIS EEFYFAQTDEEKROGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFAHLPALMQHLADN YKHWKTLLDDLCKCKSLRLPSDRLKPSHRGGLLTDKGHCESQ

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378	1117	1	3585	<p>AFLSKVEEDDYPSEELLEDENAINAKRSKEKNPGNQGRQFDVN</p> <p>LQVPDRAVLGTIHPDPEIEESKQETSMILDSEKTSETAAKGVN</p> <p>TGGREPNTMVEKERPLADKKAQRPFERSDFSISIKIQTPELGE</p> <p>VFQNKDSYDLKNDNPPEHLKTSGLAGEPEGELSKEDHENTEKY</p> <p>MGTESQGSAAEPEDDSFHWTPHTSVEPGHSDKREDLLIISFF</p> <p>FKEQQSLQRFQKYFNVHELEALLQEMSSKLKSAQQESLPYNME</p> <p>KVLDKVFRASESQILSIAEKMLDTRVAENRDLGMNENNI FEEA</p> <p>AVLDDIQDLIYFVRYKHSTAEETATLVMAPPLEEGLGGAMEEM</p> <p>QPLHEDNFSREKTAELNVQVPEEPHTLDQRVIGDTHASEVSQK</p> <p>PNTEKDLDPGPVTTEDTPMDAIDANKQPETAEEPPASVTPLEN</p> <p>AILLIYSFMFYLTKSLVATLPDDVQPGPDFYGLPWKPVFITAF</p> <p>LGIASFALFLWRTVLVVKDRVYQVTEQQISEKLKTIMKENTEL</p> <p>VQKLSNYEQKIKESKKHVQETRKQNMILSDEAIIKYKDKIKTLE</p> <p>KNQEILDDTAKNLRVMLESEREQNVKNQDLISENKKSEIKLKD</p> <p>VISMNASEFSEVQIALNEAKLSEEKVKSECHRVQEENARLKKK</p> <p>KEQLQQEIEDWSKLHAELSEQIKSFEKSQKDLEVALTHKDDNI</p> <p>NALTNCITQLNLLECESESEGQNKGGNDSDELANGEVGGDRNE</p> <p>KMKNQIKQMMDVSRQTQTATISVVEEDLKLLQLKL\RASVSTKC\</p> <p>NLEDQVKKLEDDRNSLQAAKAGLEDECKTLRQKVEILNELYQQ</p> <p>KEMALQKKLSQEEYERQERHRLSAADEKAVSAAEEVKTYKRR</p> <p>IEEMEDELQKTERSFKNQIATHEKKAHENWLKARAAERAAEE</p> <p>KREANLRHKLLDLTQKMAMLQEEPVIKPMMPGKPNTPNPPRR</p> <p>GPLSQNGSFGSPVSGGECSPPLTVEPPVRPLSATLNRRDMPR</p> <p>SEFGSLDGLPHPRWSAEASGKPSPSDPGSGTATMMNSSSRGS</p> <p>SPTRVLDEGKVNMAPKGPPFPFPGVPLMSTPMGGPVPPP IRYGP</p> <p>PPQLCGPFGPRPLPPFPFGPMRPLGLREFAPGVPPGRDLPL</p> <p>HPRGFLPGHAPFRPLGSLGPREYFIPGTRLPPPTHGPOEYPPP</p> <p>PAVRDLLPSGSRDEPPPASQSTSQDCSQALKQSP</p>

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379	1118	3	2946	MAADSEPESEVFEITDFTTASEWERFISKVEEVLNDWKLIGNS LGKPLEKGIFTS GTWEEKSDEISFADFKFSVTHHYLVQESTDK EGKDELLEDVVPQSMQDLLGMNNDFP PRAHCLVRWYGLREFVV IAPAAHSDAVLSESKCNLLSSVSIALGNTGCQVPLFVQIHKK WRRMYVGECQGGPVRTDFEMVHLRKVPNQYTHLSGLLDIFKSK IGCPLTPLPPVSIARFTYVLQDWQQYFWPQQPPDIDALVGGE VGGLEFGKLPFGACEDPISELHLATTW\PHLTEGIIVDNDVYS DLDPIQAPHWSVRVRKAENPQCLLGDVFTEFFKICRRKESTDE ILGRSAFEEEGKETADITHALSKLTEPASVPIHKLSVSNMVHT AKKKIRKHRGVEESPLNNDVLNTILLFLFPDAVSEKPLDGTTS TDNNNPPSESEDYNLYNQFKSAPSDSLTYKLALCLCMINFYHG GLKGVAHLWQEFVLEMRFRWENNFLIPGLASGPPDLRCCLLHQ KLQMLNCCIERKKARDEGKKTASDVNTIYPGDAGKAGDQLVP DNLKETDKEKGEVGKSWDSWSDSEEEFFECLSDTEELKGNQGE SGKKGGPKEMANLRPEGRLYQH GKLTLLHNGEPLYIPVTQEPA PMTEDLLEEQSEVLAKLGTS AEGAHLRARMQSACLLSDMESFK AANPGCSLEDFVRWYSPRDYIEEEVIDEKGNNVLKGELSARMK IPSNMWVEAWETAKPIPARRQRRLFDDTREAEKVLHYLAIQKP ADLARHLLPCVIHA AVLKVKEESLENISSVKKI IKQIISHSS KVLHFPNPEDKLEEIIHQITNVEAL IARARSLKAKFGTEKCE QEEEEKEDLERFVSC LLEQPEVLVTGAGRGHAGRI IHKLFVNAQ RAAAMTPPEEELKRMGSPEERRQNSVSDFP PPAGREFILRTTV PRPAPYSKALPQRMYSVLT KEDFRLAGAFSSDTSFF
380	1119	2333	670	SPTRTGDRSVSLIVFLTEGKPTVGETHTLKI LNNTREAAARGQV CIFTIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGF YDEIRTPLLSDIRIDYPPSSVVQATKTLFPNYFNGSEII IAGK LVDRKLDHLHVEVTASNSKKFII LKTDVPVRPQKAGKDVGTGSP RPPGGDGEGDTNHIERLWSYLT'TKELLSSWLQSDDEPEKERLRQ RAQALAVSYRFLTPFTSMKLRGPVPRMDGLEEAHGMSAAMGPE PVVQSVRGAGTQPGPLLKKPYQPRIKISKTSVDGDPHFVVDFF LSRLTVCFNIDGQPGDILRLVSDHRDSGVTNGELIGAPAPPN GHKKQRTYLRITITILINKPERSYLEITPSRVILDGGDRLVLP NQSVVVGSGLEVSVSANANVTVTIQGSIAFVILIHLYKKPAP FQRHHLGFYIANSEGLSSNCHGLLGQFLNQDARLTEDPAGPSQ NLTHPLLLQVGEGPEAVLTVKGHQVPVWVKQRKIYNGEEQIDC WFA RNAAKLIDGEYKDY LASHPFDTGMTLGQMSREL
381	1120	102	426	VPLESLSCSHADNWKQELTKFISPDQLPVEFGGTM TDPDGNPK CLTKINYGGEVPKSYLLCKQVRLQYEHTRS VGRGSSSLQVENEI LFPGCVLRCP EVLQHLQPGSF

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382	1121	3	3726	<p>PAAPEHTDPSEPRGSVSCCSLLRGLSSGWSSPLLPAVPCNPKNK AIFTVDAKTTEILVANDKACGLLGYSSQDLIGQKLTQFFLRSD SDVVEALSEEHMEDGHAAVVFQTVVDIISRSGEKIPVSVWMK RMRQERRLCVVLPEPVERVSTWVAFQSDGTVTSCDSLFAHLH GYVSGEDVAGQHITDLIPSVQLPPSGQHIPKNLKIQRSVGRAR DGTTFPLSLKLKSPSSEEAATTGEAAPVSGYRASVWVFCTISG LITLLPDGTIHGINHSFALTTFGYGKTELLGKNITFLIPGFYS YMDLAYNSSLQLPDLASCLDVGNESGCGERTLDPWQGDPAEG GQDPRINVLAGGHVVPDEIRKLMSQDI FTGTQTETLIAGGQ LLSCLSPQAPGVNDVPEGSLPVHGEQALPKDQQITALGREEP VAIESPGQDLLGESRSEPVVKPFASCEDSEAPVPAEDGGS DA GMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPAKQLAGGS LLMHCPCYGSEWGLWRSQDLAPSPSGMAGLSFGTPTLDEPWL GVENDREELQTC LIKEQLSQLSLAGALDVPHAELVPTECAV APVSSCDLGGRLCGGCTGSSSACYALATDLPGGLEAVEAQEV DVNSFSWNLKELFFSDQTDQTSSNCSCATSELRETPSSLA VGS DPDVGSLQE QGSCVLDRELLLLTGTCVDLQGRRFRES CVGH DPTEPLEVCLVSSEHYAASDRESPGHVPSTLDAGPEDT CPSAE EPRLNVQVTSTPVI VMRGAAGLQREIQEGAYSGSCYHRDGLRL SIQFEVRRVELQGPTPLFCCWLKDLLHSQORDSAARTRFLAS LPGSTHSTAAELTGPSLVEVLRARPWFEEPPKAVELEGLAACE GEYSQKYSTMSP LGSGAFGFVWTAVDKEKNKEVVVKFIKKEKV LEDCWIEDPKLGKVTLEIAILSRVEHANI IKVLDIFENQGFQ LVMEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAG\QSRLV SAVGYLRLKDI IHRDIKDENVIAEDFTIKLIDFGSAAYLERG KLFYTFCGTIEYCAPEVLMGNPYRGPELEMWSLGVTLYTLVFE ENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQPVPERRTTL EKLVTDPWVTQPVNLADYTWEEVFRVKNKPESGVL SAASLEMGN RSLSDVAQAQELCGGPVPGEPNGQCLHPGDPRL LTS</p>
383	1122	177	1365	<p>PGTSAATCRFLSPFVISLSFTGLCISDLVVAVNGVWILVETFM LKGGNFFSKHVPWSYLVFLTIYGVFLKLVAGLGPVEYLSGW NLFDFSVTVF AFLGLLALALNMEPFYFIVVLRPLQLRLFKLK ERYRNVLDTMFELLPRMASLGLTLLIFYYSFAIVGMEFFCGIV FPNCCNTSTVADAYRWRNHTVGNRTVVEEGYYLNNFDNILNS FVTFLFELTVVNNWYI IMEGVTSQTS HWSRLYFMTFYIVTMVVM TIIIVAFILEAFVFRMNYSRKNQDSEVDGGITLEKEISKEELVA VLELYREARGASSDVTRLLLETLSQMERYQQHSMVFLGRRSRTK SDLSLKM YQEEIQEWYEEHAREQEQQRQLSSSAAPAAQPPGS RQRSQTVT</p>

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384	1123	1	986	LAGVGTQAPRRPFGGEMAAGQNGHEEWVGSAYLFEVSSLDKVV LSDAYAHPPQKVAVYRALQAALAESGGSPDVLQMLKIHRSDPQ LIVQLRFCGRQPCGRFLRAYREGALRAALQRLAALAAHQHSVP LQL\DLRAGAERLEALLADEERCLSCILAQQPDRLRDEELAEL EDALRNLCGSGARGGDGEVASAPLQPPVPSLSEVKPPPPPPPP AQTFLFQGGPVVNRPLSLKDQQTFAFSVGLKWRKVGRSLQRC RALRDPALDSLAYEYEREGLYEQAQQLLRFFVQAEGRRATLQR LVEALEENELTSLAEDLLGLTDPNGGLA
385	1124	2409	399	SSKPKLKKRFSLSVGRSVGRSVRGILQWRGTVDPSSAGPLE TSSGPPVLGGNSNSNSGGAGTVGRGLVSDGTSPGERWTHRFE RLRLSRGGGALKDAGMVQREELLSFMGAEEAAPDPAGVGRGG GVAGPPSGGGGQPPQWKCRLLLRSEGGGGGSRLEFFVPPKAS RPLRSIPCSSITDVRTTTALEMPDRENTFVVKVEGPSEYIMET VDAQHVKAWSVDIQECLSPGPCPATSPRMTLPLAPGTSFLTR ENTDSLELSCLNHSESLPSQDLLLGPSESNDRLSQGAYGGLSD RPSASISPPSASIAASHFDSMELLPPPELPPRIPIIEGPPAGTV HPLSAPYPPLDTPETATGSFLFQG\EPEGGEQDQLSGYPWFH GMLSRLKAAQLVLTGGTGSFGVFLVRQSETRRGEYVLTFFNFQ KAKHLRLSLNEEGQCRVQHLWFQSFIDMLEHFRVHPIPLESGG SSDVVLVSYPSSQRQQEQSRASAGEEVPVHPRSEAGSRLGAM RGAREMDATPNASCTLMFPGASDC\EPTTSHDPPQPPEPPSW TDPPQPGEE\EASR\APGSGGQAAAAAKERQEKEKAGG\GGV PEE\LVPVV*LVPVGELGEGHRPQAQEAQRLGPGGDAGVPP\ MVQLQQSPLGG\DGEEGGHPR\AI\NNQYSFV
386	1125	2204	1042	FRAPVGTAAASPQVVIRRLPPGLTKEQLEEQLRPLPAHDYFEF FAADLSLYPHLYSRAYINFRNPDDILLFRDRFDGYIFLDSKDP EYKKFLETYCVEEKTSANPETLLGEMEAKTRELIARRTTPLL EYIKNRKLEKQRIREEKREERRRRELEKKRLREEKRRRREEE RCKKKETDKQKKIAEKEVRIKLLKKPEKGEEPTTEKPKERGE IDTGGGKQESCAPGAVVKARPMEGSLEEPQETSHSGSDKEHRD VERSQEQSESAQRYHVDDGRRHRAHHEPERLSRRSEDEQRWGK GPGQDRGKKGSGDSGAPGEAMERLGRAQRCDSPAPRKEERLAN KDRPALQLYDPGARFRARECGGNRRICKAEGSGTGPEKREEAE
387	1126	176	800	GVWGVCSVGLLQVGSQRAQAWRAWSPMETPLTGTFLWPHIPQG LFFDDSYGFYPQVLIQPAKIFSSVQWLSGVKPVLSKSKFRV VVEEVQVVELKVTWITKSFCPGGTDSVSPP/PSVITQENLGRV KRLGCFDHAQR/HAWGALSVCLPSQGRASQDCLGMSRKKLRPG GGLYGQEGEAPVEEAGCADHVMLPRHPVFPFGPFHGRPR

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388	1127	1	2017	FRDSSPCSAFEFHCLSGECIHSSWRCDGGPDCKDKSDEENCAV ATCRPDEFQCS DGNCIHGSRQCDREYDCKDMSDEVGCVNVTLC EGPNKFKCHSGECITLDKVCNMARDCRDWSDEPIKECGTNECL DNNGGC SHVCNDLKIGYECLCPDGFQLVAQRRCEDIDECQDPD TCSQLCVNLEGGYKCQCEEGFQLDPHTKACKAVGSIAYLFFTN RHEVRKMTLDRSEYTS LIPNLRNVVALDTEVASNRIYWSDL SQ RMICSTQLDRAHGVS SYDTVISRDIQAPDGLAVDWIHSNIYWT DSVLGTVSVADTKGVKRTLFRENGSKPRAIVDPVHGFMYWT DWGTPAKIKKGG LNVVDIYSLVTENIQWPNGITL DLLSGRLYW VDSKLHSSISIDVNGGNRKTILEDEKRLAHPFSLAVFEDKVFW TDIINEAIFSANRLTGSDVNLLAENLLSPEDMVL FHNLTQPRG VNW CERTT LSNGGCQYLCLPAPQINPHSPKFTCACPDGMLLAR DMRSC LTEG\ EAAVATQETSTVRLKVS STAVRTQHTTTTRVPD TSRLPGATPGLTTVEIVTMSHQALGDVAG\ RGN\ EKKPSSVRA LSIVLP IV\ LLVFLCLGVFLLWKNWRLKNINS INFDPVYQKT TEDEVHICHNQDGYSYPSRQMVSL EDDVA
389	1128	2299	1148	RIPGLGPPGSPPPPPHVRGMPGCPGCGMAGPRLLFLTALAL ELLGRAGGSQPALRSRG TATACRLDNKESSESWGALLSGERLDT WICSLILGSLMVGLSGVFLLVI PLEMGTMLRSEAGAWRLKQLL SFALGGLLGNVFLHLLPEAWAYTCSASPGGEGQSLQQQQQLGL WVIAGILTFLALEKMFLDSKEEGTSQAPNKDPTAAAAALNGGH CLAQPAAEPLGAVVRSIKVSGYLNLLANTIDNFTHGLAVAAS FLVSKKIGLLTTMAILLHEIPHEVGDFAILLRAGFDRWSAAKL QLSTALGGLL GAGFAICTQSPKGVEETAAWVLPFTSGGFLYIA LVNVLPDLLEEDPWRS LQQLLLLCAGIVVMVLFSLFVD
390	1129	1	523	GKVSAGQAGADRTLRRAP EPRFSQEPTGNSAYPQLRPFLDPQG RDLKPSALVPPTRSHTGRRPWLHTQPLPGPQGRAWGPTC/TPA CVDRVLESEEGRREYLAFPTSKSSGQKGRKELLKGNRRIDYM LHAEGLCPDWKAEEVEEFSFITQLSGLTDHLPVAMRLMVSSGE EEA
391	1130	1459	765	PCGGIRLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGS AVIKFCLFCTVVSLLGILVFSLHCPSPVMAGVTASYGGSLLPE GHLNLTAPCNAACSCQPEHYS PVCSDGLMYFSLCHAGCPAAT ETNVDGQKVSGAAAYRPCPLDPGKGPCLPLVIGAIVGLPRC TETVAVSLRIFPLVLAM\HCREMHFNLSKAPP SGFHIRCNFL YIPQOHSCTNGNSTMCP
392	1131	1668	962	LLRKVGAPGGARGVIRLLDWFERPDGFLLVLERPEPA\QD\LF DFITERGALDEPLARRF\FAQVLA AVRHCSCGVVHRDIKDEN LLVDLRS GELKLIDFGSGALLKDTVYTD FGDTRVYSPPEWIRY HRYHGRSATVWSLGVLLYDMVCGDIPFEQDEEILGRLLFRRR VSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADGGAPESC DLRLCTLDPDDVASTTSSSESL

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393	1132	3	817	GKNSQKASPVDDEQLSVCLSGFLDEVMKKYGSIVPLSEKEVLGRLKDVFNEDFSNRKPFINREITNYRARHQCENFRIFYNKHM LDMDDLATLDGQNLNDQVINMYGELIMDAVPDKVHFFNSFFHRQLVTKGYNGVKRWTKKVDLFKKSLLLIPIHLEVHWSLITVTLSNRIISFYDSQGIHFKFCVENIRKYLLTEAREKNR\LNQGWQTA VTKCIPQQKNDSDCGVFLQYCKCLAL\KQPFQFSQEDMPVRVKRIYKELCECRLMD
394	1133	1252	628	PPGG*QGSAAKHR/FP/KGYRHPALEARLGRRTVQEARALLRCRRAGISAPVVFVDYASNCLYMEEIEGSVTVRDYIQSTMETE K\TPQGSLNLAKTIGQVLARMHDEDLIHGDLTTSNMILLKPPLEQLNIVLIDFGLSFISALPEDKGVLDLYVLEKAF LSTHPNTETVF EAF LKSYSTSSKKARPVLKKLDEVRLRGKKRSMVG
395	1134	2	1595	RACVFRPEDMMQGEAHPASLIDRTIKMRKETEARKVVLAWGL LNVSMAGMIYTEM TGKLISYYNVTYWPLWYIELALASLFS LNALFD FWR YFKYTVAP TSLV VSPGQQ TLLGLKTAVVQTTPPHDL AATQIPPAPPSPSIQGQSVLSYSPSRSPSTSPKFTTSCMTGYS PQLQGLSSGGSGSYSPGV TYSVSGYNKLASFSPSPSPYPTT VGPV ESSGLRSRYRSSPTVYNSPTDKEDYMTDLRTDLTFLRSE EEKQHRVKLGSPDSTSPSSSPTFWNYSRSMGDYAQTLKKFQYQ LACRSQAPCANKDEADLSSKQAAEEVWARVAMNRQLLDHMSW TAKFRNWINETILVPLVQEIESVSTQMRMGCPELQIGEA SIT SLKQAALVKAPLIPTLNTIVQYLDLTPNQEYLFERIKELSQQG CMSSFRWNRGGDFKGRKWD TDLPTDSAIIMHVFCTYLD SRLPP HPKYPDGKTFTTSQHVFQTPNKP DVTNENVF CIYQSAINPPHYE LIYQRHVYIPAKGQK
396	1135	16	1542	SSAVEFINRNSVVQVLLAAGADPNLGDDFSSVYKTAKEQGIH SLEVLITREDDFNNRLNNRASFKGCTALHYAVLADDYRTVKEL LDGGANPLQRNEMGHTPLDYAREGEVMKLLRTSEAKYQEKQRK REAEERRRFFLEQRLKEHIIQESAIATVGAAIRRKENGWYDE EHPLVFLFLGSSGIGKTELAKQTAKYMHKDAKGFIRLDMSEF QERHEVAKFIGSPPGYVGHEEGQLTKKLKQCPNAVVLDFEVD KAHDPVLTIMLQLFDEGRITDGKGK TIDCKDAIFIMTSNVASD EIAQHALQLRQEALEMSRNR IAENLGDVQISDKITISKNFKEN VIRPILKAHFRRDEFLGRINEIVYFLPFCHSELIQLVNKELNF WAKRAQRHNITLLWDREVADVLVDGYNVHYGARS IKHEVERR VGNQLAAAYEQDLLP\GGCTLRITVEDSDKQLLKSPELSPQA EKRLPKLRLEI IDKDSKTRRLDIRAPLHPEKVCNTI
397	1136	1848	1602	SSCDRERHSGSLGMMSGSFILCLALVTRWSPQASSVPLAVYESK TRKSYSQRDRDGKDRSQGMGLSLLVETRKL LLSANQG

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398	1137	1497	717	HTPMA/FFL/SFLSTSET/VYTFVILPKMLINLLSVARTISFN CCALQMFFFLGFAITNCLLLGVMGYDRYAAICHPLHYPTLMSW QVCGKLAACAIGGFLASLTVVNLVFSLPFCSTNKVNHYFCDI SAVILLACTNTDVNGFVIFICGVLVLVVPFLFICVSYFCILRT ILKIPSAEGRRKAFSTCASHLSVVIVHYGCASFIYLRPTANYV SNKDLVTVTYTIVTPLLNPVYSLRNKDVQLAIRKVLGKKGS LKLYN
399	1138	2	1185	RPPAATRYPREKLKSMTSRDNYKAGSREAA\AAAAA\AAAAA AAAAAEPYPVSGAKRKYLEDSDPERSDYEEQQLQEEEEARKVK SGIRQMRLFSQDECAKIEARIDEVVSRAEKGLYNEHTVDRAPL RNKYFFGEGYTYGAQLQKRGPGQERLYPPGDVDEIPEWVHQLV IQKLVEHRVIEGFFVNSAVINDYQPGGCIVSHVDPIHIFERPI VSVSFFSDSALCFGCKFQFKPIRVSEPVLSLPVRRGSVTVLSG YAADEITHCIRPQDIKERRAVIILRKTRLDAPRLETKSLSSSV LPPSYASDRLSGNNRDPALKPKRSHRKADPDAAHRPRILEMDK EENRRSVLLPTHRRRGFSFSENYWRKSYESSEDCSEAAGSPAR KVKMRRH
400	1139	60	1699	VTWHFYFCSDHKNGHYIIPQMADRSRQKCMSQSLDLSELAKAA KKKLQALSNRLFEEAMDVYDEVDRRENDVWLATQNHSTLVT ERSAVPFLPVNPEYSATRNGRQKLARFNAREFATLIIDILSE AKRRQQGKSLSSPTDNLELSLRSQSDLDQHDYDSVASDETD QEPLRSTGATRSNRARSMDSSDLSDGAVT\LQEYLELKKALAT SEAKVQQLMKVNSSLSD\RLQREHFAP\IHKLQAE NLQL RQPPGPVPTPPLPSERAHTPMAPGGSTHRRDRQAFSMYEPGS ALKPFGGPPGDELTTTLQPFHSTELEDDAIYSVHVPA GLYRIR KGVASASAVPFTPSSPLLSCSQEGSRHTSKLSRHGSGADSDYEN TQSGDPLLGLEGKRFLGKEEDFHPELES LDGDLDPGLPSTE DVILKTEQVTKNIQELLRAAQEFKHDSFVPCSEKIHAVTEMA SLFPKRPALPVRSSLRLLNASAYRLQSECRKTVPPPEPGAPVD FQLLTQQVIQCAVDIAKAAQLVTITTREKKQ

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401	1140	1	1863	<p>RYLSYGSGPKRFPLVDVLQYALEFASSKPVCTSPVDDIDASSP PSGSIPSQTLPTSTTEQQGALSSELPTSTSPSSVAAISSRSVIHK PFTQSRIPPDLPMPAPRHITTEELSVLESCLHRWRTEIENDT RDLQESISRIRHTIELMYSKSMIQVPYRLHAVLVHEGQANAG HYWAYIFDHRESRWMKYNDIAVTKSSWEELVRDSFGGYRNAS YCLMYINDKAQFLIQEEFN/K/ETGQPLVGIETLPPDLRDFVE EDNQRFKELEEWDAQLAQKALQEKLLASQKLRESETSVTTAQ AAGDPKYLEQPSRSDFSKHLKEETIQIITKASHEHEDKSPETV LQSAIKLEYARLVKLAQEDTPPETDYRLHHVVYFIQNQAPKK IIKTLLEQFGDRNLSFDERCHNIMKVAQAKLEMIPKEEVNLE EYEEWHQDYRKPRETTMYLIIGLENFQRESYIDSLLFLICAYQ NNKELLSKGLYRGHDEELISHYRRECLLKLNEQAELFESGED REVNNGLIIMNEFIVPFLPLLLVDEMEEKDILAVEDMRNRWCS YLGQEMEPHLQEKLTDFLPKLLDCSMEIKSFHEPPKLPSTH ELCERFARIMLSLSRTPADGR</p>
402	1141	1	465	<p>AQVYVRMDSFDEDLARPSGLLAQERKLCRDLVHSNKKEQEFRS IFQHIQSAQSQRSPSELFAQHM\VPVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAANKKSPEIHRRIDISPSTFRKHGLA HDEMKSREPFGYKDGHNKSNELQVRNFI</p>
403	1142	2	369	<p>TYTFCFSLMI\ILLTIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTPVPHGFETHTLQEHNLANYLFFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN</p>
404	1143	3115	557	<p>FRKGGGGPKDFGAGLKYNSRHEKVNGLLEEGVEFLPVNNVKKV EKHGPGRWVLA AVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSQVFP LGPYHKESAVTAFSEGSVIAYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTQRTQDNSCSFGLH ARGVELMRFTTPGFDPSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFSNYPYPGHYPNIDCTWNIEVPNNQHVVKVRKFF YLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSSNKITVR FHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRC DGWADCTDHSDELNCSCDAGHQFTCKNKFCCKPLFWVCDLND GDNSDEQGCSCP\AQTFRCNKGKLSKSKQCNKGDDCGDGSDE ASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSGDSDE KDCDCGLRSFTRQARVVGTDADGEWEPWQVSLHALGQGHICG ASLISPWLVSAAHCYIDDRGFYSQDPTQWTAFLGLHDQSQRS APGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVR PICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVI NQTTCEENLLPQQITPRMTCVGLSGGVDSCQDSSGGPLSSVEA DGRIFQAGVVSWDGCAQRNKPGVYTRLPFRDWIKENTGV</p>

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405	1144	1	424	RHEEDLGNLWENTRFTDCSFFVRGQEFKAHKS VLAARSPVFNA MFEHEMEESSKKNRVEINDLDPEVFKEMMRFIYTGRAPNLDKMA DNLLAAADKYALERLKMCEKALCSNLSVENVADTLVLADLHS \AEQLKAQAI DFINRCSVLRQLGCKDGKNWNSNQATDIMETSG GKSMIQSHPHLVAEAFRALASAQGPQFGIPRKRLKQS*NLGNL WENTRFTDCSFFVRGQEFKAHKS VLAARSPVFNAMFEHEMEESS KKNRVEINDLDPEVFKEMMRFIYTGRAPNLDKMA DNLLAAADK YALERLKMCEKALCSNLSVENVADTLVLADLHSGRTVESTSH RLY
406	1145	1	1021	QRGGIPGKFQEDSGSVDWALGPFWGIFQADFGCMRFYLSAQTS DPVLRM*WGPSPISHPTSLCPGGGGAGQTTGSLCLGQQCCPLS CPNIPSRHKRWRL*AALVAGSRGSCTLR*RTPLPVTRNLP R/CHLHLHPTGDLRVHGHQCLLHGHVPPGAALLQCGGCDLRG EAAGLLFLGHACLGRSVNLRDQWLPV\PYSRLCFSGAREGHL PSLAMIHVHCTPIPALVC\PIKVNLLIPVAYLVFWAFLLV FFSFISEHMCVGVGVIIILTGVPFIFFLGFWRSKPKCVHRLTES MTHWGQELCFVVPQDAPEEEENGPCPPSLLPATDKPSKPQ
407	1146	2	1280	AAALVAEYLALLEDHRHLPVGCVSFQNISSNVLEESAISDDIL SPDEEGFCSGKHFTLGLVGLLEQAAGYFTMGGLYEA VNEVYK NLIPILEAHRDYKKLAAVHGLQEAFTKIMHQSSGWVRFGT Y FRVGFYGAHFGDLDEQEFVYKEPSITKLAEISHRLEEFYTERF GDDVVEIIKDSNPVDKSKLDSQKAYIQITYVEPYFDTYELKDR VTYFDRNYGLRTFLCTPFTPDGRAHGE LPEQHKKRKTLLSTDH AFPIYIKTRIRVCHREETVLTP\VEVAIEDMQKKTRELAFATEQ DPPDAKMLQMV LQGSVGP TVNQGPLEVAQVFLAEIPEDPKLFR HHNKLRLCFKDF*KKCEDALRKNKALIGPDQKEYHRELERNY CRLREALQPLLTQRLPQLMAPTPPGLRNSLNRSFRKADL
408	1147	55	651	GEGQQWQSTPLSPLOPTVADFLNLAWWTSAAAW*VLSGRWVEK VLPREGGSEK*GMASSADHLHSAPRALQ\SLFQQLLYGLIY HSWFQAGR*GFGGASSSPGPQSELRLHGE GGVYD*GRPETLP GSVGGAEALWALADPAEAE GSPETRESSCVMKQTQYYFGSVNA SYNAIIDCGNCSRCWQWGGTRGQGRNL
409	1148	1855	904	VAGIPACFDN/FTEALAEACRQMGYSSKPTFRAVEIGPDQDL DVVEITENSQELMRNSSGPCLSGSLVSLHCLACGESLKTFRV VGEEASVDSWPWQVS IQYDKQHVC GGS ILDPHWLTAACHFR KHTDVFNWKVRAGSDKLSFPSLAVAKIIIEFNPMYPKDNDI ALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIIGWGF TKQ NGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE GGVDTCCQGDSSGPLYQSDQWHVVGIVSWGYCGGPGSTPGVYT KVSAYLNWIYNVWKAEL

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410	1149	3	964	TISTVRWNSRIGMVLGVAIQKRAV\PGLY\AFEEAYARADKEA PRPCHKGSWCSSNQLCRECQAFMAHTMPKLKAFSMESSAYNAYR AVYAVAHGLHQLLGACASGACSRGRVYPWQLLEQIHKVHFLHKK DTVAFNDNRDPLSSYNIIAWDWNGPKWTFITVLGSSTWSPVQLN INETKIQWHGKDNQVPKSVCSDDCLEGHQRVVTFGHHCCFECV PCGAGTFLNKS/SYLGKDLDPENYNEAKCVTFSLLEFNFVSWIAF FTTASVYDGKYLPAANMMAGLSSSLSSGGFYFLPKCYVILCRP DLNSTEHFQASIQDYTRRCGST
411	1150	2	1378	VARGAFHPKMGPSFPPSPKPGSERLSFVSAKQSTGQDTEAELQD ATLALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQ AEAQKVTFSDPTTVALCISKEGRPPARISWLSLDWEAKETQ VSGTLAGTVTVTSRFTLVPSGRADGVTVTCKVEHESFEPPALI PVTLSVRYPPPEVSISGYDDNWYLGRTDNLSCDVRSNPEPTGY DWSTTSGTFPPTSAVAQGSQLVIAVDSLNTTFVCTVTNAVGM GRAEQVIFVRETPNTAGAGATGGIIGGIIAAIATADA\TGIL ICRQQRKEQTLQGAEEDEDELEGGPSYKPPTPKAKLEAQEMPSQ LFTLGASEHSPLKTPYFDAGASCTEQEMPRYHELEPTLEERSGP LHPGATSLGSPIPVPPGPPPAVEDVSLDLEDEEGEEEEEEYLDKI NPIYDALSYSSPSDSYQKGKGFVMSRAMYV
412	1151	1	1828	GTRLREDKNHNMVYVAGCTEVEVKSTEEAFVFWRGQKKRRRIAN THLNRESSRSHSVFNILVQAPLDADGDNVLQEKEQITISQLS LVDLAGSERTNRTAEGNRLREAGNINQSLMTRLTCMDVLREN QMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMIVCVNPKAEDY EENLQVMRFAEVTQEEVEVARPVDKAICGLTPGRRYRNQPRGP\ IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRLEALEKRH NLRQMMIDEFNKQSNFAKALLQEFDNAVLSKENHMQGKLENEKE KMISGQKLEIERLEKKNKTLEYKIEILEKTTTIYEEDKRNLOQ ELETQNQKLQRFSDKRRLEARLQGMVTETTMKEKECERRVA AKQLEMQNKLVWKDEKLKQLKAIIVTEPKTEKPERPSRERDREK VTQRSVSPSPVPLLFQPDQONAPPILRLRHRRSRSAGDRWVDHKP ASNMQTETVMQPHVPHAITVSVANEKALAKCEKYMILTHQELAS DGEIETKLIKGDYKTRGGGQSVQFTDITLQKESPNGSRKRR SSTVAPAQPDGAESEWTDVETRCSVAVEMRAGSQLGPGYQHHA QPKRKKP
413	1152	1	336	PFSSSSVSSKGSDFPGTLDPPFGSGSFNSAEGFADFSQMS/KGK STPVSQGLGSADFPPEADPFQPLGADSGDPFQSKKGFDPFSGK DPFVPSAAKPSKASASGFADFTSVS

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414	1153	1	1334	MSLMVVSMACVGLFLVQRAGPHMGGQDKPFLSAWPSAVVPRGG HVTLRCHYRHRFNNFMYLKEDRIHIPIFHGRIFQESFNMSPVT TAHAGNYTCRGSHPHSPTGWSAPSNPVVIMVTGNHRKPSLLAH PGPLVKSGERVILQCWSDIMFEHFFLHKEGISKDPSRLVGQIH DGVSKANFSIGPMMQDLAGTYRCYGSVTHSPYQLSAPSDPLDI VITGLYEKPSLSAQPGPTVLAGEVTLSCSSRSSYDMYHLSRE GEAHERRFSSAGPKVNGTFQADFPGLPATHGGTYRCFGSFRDSP YEWSSNDPLLVSVTGNPSNSWPSPTEPSSETGNPRHLHVLI TSVVIILFILLFFLLHRWCN\KKNAAVMDQESAGNRTANSE DSDEQDPQEVITYTQLNHCVFTRQKITRPSQRPKTPPTDIIVYT ELPNAESRSKVVSCP
415	1154	1	1570	MSLRVHTLPTLLGAVVRPGCRELLCLLMITVTVGPASGVCPT ACICATDIVSCTNKNLSKVPGNLFRLIKRLDLSYNRIGLLDSE WIPVSFAKLNTLILRHNNITSISTGSFSTTPNLKCLDLSSNKL KT\VKNAVFQELKVLEVLLLYNNHISYLDPSAFGGLSQLQKLY LSGNFLTQFPMDLYVGRFKLAELMFLDVSYNRIPSPMPHHINL VPGKQLRGIYLGHPNFVCD\CSLVSLLVFWYRRHFSSVMDFKN DYTCRLWSDSRHSRQVLLQLQDSFMNCSDSIINGSFRALGFIE AQVGERLMVHCDSTGNANTDFIWVGPDRLLLEPKEMENFYV FHNGSLVIESPRFEDAGVYSCIAMNKQRLNETVDVTINVSNF TVSRSHAHEAFNTAFTTLAACVASIVLVLLYLTPCPCKCKT KRQKNMLHQSNHSSILSPGPASDASADERKAGAGKRVVFLEP LKDTAAGQNGKVRFLFPSEAVIAEGILKSTRGKSDSDSVNSVFS DTPFVAST
416	1155	2	1928	ASDFIRSLDHCYLSLEGVFSHKFDLQDVSSVNEDVLLTTG LLCKYTAQRFKPKYKFFHKSFOEYTAGRRLSSLLTSHEPEEVT KNGYLVQKMVSISDITSTYSSLLRYTCGSSVEATRAVMKHLAA VYQHGCLLGLSIAKRPLWRQESLQSVKNTTEQEILKAININSF VECGIHLYQESTSKSALSQEFEAFFQGKSLYINSIGNIPDYLF FFEHLPCASALDFIKLGFYGGAMASWEKAEDTGGIHMEAP ETYIPSRVAVSLFFNWKQEFRTLEVTLRDFSGLNKQDIRYLGKI FSSATSLRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLTI EDERHITSVTNLKTLSDHDLQNRQLPGGLTDSLGNLKNLTKLI MDNIKMNEDAIKLAEGKLNKKMCLFHLTHLSDIGEGMDYIV KSLSEPCDLEETQLVSCCLSANAVKILAQNLHNLVKLSILD SENYLEKDGNEALHELIDRMNVLEQLTALMLPWGCDVQGSLS LLKHLEVPQLVKLGKLNWRITDTEIRILGAFFGKNPLKNFQQ LNLAGNRVSSDGWLAFMGVFENLQVLVFFDFSTKEFLPDPALV RKLSQVLSKLTFLQEARLVGWQFDDDDLSVITGAFKLVT
417	1156	342	718	ASDRKVAMTCDCFWFRMTLDQHASCMVEVGTERERQAG/GLVMF DPSGFPTGEKVLQDDEFTCDLFRFLQLLCEGHNSGL*VPGTSD DTKA*IMFSSQ**QEPVSSNYASF*RQQIILEHGSALGSG

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418	1157	1	135	EITHIVGETAAFLCPRLRLRRGGKDGSPKPGFLASVIPVDRRP GE*DITHIVGETAAFLCPRLRLRRGGKDGSPKPGFLASVIPVD RRPGE
419	1158	173	943	SKFIFYVDSQSMIFFFQTPTRHKVLIMEFCPCGSLYTVLEEPS NAYGLPESEFLIVLRDVVGGMNLRENGIVHRDIKPGNIMRVI GEDGQSVYKLTDFGAARELEDDEQFVSLYGTEEYLHPDMYERA VLRKDHQ\KKYGAT\VDLW\SIGVTIFYQGKPTGS\LAI*HPFE GASVRNKASDGIKIITGKGLLGAI\SIGVTIFYQGKPTGS\LAI*HPFE EDMPVSCSPSSGVLRVNLPVLA\NILESRSRKKCWGF*PSF LQEN
420	1159	987	500	GSTISCERSLRSWTAHWALPEMDSRIPYDDYPVVFLPAYENP PAWIPPHERVHHPDYNNELTQFLPRTITLKKPPGAQLGFNIRG GKASQLGIFISKVIPDSDAHRAQLQEGDQVLAVNDVDFQDIEH SKAVEILKTAREISMRVRFPPYNYHRQKERTVH
421	1160	3	890	HEQVSALHRRRIKAVEVAAMCGVNIICFQEAWTMPFAFCTREK LPWTEFAESAEDGPTTRFCQKLAKNHDMVVVSPILERDSEHGD VLWNTAVVISNSGAVLGKTRKNHPRVGDFFNESTYYMEGNLGH PVFQTQFGR IAVNICYGRHPLNWL MY SINGAEIIFNPSATIG ALSESLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTSGDGK KAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDLNL CQQVNDVWNFKMTGRYEMYARELAEAVKS NYSPTIVKE

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422	1161	5214	352	MAKSGGCGAGAGVGGGNGALTWVNNAAKKEESETANKNDSSKK LSVERVYQKKTQLEHILLRPDTYIGSVEPLTQFMWVYDEDVGM NCREVTFVPGLYKIFDEILVNAADNKQRDKNMTCKIVSIDPES NIISIWNNGKGIPVVEHKVEKVYPALIFGQLLTSSNYDDDEK KVTGGRNGYGAKLCNIFSTKFTVETACKKEYKHSFKQTWMNNMM KTSEAKIKHFDGEDYTCITFQPDLSKFKMEKLDKDIVALMTRR AYDLAGSCRGVKVMFNGKKLPVNGFRSYVDLYVKDKLDETGVA LKVIHELANERWDVCLTLSEKGFQQISFVNSIATTKGGRHVDY VVDQVVGKLIIEVVKKKNKAGVSVKPFQVKNIWVFINCLINP TFDSQTKENMTLQPKSFGSKCQLSEKFFKAASNCGIVESILNW VKFKAQTQLNKKCSSVKYSKIKGIPKLDDANDAGGKHSLECTL ILTEGDSAKSLAVSGLGVIGRDRYGVFPLRGKILNVREASHKQ IMENAEINNIIKIVGLQYKKSYYDDAQSLKTLRYGKIMIMTDQD QDGSIIKGLLINFIIHNWPSLLKHGFLEEFITPIVKASKNKQE LSFYSIPEFDEWKKHIENQKAWKIKYKGLGTSTAKEAKEYFA DMERHRILFRYAGPEDDAAITLAFSKKKIDDRKEWLTNFMEDR RQRLHGLPEQFLYGTATKHLTYNDFINKELILFSNSDNERSI PSLVDGFKPGQRKVLFTCFKRNDRKREVKVAQLAGSVAEMSAYH HGEQALMMTIVNLAQNFGVSGNNINLLQPIGQFTRLHGGKDAA SPRYIFTMLSTLARLLFPVADDNLLKFLYDDNQRVEPEWYIPI IPMVLINGAEGIGTGWACKLPNYDAREIVNNVRRMLDGLDPHP MLPNYKNFKGTIQELGONQYAVSGEIFVVDNRNTVEITELPVRT WTQVYKEQVLEPMLNGTDKTPALISDYKEYHTDTTVKFVVKMT EEKLAQAEAGLHKVFKLQTLTLCNSMVLFDHMGCLKKYETVQ DILKEFFDLRLSYYGRLRKEWLVGMLGAFTKLNNQARFILEKI QGKITI*NRSKKDLIQMLVQRGYESDPVKAWKEAQEKAAEED TQNQHDDSSSDSGTPSGPDFNYILNMSLWLSLTKEKVEELIKQR DAKGREVNDLKRKSPSDLWKEDLA AFVEELDKVESQEREDVLA GMSGKAIKGVGKPKVKKLQLEETMPSPYGRRIIPEITAMKAD ASKKLLKKKKGDLDTAAVKVEFDEEFSGAPVEGAGEEALTPSV PINKGPKPKREKKEPGTRVRKTPTSSGKPSAKKVKKRNPWSDD ESKSESLEETEPVVI PRDSSLRRAAAERPKYTFDFSEEDDD ADDDDDNDNDEELVKASPITNDGEDEFVPSDGLDKDEYTF PGKSKATPEKSLHDKKSQDFGNLFSFPSYSQKSEDDSAKFDSN EEDSASVFSFGLKQTDKVPSTVAACKGKPSDTPVKPKRA PKQKKVVEAVNSDSEFGIPKKTTPKGGKRGAKKRKASGSE NEGDPNPGRKTSKTTSSKKPKKTSFDQSDVDIFPSDFPTEPPS LPRTGRARKEVKYFAESDEEEDDVDFAMFN
423	1162	1	219	KGCLAASFNCIFLYTGELYPTMIR*VEA*WENDSLFLGKDILL CTGQTPELNQVHPSKAPPNTHHCKAHS

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424	1163	1454	446	ENSFECKDCGKAFSRGYQLSHHQKIHTGEKPYECKECKKAFRWGNQLTQHQKIHTGEKPYECKDCGKAFRWGSSSLVIHKRIHTGEKPYECKDCGKAFFRGDELTHQHRFHTGEKDYECKDCGKTFSRVYKLIQHKRIHSGEKPYECKDCGKAFFICGSSLIQHKRIHTGEKPYECQECGKAFTRVNYLTQHQKIHTGEKPECKECKGKAFRWGSSLVKHERIHTGEKPYKCTECGKAFNCGYHLTQHERIHTGETPYKC KECGKAFTYIGSSLVKHERIHTGVKPYGCTECGKSFSHGHLTQHKTHTSGAKSYECKECKGACNHLNHLREHQRIHNS
425	1164	826	407	HQYLLDDLYPLHVMITILLKSHFFTMLKRPVGSSEFASLPFYHQSILLRKNQMKRKKTKQDLTHINWTLQAVSIQTCIWLQKKPSSYFHQLPNQVL*PENSGPESCLYDLAAVVVHHGSG
426	1165	464	29	XLDPTLPAVATLLMDVMFYNGVKDPMATGDDCGHIRFFSFSLIEGYISLVMDVQTQQRFPNLLFTSASGELWKMVRIGGQPLGFGPVWESGPTGPTSPILPVTSSSHRQAASQVTTTKQGQWLC LKRPSARSPDHACLG*
427	1166	649	901	EAPLTSVCFSLERRFGSSSNTTSFGTLASQNAPTFGSLSQQTS GFGTQSSGFGSGTGGFSGSNNS*VSPFLSLTLIKSIK
428	1167	3	340	EEPQGSPIWVWLAGSLTSVSCFLPFQRMRIKPHQGYIGEMSF LQHHKGECPQKD*ARQENPCGPCSERRKHLLGQDPKTCCKSC KNTDSRCKARPLELNERTCRCDKPRR
429	1168	355	1312	TLWAGPGLCPQSHSSSSVPAPWEPHVERALRTDRNQQRPLLS ASWAPAPARPLFLTSPVLLPKSRAIPAARDPS*AGIFCLLEMA GGQASVVIIGSAGVLGCRWGSSGKSHSLSPSRKGNLHLLSQEP QTTVVHNATDGIKGSTESCNNTTTEDEDLKVRKQEI IKITEQLI EAINNGDFEAYTKICDPGLTSFEPEALGNLVEGMDFHKFYFEN REWVRAADILLPAPLPLCLCLLLTFSSQLPTFPFLDLRAALLL CMLVPLCPDGCRCQAPLKALLSSKCHSFCSCFVAVPVTTIKLT YFLPGAVAYACNPNTLGG
430	1169	439	728	ERAGAGGAAACRAGTRSGATSRTPWPLHRQLSMMMLAQSNPQ LFAIMGTRAGIARELERVEQQSRLEQLSAAELQSRNOGHWADW LQAYRARLGQ
431	1170	3	440	NGTLFIMVMHIKDLVSDYKE*WL*RKPLPW*EALLLRDCFFF* VTENGADENPYVKTYLLPDNHKTSKRKTKISRKTRNPTFNEML VYSGYSKETLRQRELQLSVLSAESLRENFFLGGVTLPLKDFNL SKETVKWYQLTAATYL

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432	1171	433	1824	LHRIMQLAVVVSQVLENGSSVLVCLLEEGWDITAQVTSLVQLLS DPFYRTLGEFQMLVEKEWLSFGHKFSQRSSLTLCQSGGFAPV FLQFLDCVHQVHNQYPTEFEFNLYLKFALAFHYVSNRFTKTFLL DSDYERLEHGTFLFDDKGEKHAKKGVCIEWECIDRMHKRSPFIFFN YLYSPLEIEALKPNVNVSSSLKKWDYIEETLSTGSPSYDWMMLT PKHFPSSESDSLAGEAGPRSQRRTVWPCYDDVSCTQPDALTSLF SEIEKLEHKLNAPEKWQQLWERVTVDLKEEPRTDRSQRHLSR SPGIVSTNLPSYQKRSLLHLPDSSMGEEQNSSISPSNGVERR ATLYSQYTSKNDENRSFEGTLYKRGALLKGWKPRWFVLDVTKH QLRYYDSGEDTSCKGHIDLAEVEMVIPAGPSMGAPKHTSDKAF FDLKTSKRVYNFCAQDQGSQAQQWMDKIQSCISDA
433	1172	1714	946	EVEGPRRVSPAPETLGMEEVVRPSVVFVDGQTDIPFTRLGRS HRRQSCSVARVGLGLLLLLMGAGLAVQGWFLQLHLWRLGEMVT RLPDGPAGSWEQLIQERRSHEVNPAHLTGANSLSLTGSGGPILL WETQLGLAFLRGLSYHDGALVVTKAGYYYIYSKVQLGGVGCPL GLASTITHGLYKRTPRYPPEELELLVSQQSPCGRATSSSRVWWD SSFLGGVVHLEAGEEVVVRVLDRLVRLRDGTRSYPGAFMV
434	1173	16	367	QSAELGPRRREGSRPSCTKASKPWRRRPGGPTSGLG*GPLSP GPYQCRPSLPAQLYPSLMAAATLRTPQVSAASSRPHTPSPT HVLKPSVGRACSSPRCPGSGTLRRSWVGPF
435	1174	27	1139	LWWPPLSRHAAHRQWPGPTAPRGLGHKVKGRGASPAAMWSCSW FNGTGLVEELPACQDLQLGLSLLSLLGLVGVPGVGLCYNALLV LANLHASKASMTMPDVYFVNMAVAGLVLSALAPVHLLGPSSRW ALWSVGGEVHVALQIPFNVSSLVAMYSTALLSLDHYIERALPR TYMASVYNTRHVCGFVWGALLTSFSSLLFYICSHVSTRALEC AKMQNAEADATLVFIGYVVPALATLYALVLLSRVRREDTPLD RDTGRLEPSAHRLLVATVCTQFGLWTPHYLILLGHTVIIISRGK PVDAYHLGLLHFVKDFSKLLAFSSSFVTPLLYRYMNQSFPSKL QRLMKKLPCGDRHCSPDHMGVQQVLA
436	1175	322	756	SESELFTLMPSLPTTNCVHSLQMIPPLSPAPNQELVLGLCYMS YLAFLYMTFDFCCLYFSTVYAPSFKYICVHTDTHICVCVCIYL SSVSKSSAEADGVLPQRRHPASLLIVFATSISESSLLIFSFO KTEAKLIVFAVSLAAK
437	1176	2	153	FFFLRQSLTSLSPRLECSGATSASPSAGITGMSHHSQPIVNFLR ACIPISK
438	1177	1	692	RQHAEERGRNPKTGLTLERVGPESSPYLLRRHQRGQGEHY HSCVQLAPTRGLEES/GHGPL/SLAGGPRVGGV/AAAATEAPR MEWKVKVRSDBGTRYVAKRPVRDRLLKARALKIREERSGMTTDD DAVSEMKGGRYWSKEERKQHLIRAREQRKRREFMMQSRLECLR EQONGDSKPELNI IALSHRKTMKRKNKKILDNWTIQEMLAHG ARSADGKRVYNPLLSVTTV

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439	1178	2	616	SDRGCSAAAGRNM TAVGVQAQRPLGQRQPRRSFFESFIRTLII TCVALAVVLSSVSICDGHWLLAEDRLFGLWHFCTTTNQSVPIC FRDLGQAHVPGLAVGMGLVRSVGALAVVAAIFGLEFLMVSQLC EDKHSQCKWVMGSILLVSVFLSSGGLLG FVILLRNQVTLIGF TLMFWCEFTASFLFLNAISGLHINSITHPWE
440	1179	2	540	QILPNLYLGSARDSANLESLAKLGIRYILNVTNLPNFFKNG DFHYKQIPISDHWSONLSRFFPEAIEFIDEALSQNCQGVLVHCL AGVSRSVTVTVAYLMQKLHLSLNDAYDLVKRKSNI SPNFM GQLLDFERSLRLEERHSQEQQSGGQASAA SNPPSFFTTPTSDG AFELAPT
441	1180	940	463	RKSLHENKLRLOEKVEVLEAKKEELETENQVLNRQNVFPEDY TRLOKRLKDIQRRHNEFRSLILVPMNPPTASINPVSFQSSAMG SKHGTTISSSYAGGTTSKGTLSTSQKTRRTGNNTKKTTRGTWI FRRMMFLENRQIKRGEVGD SVKLDILT CGI
442	1181	1	986	GRPGAGASELFPSVTTDL SVSKQNA CLTCVDFVT VHVMGFWG IGPALSTSCIPYPLSHGPSVKAEMLMYSQKDPLILCVRLA VLLAVTLTVPVVLFPIRRALQQLLFP GKAFSWPRHVAIALILL VLVNVLVICVPTIRDFGVIGSTSAPSLIFILPSIFYLRIVPS EVEPFLSWPKIQALCFGVLGVLFMAVSLGFMFANWATQSRMS GH*SGPAGPGCAHAHGGVRAAP*GPSCPTCGGWF*TWLSE AGDSRGCRLAHFPPPPQGCQAWIMALIPTPTPWE EEEEEEEEEEE EARSWWSLCPAQSSLPPPG
443	1182	460	27	INELRYHLEESRDKNVLLCLEERDWD PGLAIIDNMQSINQSK KTVFVLTKKYAKSWNFKTAFYLALQRLMDENMDVII FILLFPV LQHSQYLRLRQRI CKSSILQWPDNPKA EGLFWQTLRNVVL TEN DSRYNMYVDSIKQY
444	1183	1682	230	DDPIKTSWTPPRYVLSMSEERHERVRKKYHILVEGDGIPPPIK SFKEMKFPAAILRGLKKKGIIHPTPIQIQGIPTILSGRDMIGI AFTGSGKTLVFTLPVIMFCLEQEKRLPFSKREGPYGLIICPSR ELARQTHGILEYYCRLLOEDSSPLLRCALCIGMSVKEQMETI RHGVHMMVATPGRLMDLLQKKMVSLDICRYLALDEADRMIDMG FEGDIRTIFSYFKGQRQTLLFSATMPKKIQNFAKSALVKPVTI NVGRAGAASLDVIOVEYVKEEAKMVYLLECLQKTPPPVLIFA EKKADVDIAIHEYLLKGV EAVAIHGGKDQEERTKAIEAFREGK KDVLVATDVASKGLDFPAIQHVINYDMPEEIEINYVHRIGRTGR SGN TGIATTFINKACDESVM DLKALLLEAKQKVPPVLQVLHC GDESM LDIGGERGCAFCGGLGHRITDCPKLEAMQTKQVSNIGR KDYLAHSSMDF
445	1184	1	375	IETTQPS EDTNANSQDNMQPETSSQQQLSPTLSDRGGS RQD AADAGKPQRKFGQWRLPSAPKPI SHSVSSVNLRFGGRTTMSV VCKMNPMTDAASCSEVKKWWTRQLTVESDES GDDLLDI
446	1185	2	223	NDRFSACYFTLKLKEAAVRQREALKLTKN IATDSYISVNL RD VYARSIMEMLR LKGRERASTRSSGGDDFWF

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447	1186	2	1031	FTVFILGITIRPLVEFLDVKRSNKKQQA VSEEIYCR LFDHVKT GIEDVCGHWGHNFWRDKFKKFDDKYLRLKLLIRENQPKSSIVSL YKKLEIKHAIEMAETGMISTVPTFASLND CREEKIRKVTSSSET DEIRELLSRNLYQIRQRTLSYNRHS LTADT SERQAKEILIRRR HSLRESIRKDSLSNREHRASTSTSR YLSLPKNTKLPEKLQKR TISIADGNSSSDADAGTTVLNLQPRARRFLPEQFSKKS PQSY KMEWKNEVDVDSGRDMPSTPPTPHSREKGTQTSGLLQQPLL SK DQSGSEREDSLTEGI PPKPPPRLVWRASEPGSRKARFGSEKP
448	1187	3	444	HEEASGLSVWMGKQMEPLHAVPPAATLILSLLVAVFTECTSN VATTTTLFLPIFASMSRSIGLNPLYIMLPCTLSASFAMLPVAT PPNAIVFTYGH LKVADMVKTGVIMNIIGVFCVFLAVNTWGRAI FDLDHFPD WANVTHIET
449	1188	3	125	HELENNWLQHEKAPTEEGK KELLALS NANPSLLERHCAYL
450	1189	1	188	GNIIYMYMQPGARSSQDQ GKFLT LFNIVTPLL NPLIYTLRNR EVKGALGRLLL GKREL GKE
451	1190	10	1879	PLEQRSNCRVDPVRVTHMASDTSSLVQSHTYKKREPADV PYQ TGQLHPAIRVADLLQHITQMKCAEGYGFKEEYESFFEGQSAPW DSAKKDENRMKNRYGNIIAYDHSRVLQTIEGDTNSDYINGNY IDGYHRPNHYIATQGP MQETIYDFWRMVHENTASIMVTNLV EVGRVKCKYWPDDTEIYKDIKVT LIETELLA EYVIRTF AVEK RGVHEIREIRQFHFTGWPDHGVPHYATGLLGFVRQVKS KSPPS AGPLVVHCSAGAGRTGCFIVIDIMLMAEREGVVDIYN CVREL RSRRVNMVQTEEQYVFIHDAILEACLCGDTSPASQVRS LYD MNKLDPQTNSSQIKEEFRTLNMVTPTLRVEDCSIALPRNHEK NRCMDILPPDRCLPFLITIDGESSNYINAALMDSYKQPSAFIV TQHPLPNTVKDFWRLVLDYHCTSVVMLNDV DPAQLCPQYWPEN GVHRHGPIQVEFVSADLEEDIISRI FRIYNAARPQDGYRMVQQ FQFLGWPMYRDTPVSKRSFLKLIRQVDKWQEEYNGGEGRTVVH CLNGGGRSGTFC AISIVCEMLRHQRTVDVFHAVKTLRNNKPNM VDLLDQYKFCYEVALEYLNSG
452	1191	603	342	PLTYNKKYTPWWGDALGWLLALSSMVCIPAWSLYRLGTLKGP FRERIRQLMCPAEDLPQRNPAGPSAPATPRTSLRLTELESHC
453	1192	120	449	TLSESGALFSLGPPPLSLKSSSAPRPYSTLRDCLEHFAELFDL GFPNPLAERII FETHQIH FANCSLGQPTFSDPPEDVLLAMIIA PICLIPFLITLVVWRSKDSEAQA
454	1193	1838	1066	CEEREQEKDDVDVALLPTIVEKVILPKLTVIAENMWDPFSTTQ TSRMVGITLKLINGYPSVVNAENKNTQVYLKALLRMRRTLDD DVFMPLYPKNVLENKNSGPYLFFQRQFWSSVKLLGNFLQWYGI FSNKT LQELSIDGLLNRYILMAFQNSEYGD DSIIKKAQNVINCF PKQWF MNLKGERTISQLENFCRYLVHLADTIYRNSIGCS DVEK RNAREN IKQIVKLLASVRALDHAMSVASDHNVKEFKSLIEGK

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455	1194	112	1361	TPFCFLCSLVFRSRVWAEPCCLIDAAKEEYNGVIEEFLATGEKL FGPYVWGRYDLLFMPPSFPPGGMENPCLTFVTPCLLAGDRSLA DVIIIEISHSWFGNLVTNANWGEFWLNEGFTMYAQRRIISTILF GAAYTCLEAATGRALLRQHMDITGEENPLNKLRLVKIEPGVDPD DTYNETPYEKGFCFVSYLHLVGDQDQFDSFLKAYVHEFKFRS ILADDFLDIFYLEYPPELKKRVDIIPGFEFDRWLNTPGWPPYL PDLSPGDSLMPKPAEELAQLWAAEELDMKAEAVAI SPWKTYQL VYFLDKILQKSPPLPPGNVKKLGDITYPSISNARNAELRLRWGQI VLKNDHQEDFWKVKEFLHNQKQKYTLPLYHAMMGSEVAQTL AKETFASTASQLHSNVVNYVQQIVAPKGS
456	1195	1	889	CASGSSGWRPVLWAGAFMASAELDYTTIEIPDQPCWSQKNSPS PGGKEAETROPVVILLGWGGCKDKNLAKYSAIYHKGRCIVIRY TAPWHMVFFSES LGIPSLRVLAQKLELLFDYEIEKEPPLLFHV FSNGGVMLYRYVLELLQTRRFCLRLRVVGTIFDSAPGDSNLVGA LRALAA ILERRAAMLRLLLLVAFALVVVLFHVLLAPITALFHT HFYDRLQDAGSRWPELYLYSRADEVVLARDIERMVEARLARRV LARSVDVFSSAHVSHLRDYPTYTSLCVD FMR \NWVRC
457	1196	2	295	PRVRDRLPSTGVRDRKGDKPWKESGGGSVEAPRMGFTHPGHLS GCQSSLASGETGTGSADPPGGPRPGLTRRAPVKDTPGRAPAD AAPAGPSSCLG
458	1197	1299	682	QGR TSCIGLYTYQRRICKYRDQYNWFFLARPTTFAI IENLKYF LLKKDPSQPFYLGHTIKSGDLEYVMEGGIVLSVESMKRLNSL LNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGK DVFNTKSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQM HVMYGVYRLRAFG \HIFNDALVFLPPNGSDND
459	1198	779	61	HEGKPTRGRGRGGSLSLSTRGRGSEVPDSAHLAPTPLFSESGCCG LRSRFLTDCMEEGGLGGLIKMVHLLVLSGANGMQMWTFVS GFLFLRSLPRHTFGLVQSKLFPFYFHISMGC AFINLCILASQH AWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQT VEKERGLGGEVPGSHQGPDPYRQLREKDPKYSALRQNF FRYHG LSSL CNLGCVL SNGLC LA \ALPWK
460	1199	517	815	KQLDKQLRADPSGSLPPLPPSPPPPLEAGGRPPEVP/PRGPSA VPSFPSVSGDWGGPVEAG/EGGQQGRGRARARPCSLPPLPPS PVCRLSGSRAPLGCDG
461	1200	1	583	RNQLSSQKSVPWVPIKSLPLWAIIVVAHFSYNWTFYTLTLLP TYMKEILRFNVQENGFLSSLPYLGSWLCMILSGQAADNLRAKW NFSTLCVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVFLTIS TTLGGFCSSGFSINHLDIAPSYAGILLGITNTFATIPGMVGPV IAKSLTPDMGISLHRPGWSAVA
462	1201	25	383	GPSGTT HASAHSCHPGSPRGSLSRHPSSQLAGPGVEGEGTQK PRDYIILAILSCFCPMWPVNIVAFAYAVMSRNSLQQGDVDGAQ RLGRVAKLLSIVALVGGVLI I IASCVINLG VYK
463	1202	573	372	SLFLSFPPLSPKMTLNDAMRNKARLSITGSTGENGRVMTPEFP KAVHAVPYVSPGMGMNVSVTDLS

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464	1203	2018	491	DDVPPFPAPDLYDVPPGLRRPGPGTLYDVPRERVLPPEVADGGV VD SGVYAVPPPAEREAPAEGRKLSASSTGSTRSSQSASSLEVA GPGREPLELEVAVEALARLQQGVSA TVAHLLDLGASAGATGSW RSPSEPQEPVLVQDLQA AVAAVQSAVHELLEFARSAGVNAHTS DRALHAKLSRQLQKMEDVHQT LVAHGQALDAGRGGSGATLEDL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPEGGG TLHPNPTDKTSSIQSRPLPSPPKFTSQDS PDGQYENSEGGWME DYDYVHLQKKEFEKTQKELLEKGSITROGKSQLELQQLKQFE RLEQEVSRPIDHDLANWTPAQPLAPGRTGG LGPSDRQLLLFYL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILSAHK LVFIGDTLSRQAKAADVRSQVTHYSNLLCDLLRGIVATTKAAA LQYPSPSAAQDMVERVKELGHSTQQFRRVLGQLAAA
465	1204	299	189	EMEEPQKSYVNTMDLERDEPLKSTGPQISVSEFSCHCCYDILV NPPTLNCGHSFRCRHCLALWWASSKKTECPECREKWEFGPKVSI LLRDAIEKLPDAILRFEDIQQNNDIVQSLAAFQKYGNDQIP LAPNTGRANQQMG GFFSGVLTALTGVAVVLLVYHWSRESEH DLLVHKAVAKWTAEEVVLWLEQLGPWASLYRERFLSERVNGRL LLTLTEEEFSKTPYTIENSSHRAILMELERVKALGVKPPQNL WEYKAVNPGRSFLLYALKSSPRLSLLYLYLFDYTDTFLPFIH TICPLQEDSSGEDIVTKLLDLKEPTWKQWREFLVKYSFLPYQL IAEFAWDWLEVHYWTSRFLIINAMLLSVLELFSFWRIWSRSEL K*VGFRFLRLGVAALGSVEVAGLRGVVKGERPLLYGHGAGARF PHSVLLLPVAKPLPLPLPRGLC
466	1205	2	242	EKARMIYEDYISILSPKEVSLDSRVREVINRNLLDPNPHMYED AQLQIYTLMHRDSFPRFLNSQIYKSFVESTAGSSSES
467	1206	2	619	LYYSQDEESKIMISDFGLSKMEGKGDVMSTACGTPGYVAPEVL AQKPYSKAVDCWSIGVIAIYILLCGYPPFYDENDSKLFEQILKA EYEFDSPYWDIDSDAKDFIRNLMKDPNKRYTCEQAARHPWI AGDTALNKNIHESVSAQIRKNFAKSKWRQAFNATAVVRHMRKL HLGSSLDSSNASVSSSLSLASQKDCASGTFHAL
468	1207	1	352	RTRGGAVSFEDFIKGLSILLRGTQVEKLNWAFNLYDINKDGYI TKEEMLDIMKAIYDMMGKCTYPVLKEDAPRQHVETFFQKMDKN KDGVVITIDEFIESCQKDENIMRSMQLFENVI
469	1208	3	1015	PRSPHEHTPAWHEGRSLGPIMASMA DRNMKLFSGRVVPAQGE TFENWLTQVNGVLPDWNMSEEEKLRLMKTLRGPA REVMRVLQ ATNPNL SVADFLRAMKLVFGESESSVTAHGKFNTLQAQGEKA SLYVIRLEVQLQNAIQAGIIAEKDANRTRLQQLLLGGELSRL RLRLKDFLRMYANEQERLPNFLELIKMVREEDWDDAFIKRKR PKRSESMVERAVSPVAFQGSPPPIVIGSADCNVIEIDDTLDDSD EDVILVESQDPPLPSWGAPPLRDRARPQDEV LVIDSPHNSRAQ FPSTSGGSGYKNNPGEMRRARKRKHTIRCSYC GEE
470	1209	1543	1351	SVACTVPLRSMSPDPQDFDKEPDSSTKHSTPSNSSNPSPGPPS PNSPHRSQLPLEGLEQ PACDT

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471	1210	3	952	YSAVEFAERGSGGSSGDELREDDEPVKKRGRKGRGRGPPSSSD SEPEAELEEREAKKSAKKPQSSSTEPARKPGQKEKRVRPPEEKQQ AKPVKVERTRKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKF ALKVDS PDVKRCLNALEELGTLQVTSQILQKNTD VVATLKKIR RYKANKDVMKAAAEVYTRLKSRVLGPKIEAVQKV N KAGMEKEK AEEKLAGEELAGEEAPQEKAEADKPS TDL SAPVNGEATSQKGES AEDKEHEEGRDSEEGPRCGSSEDLHDSVREGPDLDRPGSDRQE RERARGDSEALDEES
472	1211	5204	2901	LAELSSLSVLR LSHNSISHIAEGAFKGLRSLRVL DLDHNEISG TIEDTSGAFSGLDLSKLT LFGN KIKSVAKRAFSGLEGLEHLN LGGNAIRSVQFD AFVKMKNL KELHISSDSFLCDCQLKWLP PWL IGRMLQAFVTATCAHPESLKGQSIFSVPPESFVCDDFLKPQII TQPETTMAMVGKDIRFTCSAASSSSSPMTFAWKDNEVLTNAD MENFVHVHAQDGEVMEYTTILHLRQVTFGHEGRYQC VITN HFG STYSHKARLTVNVLP SFTKTPHDITIRTTT MARLECAATGHPN PQIAWQKDG GTDFPAARERRMHVMPDDDVFFITDVKIDDAGVY SCTA QNSAGSISANATLT VLETPSLVVPLEDRVVS VGETVALQ CKATGNPPPRITWFKGDRPLSLTERHHLTPDNQLLVVQNVVAE DAGRYTCEMSNTLGTERAHSQLSVLPAAGCRKDGTTVGIFTIA VVSSI VLTSLVWVCIIYQTRKKSEEYSVINTDET VVPPDVPSY LSSQGTLSDRQETVVRTEGGPQANGHIESNGVCPRDASHFPEP DTHSVACRQPKLCAGSAYHKKPWKAMEKAEGTPGPHKMEHGGR VVCSDCNT EVDCYSRGQAFHPQPVSRDSAQPSAPNGPEPGSD QEHSPHHQCSRTAAGSCPECQGS LYP SNH D RMLTAVKKKPMAS LDGKGDSWTLARLYHPDSTELQPASSLTSGSPERAEAYLLV SNHLPKACDASPESTPLTGQLPGKQRVPLLLAPKS

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473	1212	2	2466	AAAGAARRVSVRCGRSGPGPGRGAAGLSPADIALASEQGASCS VRAPERKLRMKLLWQAKMSSIQDWGEEVEEGAVYHVTILKRVQI QQAANKGARWLGVGDQLPPGHTVSQYETCKIRTIKAGTLEKL VENLLTAFGDNDFTYISIFLSTYRGFASTKEVLELLLDYGNL TSPNCEEDGSQSSSESKMVIRNAIASILRAWLDQCAEDFREPP HFPCLQKLLDYLTRMMPGSDPERRAQNLLQFQKQEVETDNGL PNTISFSLEEEEELEGGESAFTCFSEDLVAEQLTYMDAQLFK KVVPHHCGLCIWSRRDKKENKHLAPTIRATISQFNTLTCKVVS TILGGKELKTQORAKIIEKWINIAHECRLLKNFSSLRAIVSAL QSNSIYRLKKTWAAVPRDRMLMFEELSDIFSDHNNHLTSRELL MKEGTSKFANLDSSSVKENQKRTQRRLLQLQKDMGVMQGTVPYLG TFLTDLTMLDTALQDYIEGGLINFKRRREFEVIAQIKLLQSA CNSYCMTPDQKFIQWFQRQQLLTEESYALSCEIEAAADASTT SPKPWKSMVKRLNLLFLGADMITSPTPTKEQPKSTASGSSGES MDSVSVSSCESNHSEAEEGYITPMDTPDEPQKKLSESSSYCSS IHSMDTNFLQGMSSLINPLSPSPSCNNNPKIHKRSVSVTSITS TVLPPVYNQQNEDTCIIRISVEDNNGNMYKSIMLTSQDKTPAV IQRAMLKHNLDSDPAEYELVQVISEDKELVIPDSANVFYAMN SQVNFDFILRKNSMEEQVKLSRSTSLTLPR TAKRGCSNRHS KITL
474	1213	1	867	AREKMDSCIEAFGTTKQKRALNTRRMNRVGNESLNRAVAKAAE TIIDTKGVTALVSDAIHNDLQDDSLYLPPCYDDAAKPEDVYKF EDLLSPAIEALQSPSEAFRNVTSSEILKMIEENSHCTFVIEA LKSLPSDVESRDRQARCIWFLDTLIKFRHRVVKRKSALGPGV PHIINTKLLKHFTCLTYNNGRLRNLISDSMKAKITAYVILAL HIHDFQIDLTVLQDLKLSEKRMMEIAKAMRLKISKRRVSVAA GSEEDHKLGLTSLPLPPAQTSDRLAKRRKIT

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475	1214	2	2621	LSLFGSRALGRSGARAMAKAKKVGARKKASGAPAGARGGPAKANSNPFEVKVNRQKFQILGRKTRHDVGLPGVSRARALRKRTQTL LKEYKERDKSNVFRDKRFGGEYNSNMSPEEKMMKRFALQQRHH EKKS IYNLNEDEELTHYGQSLADIEKHNDIVDSDDAEDRGTL SGELTAAHFGGGGGLLHKKTQQEGEEREKPKSRKELI EELIAK SKQEKRRERQAQREDALELTEKLDQDWKEIQTL LSHKTPKSENR DKKEKPKPDAYDMMVRELGFEMKAQPSNRMKTEAEELAKEEQEH LRLKLEAERLRRMLGKDEDEENVKKPKHMSADDLNDGFVLDKDDR RLLSYKDGKMNVEEDVQEEQSKEASDPESNEEEGDSSGGEDTE ESDSPDSHLDLESNVESEEEENEKPAKEQRQTPGKGLISGKERA GKATRDELPTYTFAAPESYEELRSLLLGRSMEEQLLVVERIQKC NHPSLAEGNKAKLEKLFGLLEYVGD LATDDPDLTVIDKLIVV HLYHLCQMFPEASDAIKFVLRDAMHEEMIE TKGRAALPGL DVLIY LKITGLLFPTSDFWHPVTPALVCLS QLLTKCPI LSLQ DVVKGLFVCCFLFLEYVALSQRFIPELINFLLGILYIATPNKAS QGSTLVHPFRALGKNSSELLVVSAREDVATWQQSSLSLRWASRL RAPSTSEANHIRLSCLAVGLALLKRCVLMYGS LPSFHAIMGPL RALLTDHLADCSHPQELQELCQSTLT EMESQKQLCRPLTCEKS KPVPLKLF TPRLVKVL EFGGRKQGS SKEEQERKRIHKHKREFK GAVREIRKDNQFLARMQLSEIMERDAERKRKVKQLFNSLATQE GEWKALKRKKFKK
476	1215	3	961	LTKQEDCCGSIGTAWGQSKCHKCPQLQYTGVPKPGPVRGEVGA DCPQGYKRLNSTHCDINECAMPGVCRHGDCLNPNPSYRCVCP PGHSLGPSRTQCIADKPEEKSLCFRLVSPHQCHPLTTRLTR QLCCCSVGKAWGARCQRCPTDGTAAFKEICPAGKGYHILTS HQ TLTIQGESDFS LFLHPDGPPKQQLPESPSQAPPEDTEEERG VT TDS PVSEERSVQQSHPTATTTTPARPYPELISRPSPTMRWF LPDLPPSRSAVEIAPTQVTETDECRLNQNICGHGECVPGPPDY SCHCNPGYRSHPOHRYCV

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477	1216	3652	1207	MAGGHCGSFPAAGSGEIVQLNVGGTRFSTSRQTLMWIPDSF FSSLLSGRISTLRDETGAIFIDRDPAAAFAPILNFLRTKELDLR GVSINVL RHEAEFYGITPLVRRLLLCEELERSSCGSVLFHGYL PPPGIPSRKINNTVRSADSRNGLNSTEGEARGNGTQPVLSGTG EETVRLGFPVDPKVLIVAGHHNWIVAAYAHFAVWYRIKESSG WQQVFTSPYLDWTIERVALNAKVVGPGPHGDKDKMVAASESSI ILWSVQDGGSGEIGVFSLGVPVDALFFIGNQLVATSHTGKVG VWNAVTOHWQVQDVVPITSYDTAGSFLLLGCNNGSIYYIDMQK FPLRMKDNLLVTELYHDPNDAITALS VYLT PKTSVSGNWIE IAYGTSSGAVRVIVQHPETVGS GPQLFQTFTVHRSPVTKIMLS EKHLVSVCADNNHVRTWTVTFRGMISTQPGSTPLASFKILSL EETESHGYSYSSNDIGPFGERRDDQQVFIQKVVPITNKL FVRLS STGKRICEIQAVDCTTISSTFGRECEGSSRMGSRPRRYLFTGH TNGSIQMWDLTTAMDVMNKSEDKDVGGPTEEELKLLDQCCLS TSRCATPNISPATSVVQSHSLRESNSSLOLQHDDTTHEAATYG SMRPYRESPLLARARRTESFHSYRDFQITINLRNVERAVPENG NLGP IQAEVKGATGECNISERKSPGVEIKSLRELD SGLEVHKI AEGFSESKKRSSDENENKIEFRKKGGFEGGGFLGRKKVPYLA SSPSTSDGGTDSPGTASPSPTKTTSPRHKSDSSSGQEYSL
478	1217	1	1379	RRPTRPILTDELFKRTIQPLHLKTLILNGNKLETLSLVSCFAN NTPLEHLDLSONLLQHKNDENCSWPETVVMNLSYNKLSDSVF RCLPKSIQILDNNNQIQTPKETIHLMALRELNIAFNFLTDL PGCSHF SRLSVLNIEMNFILSPSLDFVQSCQEVKTLNAGRNP RCTCELKNFIQLETYSEVMVGVSDSYTCEYPLNLRGTRLKDV HLHELSCNTALLIVTIVIMLVGLAVAFCCCLHFDLPWYLRML GQCTQTWHRVRKTTQEQLKRNVRFHAFISYSEHDSLWKNELI PNLEKEDGSILICLYESYFDPGKSI SENIVSFIEKSYKSI FVL SPNFVQNEWCHYEFYFAHNL FHENS DHI ILILLEPIPFYCIP TRYHKLKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNLAT REMYELQTFTELNEESRGSTISLMRTDCL
479	1218	1	1099	PTRPPTRPPTRPLLTPSWTSTGRMWSHLNRLLFWSIFSSVTCR KAVLDCEAMKTNEFPSPCLDSKTKVVMKGQNVSMFC SHKNKSL QITYSLFRRKTHLGTQDGKGPAIFNLSITEAHESGPYKCKAQ VTSCSKYSRDFSFTIVDPVTS PVLNIMVIQTETDRHITLHCLS VNGSLPINYTF FENHVAISPASKYDREPAEFNLTKKNPGEEE EYRCEAKNRLPNYATYSHPVTMPSTGGDSCPFCLKLLLPGLLL LLVVIILILAFWVLPKYKTRKAMRN NVPRDRGDTAMEVGIYAN ILEKQAKEESVPEVGSRPCVSTAQDEAKHSQELQYATPVFQEV APREQEACDSYKSGYVYSELNF
480	1219	1	293	FFFFEERTTGSHSVGHPRMEYSGVSMACHSLNLLGSSNSPSSA SQDARTTGACQHAQLIGFFFF\ VETAS PQVTHAG/LKHLVSRN PSAVTSQSARIKT

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481	1220	1	727	NREGARKIQNKWLRPSPRSHRTPESVSPERYSYGTSSSSSKRTE GSCRRRRQSSSSANSQQGWETGSPPTKRQRRSRGRPSGGAKR RRRGAPAAPQQQSEPARPSSEGKVTCDIRLRVRAEYCEHGPAL EQGVASRRPQALARQLDVFGQATAVLRSDLGSSVCDIKFSEL SYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLLVSV DEADYEAGRRRLLLMEEEGRRRPTAS
482	1221	1	1321	APNTAELRICRVNKNCGSVRGDEIFLLCDKVQKDDIEVRFVL NDWEAKGIFSQADVHRQVAIVFKTPPYCKAITEPVTVMQLRR PSDQEVSESMDFRYLPDEKDTYGNKAKKQKTTLFQKLCQDHV ETGFRHVDQDGLELLTSGDPPTLASQSAGITVNFPERPRPGLL GSIGEGRYFKKEPNLFSHDAVVREMPGTGVSSQAESYYPSPGPI SSGLSHHASMAPLPSSSWSSVAHPTPRSGNTNPLSSFSTRITP SNSQGIPPFLRIPVGNLDNASNACIYNNADDIVGMEASSMPSA DLYGISDPNMLSNCSVNMMTTSSDSMGETDNPRLLSMNLENPS CNSVLDPRDLRQLHQMSSSSMSAGANSNTTVFVSQSDAFEGSD FSCADNSMINESGPSNSTNPNSHGFVQDSQYSIGISMQNEQLS DSFPYEFFQV
483	1222	1	1311	RRLSLDLQLGPLGRDPPQECSTFSPTDSGEEPGQLSPGVQFQ RRQNQRFRSMEDVSKRLSLPMDIRLPQEFQLQKLMESPDLPKP LSRMSRRASLSDIGFGKLETYVKLDKLGEGTYATVFKGRSKLT ENLVALKEIRLEHEEGAPCTAIREVSLLKNLKHANIVTLHDLI HTDRSLTLVFEYLDSDLKQYLDHCGNLMSMHNKIFMFQLLRG LAYCHHRKILHRDLKPQNLLINERGELKLADFGLARAKSVPTK TYSNEVVTLYWRPPDVLLGSTYESTPIDMWGVGCIHYEMATGR PLFPGSTVKEELHKINRLLGTPTEETWPGVTAFFSEFRTYSFPC YLPQPLINHAPRLDLDGIHLLSSLLLYESKSRMSAEALSHSY FRSLGERVHQLEDTASIFSLKEIQKQDPGYRGLAFQQPGRGK NRRQSIIF
484	1223	807	356	CTPHGSSSSWKIPLWPRHMSPLHSCLPVGTSTSSGPLAVPRDC FHLCCWQQLLLISCPLACQGQCRVAGGQHVPGQALGTLSP VSLLTWAGPSLDWPHPGSLVTPRCPIPAVPVLVKGLGGWPPT RPSRAAPVSGPWDQLPYFPGL
485	1224	1199	370	LISPVWGNIQRSRSVPLFPSGLVLGGIWARGLLALLASFNI SVLNAECYLKQILHPTSHFTVSETPPLSGNDTDSLSCDSGSSA TSTPCVSRLVTGHHLWASKNGRHVLGLIEDYEALLKQISQGR LLAEMDIQTQEAPSSTSQELGTGKPHAPLSKFVSSVSTAKLT LEEAYRRLKLLWRVSLPEDGQCPLHCEQIGEMKAEVTKLHKKL FEQEKKLQNTMKLLQLSKRQEKVIFDQLVVTHKILRKARGNLE LRPGGAHPGTCSPSRPGS

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486	1225	2469	1660	LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAAEACQRQ QLPVTFGNKQKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDR EVVNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESR WGYSGTSDRIRFTVNRRIISIVGFGLYGSIHGPTDYQVNIQIIIE YEKKQTLGQNDTGFS CDGTANTFRVMFKEPIEILPNVCYTACA TLKGPDSHYGKGLKKVVHETPAASKTVFFFFSSPGMNNGTSTI EDGQIPEIIIFYT
487	1226	1193	372	SVVWNSEVKDWMQKKRRGLRNSRATAGDIAHYRDYVVKKGLG HNFVSGAVVTAVEWGTPDPSSCGAQDSSPLFQVSGFLTRNQAQ QPFSLWARNVVLATGTGFDSPARLGIPGEALPFIHHELSALEAA TRVGAVTPASDPVLIIGAGLSAADAVLYARHYNIPVIAFRRA VDDPGLVFNQLPKMLYPEYHKVHQMMREQSILSPSPYEGYRSL PRHQLLCFKEDCQAVFQDLEGVEKVFGVSLVLVLIGSHPDLSF LPGAG\LTQLQWILTSR
488	1227	756	1016	KLRPFIFSNQSLWLHSYEGAELEKTFIKGSWATFWVKVASCWA CVLLYLGLLLAPLCWPPTQKPQPLILRRRRHRIISPDKYPPV
489	1228	1	747	QLIHLSHGYQIHWTDYNVGTGRPEFGTRAHKS LAGAEKLT KDFVTVLAKLFPGRPVKKLLEMLQEWLASLPDRIPYNAVL LVNNKMRISGIFLTNHIKWVGCQGSSELRGYPCSLWKLFHTL TVEASTHPDALVGTGFEDDPQAVLQTMRRYVHTFFGCKECCGEH FEEMAKESMDSVKTPDQAILWLWKKHNMVNGRLAGEKPLGMGG SARAEGGPGPGTARTARLPWGLSLSFAASCHPLC
490	1229	4797	2398	HGGATFINAFVTTMCCPSRSSMLTGKYVHNHNVTNNENCSS PSWQAMHEPRTFAVYLNNTGYRTAFFGKYLNEYNGSYIPPGWR EWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKDYFTDLITNESI NYFKMSKRMYPHRPVMVISHAEPHGPEDSAPQFSKLYPNASQ HITPSYNYAPNMDKHWIMQYTGPMPLPIHMEFTNIIQKRLQTL MSVDDSVRLYNMLVETGELENTYIIYTADHGYHIGQFGLVKG KSMPYDFDIRVPPFIRGPSVEPGSIVPQIVLNIDLAPTILDLA GLDTPPDVDGKSVLKLDDPEKPGNRFRTNKKAKIWRDTFLVER GKFLRKKEESSKNIQQSNHLPKYERVKELCQQARYQTACEQPG QKWQCIEDTSGKLRIHKCKGPSDLLTVRQSTRNLYARGFHDKD KECSCRESGYRASRSQRKSQRQFLRNQGT PKYKPRFVHTRQTR SLSVEFEGEIYDINLEEEELQVLQPRNIAKRHDEGHKGPRDL QASSGGNRGRMLADSSNAVGPPTTVRVTHKCFILPNDSIHCER ELYQSARAWKDHKAYIDEEIEALQDKIKNLREVRGHLKRRKPE ECSCSKQSYNKEKGVKQEKLSHLHPFKEAAQEVDSKQLQF KENNRRRKKEKRRQRKGEECSLPGLTCFTHDNNHWQTAPF WNLGSFCACTSSNNNTYWCLRTVNETHNFLCFEATGFLEYFD MNTDPYQLTNTVHTVERGILNQLHVQLMELRSCQGYKQCNPRP KNLDVGNKDGGSYDLHRGQLWDGWEG

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491	1230	2480	385	HLLIAQELADRVGEGRACWSLGNAYVSMGRPAQALTFAKKHLQ ISQEIHDRHGEILTARMNVAQLQLVLGRLTSPAASEKPDLAGYE AQGARPKRTQRLSAETWDLRLPLEREQNGDSHSHSGDWRGSPSR DSLPLPVRSRKYQEGPDAERRPREGSHSPLDSADVRVHVPRTS IPRAPSSDEECFFDLLTKFQSSRMDDQRCPLDDGQAGAAEATA APTLEDRIAQPSMTASPQTEEFFDLIASSQSRRLDDQRASVGS LPGLRITHSNAGHLRGHGEPQEPGDDFFNMLIKYQSSRIDDDQR CPPPDVLPRGPTMPDEDFFSLIQRVQAKRMDEQVRDLAGGPGA GGRRPARAPAAVPAWCELRPCAHRQAHPAPTGRSSHSHSHVL PRPLPRTGTGHAAPRPPRPRATGSGQAARGGRACFHPGLAPMA LSFLPSAPAAGRTGPSACRPRPGAVRLPHPLPQALPVLPCPAK CETLLSPSPSPKVSLSRLLGPPRTGPCSVPELVLGWPCDRHA PPLQLRPGAGLPPSLSPHSPARGQQPKAPQTTGHRPGCSGSP EVPFAESQGPAGASTGAGPISKAEGMAGHELHRSKTPSQEKQ GLVLGMLTGSKSSAQSGWEVAPGSVTLTQVGGWSVEAGEASLS STLQTPHMRTPLLPPAGGDDITALSMGRGLTGHVQVRDPRTRT CWSLRWAPGA
492	1231	3	398	NSAADLAI PALWGLKPVVYLLASSFLGLGLHPISGHFVAEHYM FLKGHETYSYYGPLNWITFNVGYHVEHDFPSIPGYNLPLVRK IAPEYYDHL PQHHSWVKVLWDFVFEDSLGPYARVKRVYRLAKD GL
493	1232	1	214	QESGFSCCKGPGQNVAVTRAHPDSQGRRRRPERGARGGQVFYNS EYGELSEPSEEDHCSPSARVTFFTDNSY
494	1233	3	443	VIVHARPIRTRASKYYIPEAVYGLPAYPAYAGGGGFVLSGATL HRLAGACAQVELFPIDDVFLGMCLQRLRLTPEPHPAFRTFGIP QPSAAPHLSTFDPCFYRELVVVHGLSAADIWLMWRLLHGPHGP ACAHQPQVAAGPFQWDS
495	1234	1	897	MASAACSMDFIDSFELLDLLFDRQDGLRHVELGEGWGHVKDQ VLPNPDSDDFLSSILGSGDSLPSPLWSPEGSDSGISEDLPD PQDTPPRSGPATSPAGCHPAQPGKGPCLSYHPGNSCSTTTTPGP VIOQQHHLGASYLLRPGAGHCQELVLTEDEKKLLAKEGITLPT QLPLTKYEERVLKKIRRKIRNKQSAQESRKKKKEYIDGLETRS CCCPLPSSSSPPSALLAPT KPRALGTLRLYECSPELCTTMLPP AWLLMLCQAPRPQDPDPRLTQPEKSLQEAPGQTGASRTPRT

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
496	1235	4235	940	ARGRRSRPVWAASWGGGRGPAARRRPRGLAATMGFELDRFDGD VDPDLKCALCHKVLEDPLTTPCGHVFCAGCVLPWVWQEGSCPA RCRGRLSAKELNHVLPKRLILKLDIKCAYATRGCGRVVKLQQ LPEHLERCDFAPARCRHAGCGQVLLRRDVEAHMRDACDARVPG RCQEGCGLPLTHGEQRAGGHCCARALRAHNGALQARLGAHKA LKKEALRAGKREKSLVAQLAAQLELQMTALRYQKKFTYLSAR LDSLSRCVAAPPGGKGEETKSITLVLRHDSGSLGFNIIGGRPS VDNHDGSSSEGI FVSKI VDSGPAAKEGGLQIHDR IIEVNGRDL SRATHDQAVEAFKTAKEPIVVQVLRRTPTKMTPTPSESQ LVD TGTQTDITFEHIMALKMSSPSPVLDPYLLPEEHPSAHEYD PNDYIGDIHQEMDRELELEEVLDLYRMNSQDKLGLTVCYRTDD EDDIGIYISEIDPNSIAAKDGRIREGDRI IQINGIEVQNREEA VALLTSEENKNFSLIARAELQLDEGWMDDDRNDFLDDLHMDM LEEQHHQAMQFTASVLQKKHDEDGGTTDTATILSNQHEKDSG VGRDTESTRNDESSEQENNGDDATASNPLAGQRKLTCSDTL GSGDLPFSNKSFISPECTGAAYLGIPVDECERFRELLEKQCQV KSATPYGLYPPSGPLDAGKSDPESVDKELELLNEELRSIELEC LSIVRAHKMQQLKEQYRESWMLHNSGFRNYNTSIDVRRHELSD ITELPEKSDKDSSAYNTGESCRSTPLTLEISPDNSLRRAEG ISCPSSSEGAVGTTEAYGPASKNLLSITEDPEVGTPTYSPSLKE LDPNQPLESKERRASDGSRSPTPSQKLGSAYLPSYHHSFYKHA HIPAHQHYQSYMQLIQKSAVEYAQSQMSLVSMCKDLSSPTP SEPRMEWKVKIRSDGTRYITKRPVRDRLLRERALKIREERSGM TTDDDAVSEMKGRIYWSKEERKQHLVKAKEQRRRRREFMMQSRL DCLKEQQAADDRKEMNILELSHKMMKKRNKKIFDNWMTIQEL LTHGTKSPDGTRVYNSFLSVTTV
497	1236	2	157	FFFLVEMGFCHVGQGLTLIGSSNLPASASKSAGITGVSHCAR PDFKSCVE
498	1237	1	211	LAGRKVLLFVSGYVVGWGPITWLLMSEVLPLRARGVASGLCVL ASWLTAFLVLTKSFLPGGVSVPQAPGP
499	1238	2	345	FWAPGPPGVGAAGDASTRSLRESCPSPSPGRLRRTTAPWSSQ ARAAAPAPSSSCRGPDGASSPRDLPWRPWKILRRTPLSGDVEL SQVHPDQRI LRRLFILSRTCGNTIPGMAE
500	1239	1	523	MRRFLSKVYSFPMRKLILFLVFPVVRQTPTQHFKNQFPALHWE HELGLAFTKNRMNYTNKFLIPESGDYFIYSQVTFRGMTSECS EIRQAGRPNKPDSTIVVITKVTDSYPEPTQLLMGTSKSVCEVGS NWFQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAP LL

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501	1240	2	1277	FVWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPPGGSRVISHY AGQDATDPFVAFHINKGLVKYMNSSLIGELSPEQPSFEPTKN KELTDEFRELRATVERMGLMKANHVFFLLYLLHILLDDGAAWL TLWVFGTSFLPFLCAVLLSAVQAQAGWLQHDGHLVSFSTSK WNHLLHHFVIGHLKGAPASWWNHMHFQHHAKPNCFRKDPDINM HPFFFALGKILSVELGKQKKKYPYNNHQHKYFFLIGPPALLPL YFQWYIFYFVIQRKKWVDLAWMITFYVRFFLTYPVLLGLKAF GLFFIVRFLESNWFVWVTQMNHIPMHIDHNRMDWVSTQLQAT CNVHKSANFDFSGHLNFQIEHHLFPTMPRHHYHKVAPLVQSL CAKHGIEYQSKPLLSAFADIHSLKESGQLWLDAYLHQ
502	1241	999	540	QCGGIPYNTTQFLMNDRDPEEPNLDVPHGISHPGSSGESEAGD SDGRGRAHGEFQKDFSETYERFHTESLQGRSKQELVRDYLEL EKRLSQAEEETRLQLQACTGQQSCQVQEEELAAEVQRLRTEN QRLRQENQMWNRREGCRCDDEPGT
503	1242	1448	875	SPERSSSLVSGREKAMEVPPAPRSFLCRALCLFPRVFAAEAVT ADSEVLEERQKRLPYVPEPYYPESGWDRLRELFGKD\VTGSLF RINVGLRGLVAGGIIGALLGTPVGGLLMAFQKYSGETVQERKQ KDRKALHELKLEEWKGRQLQVTEHLPEKIESSLQEDPENDAKK IEALLNLPRNPSVIDKQDKD
504	1243	149	1293	RSLGLAVTEMVPWVRTMGQKLKQRLRLDVGREICRQYPLFCFL LLCLSAASLLLNRYIHILMIFWSFVAGVVTFYCSLGPDSLLPN IFFTIKYKPKQLGLQELFPQGHSCAVCGKVCKRHRPSLLLEN YQPWLDLKISSKVDASLSEVLELVLENFVYPWYRDVTDDES DELRLITLRFASVLIRRIHKVDIPSIIITKKLLKAAMKHIEVIV KARQKVKNTEFLQQAALAEYGPPELHVALRSRRDELHYLRKLT LLFPYILPPKATDCRSLTLLIREILSGSVFLPSLDFLADPDTV NHLLIIIFIDDSPPEKATEPASPLVPFLQKFAEPRNKKPSVLKL ELKQIREQQDILLFRFMNFKQEGAVHVLHVLFDCCGI
505	1244	2	1116	QSLAEVLQQLGASSELQAVLSYIFPTYGVTPNHSAFSMHALLV NHVMKGGFYPRGVTSEIAFHTIPVIRAGGAVLTATVQSVLL DSAGKACGVSVKKGHELNIYCPVVSNAGLFNTYEHLLPGNA RCLPGVKQQLGTVRPGLGMTSVFICLRGTEDLHLPSTNYVYV YDTDMQAMERYVSMFREEAAEHIPLLFFAFPSAKDPTWEDRF PGRSTMIMLIPTAYEFEEWQAEKKG\RGSDYETFKNSFVEA SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGAD HDLGRLHPCVMASLRAQSPINLYLTGQDIFTGCLVGLALQAL LCSSTILKRNLYSDLKNLDSRIRAQKKKN
506	1245	1759	873	RPQETRVLQVSCGRAHSLVLTDRGVFSMGNNSYGQCGRKVVE NEIYSESHRVHRMQDFDQVQVQACGDHSLFLTDKGEVYSCG WGADGQTGLGHYNITSSPTKLGGDLAGVNVIQVATYGDCCCLAV SADGGLFGWGNSEYLQLASVTDSTQVNVPRCLHFSGVGKVRQA ACGGTGCAVLNNGEGHVFVWGYGILGKGNLVESAVPEMIPPTL FGLTEFNPEIQVSRIRCGLSHFAALTNGELFVWGKNIRGCLG IGRLEDQYFPWRVTMPGEPVDVACGVDMVTLAKSFI

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507	1246	520	2	LPFREWLMIVVSLSAAAVAAAFMAKCRMVLSRRYFCSHFVMSA SRARIRSSFSRTSSRRAGALYSGMLAGWPFPCFCWVLSASSSL SSQVRLRSICSRFSHADCSWVRACCSFSTFSTYACFSRNSSS SLMTLAWALLKAWSRISMCLRWSSLAVRTAANSISNFSFSFKN
508	1247	1	1083	MQAVRATASQSLSCARAPREPTQHALRAHWFPAAAVQSPHS GVAAAAGTWSSAFRGEHPLVSSGLLLGVREQSFRLLRKAGTH MYLEHTSHCPHHDDDTAMDTPLPRPRPLLAVERTGQRPLWAPS LELPKPDMPQLPAGAFLEEVAEGTPAQTESEPKVLDPEEDLLC IAKTFSYLRESGWYGSITASEARQHLQKMPEGTFVLVDSTHP SYLFTLSVKTTTRGPTNVRIEYADSSFRLDSNCLSRPRILAFPD VVSLVQHYVASCTADTRSDSPDPAPTALPMPKEDAPSDPALP APPPATAVHLKLVQPFVRRSSARSLSQHLCLRLVINRLVADVDC PLPRRMADYLRQYFPQL
509	1248	2	841	FVDIFQRWKECRGKSPAQAELS YLNKAKWLEMYGVD MHVVRGR DGCEYSLGLTPTGILIFEGANKIGLFFWPKITKMDFKKSKLTL VVVEDDDQGREQHTFVFRLDSARTCKHLWKCAVEHHAFFRLR TPGNSKSNRSDFIRLGSRFREFSGRTEYQATHGSRLRRTSTFER KPSKRYPSRRHSTFKASNPNVIAAQLCSKTNPVHNYPQYHPN IHPSQPRWHPHSPNVRPSFQDDRSHWKASASGDDSHFDYVHDQ NQKNLGGMQSMMYRDKLMTAL
510	1249	2	763	GGIRLIQKLTWRSRQQDRENCAMKGKHKDECHNFIKVFVPRND EMVFVCGTNAFNP MCRYRVSIFYVICFF*STFLPSLICC*S* NLSAFQ*FVLSLVQ*KNKDRILQMEF*YK*NSIAFKRAR*IDM TLAIYFSFV\LSTL*YDGEEISGLARCPFDARQTNGALFADGK LYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKE/PHFL YAIK/Y/GNYVYFSFREIVAT**LG/KAVDS/RVARYEKQLVG PTV
511	1250	1555	629	ARALARERESESARADDVTLGVSAILAVDRGGNLGSA\DGWAY IDVEVRRPWAFVGP GCSRSSGNGSTAYGLVGS PRWLS PFHTGG AVSLPRRPRGPGPVLGVARPCLRCVLRPE\HYEPGSHYSGFAG RDASRAFVTGDCSEAGLVDDVSDLSAAEMLTLHNWLSFYEKNY VCVGRVTGRFYGEDGLPTPALTQVEAAITRGLEANKLQLEKQ TFPPCNAEWSSARGSLWCSQKSGGVS RDWIGVPRKLYKPGAK EPRCVCVRTTGPPSGQMPDNPPHRNRGDL DHPNLA EYTGCPPL AITCSFPL
512	1251	1100	798	YFIICRDGVLLFCPGWSQTPGAQAILLHWATQNAGMTDMSHSA QPIYLFYILIRTRSHYVAQAGQLLDSNDSPNVASQNVGITGMS HHAWLKIVLYFCII

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513	1252	3	1395	PAARPPSLVRLSPSPPKPRARARAPQSVEPAAPLVARGSSPPA RPAPAMVRPRAPYRSGAGGPLGGRGRPPRPLVVRVRSR ASPRGPQPPR\IRARSAPPMEGARVFGALGPIGPSSPGLTLGG LAVSEHRLSNKLLAWSGVLEWQEKRRPYSDSTAKLKRTPCQA YVNQGENLETDQWPQKLIMQLIPQQLLTTLGPLFRNSQLAQFH FTNRDCDSLKGLCRIMNGFAGCMLFPHISPCEVRVLMMLYSS KKKIFMGLIPYDQSGFVSAIRQVITTRKQAVGPGGVNSGVPQI VNNKFLAWSGVMEWQEPREPEPNSRSKRWLPSHVYVNOGEILRT EQWPRKLYMQLIPQQLLTTLVPLFRNSRLVQFHFTKDLETLS LCRIMNGFAGCVHFSYKASCEIRVLMMLYSSEKKIFIGLIPH DQGNFVNGIRRVIANQQQVLQRNLEQEQQQRGMGG
514	1253	320	964	GRPALGREAPPQAGLSSTPPPCSETCTMGPHSILRTVHCRPTK TPPEPSAEPHPLSLTSSNTSLAGTSLGRDLTPGGGKPPSGQT PRNPESPRHRLGSPRGRRLASPTPTGSGRSGPASRGQRRLSC AAQDPTSEGASVGAMEAGLGPPTAAPRGVVSEAAESLGGTSLW GAWGRPPAGPSGLAGRRSRREALRPDRKEASVMAAVSAIQP
515	1254	704	107	PGVPTHGWPRSRVLTTRVGRSGSGKMAAAVLAAGLRAARRAV AATGVRGGQVRGAAGVTDGNEVAKAQATPGGAAPTIFSRILD KSLPADILYEDQQCLVFRDVAPQAPVHFLVIPKKPIPRISQAE EEDQQ/LTYVPPLSL*LLGHLLLVAKQTAKAEGLDGYRLVIN DGKLGAAQSVYHLHIHVLGGRQLQWPPG
516	1255	2299	924	VPNYLPSVSSAIGGEVPQRYVWRFCIGLHSAPRFLVAFAYWNH YLSCTSPSCYRPLCRLNFGNLNVENLALLVLTYSSEDF/T WVPG*GRSGEVFPEGTGLPLPHSDLPTSWCGHSLQCGSQSSFP PAIHENAFIVFIASSLGHMLLTCILWRLTKKHTVSQE\DGLSL AGAPRQPRRKSRTSVLRIRVMVRWELSSNGNPGRGVLGLGLGL GNKLRVVGQNLGL*HCVVWVWETGE*KRWRLOMGIE*GVASRR Q*VRNSVRGLVCHNSSAPPYMGFFSPTVFGGVGG*LVHTFI LHPPEVEAAGIPLLLGPSLPQROGREHIVVILAAPACAPFHDR *WEPREIRPSP*ELGLRGEPTLSYPASCRVIRQPI*DRKSYS WKQRLFIINFISFFSALAVYFRHNMYCEAGVYTIFAILEYTVV LTNMAFHMTAWWDFGNKELLITSQPEEKRF
517	1256	3	254	IDLLEIRNGPRSHESFQEMDLNDDWKLKDEVKAYLKKEFEKH GAVVNESHDLVEDIFDKEDEKDGFIISAREFTYKHDEL
518	1257	2	611	PRVRGRVKGEGAAAKPRSLRRFQLLSWSVCGGNKDPWVQELM SCLDLKECGHAYSGIVAHQKHLPTSPPIQASEGASSDIHTP AQMLLSTLQSTQRPPLPVGSLSSDKELTRPNETTIHTAGHSLA AGPEAGENQKQPEKNAGPTARTSATVPVLCLLAIIFILTAALS YVLCRRRGQSPOSSPDLPVHYIPVAPDSNT
519	1258	1002	418	LIISNFLKAKQKPGSTPNLQKKSQARLAPDIVSASQYRKFE FQTGILIYELLHQPNPFVRAQLRERDYRQEDLPPLPALSLYS PGLQQLAHLLEADPIKRIRIGEAKRVLQCLLWGPRELVOQP GTSEALCGTLHNWIDMKRALMMMKFAEKAVDRRRGVELEDWL CCQYLASAEPGALLQSLKLLQLL

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520	1259	2	2019	KRGLIVVMAHEMIGTQIVTERGVALLESgtekvLLIDSRPFVE YNTSHILEAININCSKLMKRRLQDQKVLITELIQHSAKHKVDI DCSQKVVVDQSSQDVASLSSDCFLTVLLGKLEKSFNSVHLLA GGFAEFSRCFPGLCegKSTLVPTCISQPCLPVANIGPTRLPN LYLGCQRDVLNkELMQONGIGYVLNASNTCPKPDFIPESHFLR VPVNDSFCEKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRS ATIAIAYIMKRMDMSLDEAYRFVKEKRPTISPNNFLGQLLDY EKKIKNQTGASGPKSKLKLHLEKPNPVPVAVSEGGQKSETPL SPPCADSATSEAGQRPVHPASVPSVPSVQPSLLEDSPLVQAL SGLHLSADRLEDsnKLKRSFSLDIKSVSYSASMAASLHGFSSS EDALEYYKPSTTLDTGNKLCQFSPVQEL/CGADSRNQS**GGS Q/PSPRSCRPPGLQTARASDCIRSEPAAVAPPRGPFYLHCIEV GAWRTITTPASFSAFPP\PAAPHEVCWPGP*GLA\PDILAPQT STPSLTSSWYFATESSHFYASAIYGGSASYSAYSCSQLPTCG DQVYSVRRRQKPSDRADSRRSWHEESPFEKQFKRRSCQMEFGE SIMSENRSREELGKVGSSQSSFSGSMEEIEVS
521	1260	20	803	ASSSKRVSRQKMLQLWKLVLGCVLTGTSESLLDNLGNDLSNV VDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLOKSSAWQLAK QKAQEAekLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPID DGKGLNLSFPVTANVTEAGPIIDQIIN\LRASLDLLTAVTIET DPQTHHPVAGLGEcARDPTSISLCLLDKHSQIINKFVNSVINT LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQ TLI
522	1261	1246	411	CSLRRPRSAEPDADHVPLLGLLRLQLRAARQPGAMRPGGPA SPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLY NGMCLQGPGVPGRDGSPGANGIPGTPGIPGRDGFKEGECCL RESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSAL RVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQ GSPERNSTINIHTSSVEGLCEGIGAGLVDAIwVGTCSDPYK GDASTGWNsvSRIIEELPK
523	1262	2009	921	MHSAMLGTRVNLsvSDFWRVMMRVCWLVRQDSRHQRIRLPHLE AVVIGRGPETKITDKKCSRQVQLKAECNKGyVKVKQVGVNPT SIDSVVIGKDQEVKLQPGQVLHVNELYPIVEFEKEAKNPGL ETHRKRKRSGNSDSIERDAAQEAeAGTGLEPGSNGQCSVPLK KGKDAPIKKESLGHWSQGLKISMQDPKMqVYKDEQVVVIKDKY PKARYHWLVLPWTSISSLKAVAR\EHLELLKHMHTVGEKVIVD FAGSSKLRFRLGYHAIPSMshVHLHVISQDFDspCLKNKKHWN SFNTEYFLESQAVIEMVQeAGRVTVRDGMPELLKLPLRCHecQ QLLPSIPQLKEHLRKHWTQ

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524	1263	2067	198	DMSDTSESGAGLTRFOAEASEKDSSSMQTLTTLVTQNVEVPET PKASKALEVSEDVKVSKASGVSKATEVSKTPEAREAPATQASS TTQLTDTQVLAAENKSLAADTKKQADPQAVTMPATETKKVSH VADTKVNTKAQETEAAPSQAPADEPEPEPESAAAQSQENQDTRPK VKAKKARKVKHLDGEEDGSSDQSQASGTTGGRRVSKALMASMA RRASRGPIAFWARRASRTRLACFGPGEPPLSPWRSP\KARROR GFAVRVAKFQ\SSQEPEAPPFW\DVALLQGRAN\DLVKYLLAK DQTKIPIKRS\DMKDIKEYTDVYPEII\ERAGYSLE\KVFG IQLKEIDKNDHLYILLSTLEPTDAGILGTTKDSPKLGLLMVLL SIIF\MNGNRS\SEAVIWEVLR/RSLGLRLGIHHS\LLGDVK\ KLITDEV\VKQKYL\DYARVPHSNP\EYEFFWG\LRSYEDQ QR*KSFKFACK\VQK\KDPK\EWAAQSPPGKAR/ERMEAD\LK AAS*GSPWKPRLRAEIKARMGIGLSENAAGPCNWDEADIGPW AKARIQAGAEAKAKAQESGSASTGASTSTNNSASASASTSGGF SAGASLTATLTFGLFAGLGGAGASTSGSSGACGFSYK
525	1264	1	1397	ARPPVCTGSTMSLTVVSMACVGFLLQGAWPLMGGQDKPFLSA RPSTVVPRGGHVALQCHYRRGFNNFMYLYKEDRSHVPIFHGRIF QESFIMGPVTPAHAGTYRCRGRPHSLTGWSAPSNNPLVIMVTG NHRKPSLLAHPGPLLKSGETVILQCWSDIMFEHFFLHKEGISK DPSRLVGQIHDGVSKANFSIGPMMLALAGTYRCYGSVTHTPYQ LSAPSDPLDIVVTGPYEKPSLSAQPGPKVQAGESVTLSCSSRS SYDMYHLSREGGAHERRLPAVRKVNRTFQADFPLGPATHGGTY RCFGSFRHSPYEWSDPSDLLVSVTGNPSSSWPSPTEPSSKSG NLRHLHLIGTSVVKIPFTILLFFLLHRWCSNKK\NAAVMDQE PAGNR\VNSED\$DEQDHQEVSY*LEHCVFTQRKITRPSQRPK TPPTDTSMYIELPNAEPRSKVVFPCRAPQSGLEGIF

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526	1265	6657	988	<p>LHNLRLERYFSGLIYTYSGLFCVVVNPYKHLPIYSEKIVDMYKG KKRHEMPPIHYAIADTAYRSMQLDREDQSILCTGESGAGKTEN TKKVIQYLAVVASSHKGKKDTSITGELEKQLLOANPILAEFGN AKTVKNDNSSRFGKFI RINFDTVGYIVGANIETYLLEKSRAIR QARDERTFHI FYMIAGAKEKMRSDLLLEGFNNTFLSNGFVP IPAAQDDMFQETVEAMAIMGFSEEEQLSILKVSSVLQLGNI VFKKERNTDQASMPDNTAAQKVCHLMGINVTDFTRSILTPRIK VGRDVVQKAQTKEQADFAVEALAKATYERLFRWILTRVNKALD KTHRQASFLGILDIAGFEIFEVNSFEQLCINYTNEKLOQLFN HTMFIL\EQEEYQREGIEWNFIDFGLDLQPCIELIERPNNPPG VLALLDEECWFPKATDKSFVEKLCTEQGSHPKFQKPKQLKDKT EFSIIHYAGKVDYNASAWLTKNMDFLNDNVTSLLNASSDKFVA DLWKDVDRIVGLDQMAKMTESLPSASKTKKGMFRTVQGQLYKE QLGKLMTTLRNTTPNFVRCIIPNHEKRSGLDAFLVLEQLRCN GVLEGIRICRQGFNRI VFQEFQRQYEILAANAIPKGFMDGKQ ACILMIKALELDPNLYRIGQSKI FFRGTGVLAHLEERDLKITD VIMAFQAMCRGYLARKAFARQQQLTAMKVIQRNCAAYIKLRN WQWCRLFTKV*PLLQVTRQE*EMQAKEDLQKTKERQQAENE LKELEQKHSQLTTEKNLLQEQLQAETELYAEAEEMRVRLAAKK QELEEILHEMEARLEEEEDRGQQLQAERKKMAQOMLDLEEQL EEEEARQKLQLEKVTAEKIKKLEDEILVMDDQNNKLSKERKL LEERISDLTTNLAEEEEKAKNLTCLKNKHESMISELEVRLKKE EKSRQELEKLRKLEGDASDFHEQIADLQQAIAELKMQLAKKE EELQAALARLDDEIAQKNNALKKIRELEGHISDLQEDLDSERA ARNKAQKQKRD LGEELEALKTELEDTL DSTATQQLRAKREQE VTVLKR\ALNEETR SHEAQVQEMRQKHAQAVQSLTEQLEQ*K RAKANLDKNKQTLKENTD\LAGELRVLGQA\KQEVHRMKKL QAQVQELQSKCSDGERARAELNDKVHK\QNEVESVTG\MLNE AEGKAIKLAKDVASLSSQL\QDTQELLQEE SRQKLNVT\SLR \QLEEEERNSLQDQLDEEMEAKQNLERHISTLNIQLSDSKKKLQ DFASTVEALEEGKKRFQKEIENLTQQYEEKAAAYDKLEKTKNR LQQELDDLVDLDNQRQLVSNLEKKQRKFDQLLAEKNISSKY ADERDRVEAEAREKETKALS\ARALEEAELEKEELERTNKML KA\EMGRPGSASKD\DVQELSHDL\EKSK\RALGDPRL EEMK T\QLEELGRTELASPRRDA\KLRLEVNMQAPSASFER\DLQA RTEQNE\ESRR\HLQRQLHEYETELEDERKQRAAAAAIKIG WDPVRTLDL*ADSAIKGRGGKAIKQLRKLQAQMKDFQRELEDA \RASRDEIF\ATA\KENEKKA KSLEA\DLMLQLE\DLAAAE RKQ\ADLE\KEELAEEL\ASSLSGRNALQDEKRRL EARIAQLE EELEEEQGNMEAMSDRVKATQQAQELSNE LATERSTAQKNES ARQQLERQNKELRSKLHEMEGAVKSKFKSTIAALEAKIAQLEE QVEQEAEREQAATKSLKQDKKLLKEILLQVEDERKMAEQYKEQ AEKGNARVKQLKRQLEEAEEESQRINANRRKLQRELDEATESN EAMGREVNALKSKLRRGNETSFVPSRRSGRRVIENADGSEEE TDTRDADFNGTKASE</p>

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527	1266	1	775	KLHFAKSLNSELSCSTREAMQDEDEGYITLNIKTRKPALVSVGP ASSSWVRVMA LILLILCVGMVVLVALGIWSVMQRNYLQDENE NRTGTLQQLAKRFCQYVVKQSELKGTFGHKCSPCDTNWRYYG DSCYGGFRHNLTWEEKQYCTDMNATLLKIDNRNIVEYIKAR\ THLIRWVGLSRQKSNEVWKWEDGSVISENMFEELEDGKGNMNC AYFHNGKMHPTFCENKHYL\MCE\RKAGHDPRTWQLPLMPKRW TG
528	1267	1053	424	NQGLRDVGLCRTCLVNKIFASSILGKSHHSLVSNQGHNA PW KAAGS\LPLKAAAYC\QGFSPCDCLKYG\SWDEKDLMPQPDTH KGSVLRWISKRGKPLAVEME EGHCL\CLPLGTECLGVKP\IVH LFNSEMG EK\RPVAG\ARHVGSSAALLFFTPLRCLGGEKHKSG LRARPGIVPSLELNYDIDSFAHMF/SVDLLLIITLLSYTIPF C
529	1268	1435	1560	MWWRLAPTQAIWRAAGCCMRFSRRRSTCCCLASCIFFLYKIVR GDQPAAKRRQRRRRAAPSAPPQAARLHPPPKLRRFDGVQDPAP YSWAINGKVFDTQRPANFLRGPRGPETLSDWESQFTFKYHHV GKLLKEGEEPTVYSDEEPEKDESARKND*
530	1269	705	166	GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCL GASPTPGEVQRHLQTHGIDNGELDFSTFLTIMHMQIKQEDPK KEILLAMLMDKEKKGVMASDLRSKLTSLGEKLTHKEV\DDL FRE\ADIEPNGKVYDEFIHKI/TLLPGRDLLKEENGRASPGP ENLEQLIFL
531	1270	25	1396	ADPHTTVIRFFPAASATKRVLPVLRVSSPRTWNPVNPESPRI PAPRLPKRMSGAPTAGAALMLCAATAVLLSAQGGPVQSKSPRF ASWDEMNVLAHGLLQGLQGLREHAERTRSQLSALERRLSACGS ACQGTGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFH KVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKR LPEMAQPVDPAHNVSRHLRLPRDCQELFQVGERQSGLFEIQPQ GSPFFLVNCKMTSDGGWTVIQRHDGSDVFNRPWEAYKAGFGD PHGEFWLGLEKVHSITGDRNSRLAVQLRDWDGNAELLQFSVHL GGEDTAYSLQLTAPVAGQLGATTVPVPSGLSVFPSTWDQDHLR RDKNCAKSLSGGWFGTCSHSNLNGQYFRSIPQQRQKLKKGIF WKTWRGRYYPLQATTMLIQPMAAEAAS
532	1271	1276	90	ALDFGDSQWPRPQDTMKQLPVLEPGDKPRKATWYTLTVPGDS PCARVGHSCSYLPPVGNARGKVFI VGGANPNRSFSDVHTMDL GKHQWDLDTCKGLLPRYEHASFIPSCPTDRIWVFGGANQSGNR NCLQVLNPETRTWTTPEVTSPPPSPTFTTSSAIGNQLYVFG GGERGAQPVQDTKLHVFDANTLTWSQPETLGNPPSPRHGHVMV AAGTKLFIHGGLAGDRFYDDLHCIDISDMKWQKLNQYTGAA\PA GCAS/HTPAVAMGK\HVIYI\FGGMTPAGAPGTQCTQYHTEQH WDPCLKF\DTPSYPPGTIGTHSHVVSFPW\PVTCASEKEDS\N SLTLNHEAEKEDSADKVM SHSGDSHEESQTATLLCLVFGGMNT EGEIYDDCIVTVVD

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533	1272	1169	639	GFSIGKATDRMDAFRKAKNRAVHHLHYIERYEDHTIFHDISLR FKRTHIKMKKQPKGYGLRCHRAIITICRLIGIKDMYAKVSGSI NMLSLTQGLFRGLSRQETHQQLADKKGLHVVEIREECGPLPIV VASPRGPLRKDPEPEDEVDPVKLDWEDVKTAQGMKRSVWSNLK RAAT
534	1273	25	1396	ADPHTTVIRFFPAASATKRVLPVLRVSSPRTWNPVNPESPRI PAPRLPKRMSGAPTAGAALMLCAATAVLLSAQGGFVQSKSPRF ASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGS ACQGTGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFH KVAQQQRHLEKQHLRIQHLSQFGLLDHKHLDHEVAKPARRKR LPEMAQPVDPAHNVSRHLRLPRDCQELFQVGERQSGLFETIQPQ GSPPFLVNCKMTSDGGWTVIQRHDGSDVFNRPWEAYKAGFGD PHGEFWLGLEKVHSITGDRNSRLAVQLRDWDGNAELLQFSVHL GGEDTAYSLQLTAPVAGQLGATTVPSPGLSVPFSTWDQDHLR RDKNCAKSLSGGWFFGTCSHSNLNGQYFRSIPQQRQKLKKGIF WKTWRGRYYPLQATTMLIQPMAAEAAS
535	1274	23	1102	TLRSRPAGEAGYLGDPEQAGEGSALS RPGAMAALMTPGTGAP PAPGDFSGEGSQGLPDPSPEPKQLPELIRMKRDGGRLSEADIR GFVAADVNGSAQGAQIGAWGGLGVPDPDWEVSPRDFGSLGVRR CPTTSTGPRVPHRCGLPPSRVPPHTRG\MLMAIRLRGMDLEET SVLTQALAQSGQQLWEPEAWRQQLVDKHSTGGVGDKVSLVLAP ALAACGCKVINHLLSRREPIPHMQQPVHPQAAPNLKPGPKPPR PYQGFSPPCSPAQFSPPRSPAQRLGPLWLQTRPLGAGKRSTDG IQTPFPLGPPQTAPPREELRTSLPLPQALFPQGGVPTSSPTDTS QPRKLPFHSLTSWAPL
536	1275	3	439	RALRELRRVTHGLAEAGRDREDVSTELYRALEAVRLQNSEGS CEPCPTSWLPFGGSCYYFSVPKTTWAEAQGHCADASAHLA/IV GGLGEQDFLSRDTSALEYWIGRRVQHLRKVQGYSWVDGVPLS FR*/WEG/HPGETWGPQVRL
537	1276	1	564	RWPRSWPPRAGAARGAAEAAMVGALCGCWFRLLGGARPLIPLGP TVVQTSMSRSQVALLGLSLLLMLLLYVGLPGPPEQTSCLWGD NVTVLAGLTPGNSPIFYREVLPLNQAHREVEV\CCFMERPLTLT RGSSWAHCSYCHRGATGPWPLTFQVLGTRHLQRRQAQRQGGQR CWSGRCGTWRYRMPCW

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538	1277	102	1549	QENQLEKKMKFLIFAFFGGVHLLSLCSGKAICKNGISKRTFEE IKEEIASCGDVAKAIINLAVYGKAQNRSYERLALLVDTVGPRL SGSKNLEKAIQIMYQNLQODGLEKVHLEPVRIHPWERGEESAV MLEPRIHKIAIILGLGSSIGTPEGITAEVLVVTSFDELQRRAS EARGKIVVYNQPYINYNSRTVQYRTQGAVEAAKVGALASLRSV ASFSIYSPHTGIQEYQDGVPKIPTACITVEDAEMMSRMASHGI KIVIQLKMGAKTYPDTDSFNTVAEITGSKYPEQVVLVSGHLDS WDVGQGAMDDGGGAFISWEALSLIKDLGLRPKRTLRLVLWTAE EQGGVGAFQYYQLHKVNISNYSLVMESDAGTFLPTGLQFTGSE KARAIMEEVMSLLQPLNITQVLSHGEGTDINFWIQAGVPGASL LDDLKYFFFFHSHGDTMTVHGIQTQMNVA\AAAV\WAVVS\YV\ VADMEEMLPRS
539	1278	2438	1148	TKPKRRRHQPASQRPWSSDSTGDLARGKGRKEENKGS DRV SLAPPSLRPMMQCSEARQGPPELRAAKWLHFPQLALRRRLGQL SCMSRPALKLRSWPLTVLYLLPFGALRPLSRVGRVSRVAL YKSVPTRLLSRAWGRNLQVELPHWLRPPVYSLYIWTFGVNMKE AAVEDLHHYRNLSFFRRKLKPQARPVCGLHVSISPDSGRILN FGQVKNCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCD SF KNQLVTREGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFP SLMSVNPGMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\ NWGSIRIYFDRDLHTNSPRHSGSYNDFSFTVHTNREGVPMRK GEHLGEFNLGSTIVLIFEAPKDFNFQLKTGQKI\RFGEALGSL
540	1279	3	1911	LPERAFGPRTPPAPRRRRRRLLSPPPRPPPPPLDREPRAPGPW LCPSRAGTAQDPARIRERRGRVAGGAAGPAMELRARGWLLCA AAALVACARGDPASKSRSCGEVRQIYGAKGFSSS\DVQAEIS GELRICPQGYTCCTSEMEENLANRSHAELETALRDSSRVLQA MLATQLRSFDDHFQHLNDSERTLQATFPFAGFELYTQNRARF RDLYSELRLYYRGANLHLEETLAEFWARLLERLFKQLHPQLLL PDDYLDCLGKQAEALRPF\GEAP\RELRLRAT\RA\FVAAR\S FVQGLGVAS\DVVRKVAQVPLG\PEC\SRAVIEAGSYC\ALHC VGVPGARPCPDYCRNVKGC LANQADLDAEWRNLLDSMVLITD KFWGTSGVESVIGSVHTWLAEAINALQDNRDILTAKVIQGC GN PKVNPQGPPEEKRRRGKLA PRERPPSGTLEKLVS EAKAQLRD VQDFWISLPGTLCSEKMALSTASDDRCWNGMARGRYLPEVMGD GLANQINNPEVEVDITKPDMTIRQQIMQLKIMTNRLRSAYNGN DVDFQDASDDGSGSGSGDGCLDDLCGRKVSRSKSSSRTPLTHA LPGLSEQEGQKTSAA SCQPPTFLLPLLLFLALTVARPRWR
541	1280	590	189	ATELTRAGMEASALT KSA\VTSAKVVR\VASGS AVVLP LARI ATSCD*RVGGP/VQAVPMVL\SAMGLQLRAGIASSSIAAKMMS AAAIA\NGGGVSPGQPLWLLLQSLGATGL\SGLT KFILGSIGS AIA\AVIARFY

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542	1281	41	1415	TNGRNL LHHWILGVCGMHPHQETLKKNRVVLAKQLLLSELLE HLEKDIITLEMRELIQAKVGSFSQNVLLNLLPKRGPQAFDA FCEALRETKQHLEDMLLTTL SGLQHVL PPLSCDYDLSL PFPV CESCPLYKKLR LSTDTVEHSLDNKDG P VCLQVKPCTPEFYQTH FQLAYRLQSRPRGLALVLSNVHFTGEKELEFRSGGDVDHSTLV TLFKLLGYDVHVLCDQTAQEMQEKLQNFALPAHRVTDSCIVA LLSHGVEGAIYGV D G K L L Q L Q E V F Q L F D N A N C P S L Q N K P K M F F IQACRGGAGISLG H L L L F T A A T A S L A L \ E T D R G V D Q Q D G K N H A GSPGCEESDAGKEKL P K M R L P T R S D M I C G Y A C L K G T A A M R N T K RGSWYIEALAQVFSE R A C D M H V A D M L V K V N A L I K D R E G Y A P G T EFHRCKEMSEYCS T L C R H L Y L F P G H P P T
543	1282	862	275	VRGKEVMAALCRTRAVAAESHFLRVFLFFRPFRGVGTESGSES GSSNAKEPKTRAGGFASALERHSELLQKVEPLQKGSPKNVESF ASMLRHSPLTQMGP AKDKLVIGRI F H I V E N D L \ Y I D F G G K F H C VCCRPEVDGEKY \ Q K G T R V R \ L R L L D L E L T S R F L G A T T D \ T T V LEANAVLLGIQESKDSRSKEEHLEKYI

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544	1283	2	4503	<p>IPGASAPARRAAPRLRLGLRLASGWARAPGGVSPVPGPGMGGDA PTMARAQALVLELTFQLCAPETETPEVGCTFEEGSDPAVPCEY SQAQYDDFQWEQVRIHPGTRAPADLPHGSYLMVNTSQHAPGQR AHVIFQSLSENDTHCVQFSYFLYSRDGHSPTGLGVYVRVNGGP LGSAVWNMTGSHGRQWHQAE LAVSTFWPNEYQVLFEALISPD RGYMGDDILLLSYPCAKAPHFSRLGDVEVNAGQNASFQCMMA GRAAEAEERFLLQRQSGALVPAAGVRHISHRRFLATFPPLA AEQDLYRCVSQAPRGRGTSLNFAEFMV/KEPPTPIAPPQLLRA GPTYLIIQLNTNSIIGDGPVIRKEIEYRMARGPWAEVHAVSLQ TYKLWHLDPDTEYBISVLLTRPGDGGTGRPGPPLISRTKCAEP MRAPKGLAFAEIQARQLTLQWEPLGYNVTRCHTYTYSVCYHYT LGSSHNQTI\RECVKTEQGVSRYSYTMKNLLPYRNVHVRVLVLTNP EGRKEGKEVTFQTDDEVP SGIAAESLTFTPLEDMIFLKWEEPQ EPNGLITQYEISYQSIESSDPAVNVP GPRRTISKLRNETHYVF SNLHPGTTYLFSVRARTGKGFGQAALTEITTNISAPSFYADM SPPLGESENTITVLLRPAQGRGAPISVYQVIVEEEQGSRRRLR EPGGQDCFPVPLTFEALARGLVDFGAELAASSLPEAMPFTV GDNKTYRGFWNPPLPRKAYLIYFQAASHLKGETRLNCIRIAR KAACKESKRPLEVSQRSEEMGLILGICAGGLAVLILLGAIIV IIRKGRDHYAYSYPKPVNMTKATVNYRQEKTHMMSAVDRSFT DQSTLQEDERLGLSFMDTHGYSTRGDQRSGGVTEASSLLGGSP RRPCGRKGSFYHTGQLHPAVRVADLLQHINQMKTAEQYGFQKE YESFFEGWDATKKKDKVKGSRQEPMPAYDRHRVKLHPMLGDPN ADYINANYIDIRINREGYHRSNHFIATQGPKEPMVYDFWRMVW QEHCSIVMITKLVEVGRVKCSRYWPEDSDTYGDIKIMLVKTE TLAEYVVRTFALERRGYSARHEVRQFHFTAWPEHGVPHYATGL LAFIRRVKASTPPDAGPIVIHCSAGTGRGTGCYIVLDVMDMAE CEGVVDIYNCVKTLCSSRVNMIQTEEQYIFIHDAILEACLCGE TTIPVSEFKATYKEMIRIDPQSNSSQLREEFQTLNSVTPPLDV EECSIALLPNRDKNRSMDVLPDRCLPFLISTDGDSSNNYINA ALTDSTYTRSAFIVTLHPLQSTTPDFWGLVYDYGCTSIIVMLNQ LNQSNSAWPCLQYWPEPGRQQYGLMEVEFMSGTADEDLVARVF RVQNISRLQEGHLLVRHFQFLRWSAYRDTDPDSKKAFLHLLAEG DKWQAESGDGRTIVHCLNGGGRSGTFCA\CATVLEMIRCHNLV DVFFAAKTLRNYKPNMVETMDQYHFCDVALEYLEGLESR</p>

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545	1284	2443	1152	TKPRKRRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGS DRV SLAPPSLRRPMMCQSEARQGP ELRAAKWLHFPQLALRRRLGQL SCMSRPALKLRSWPLTVLYLLPFGALRPLSRVGRVPVSRVAL YKSVPTRLLSRAWGRNLNQVELPHWLRPVSLSYIWTFGVMNME AAVEDLHHYRNLSEFFRRKLKPQARPVCGLHVSIPSDGRILN FGQVKNCEVEQVKGVTSLESFLGPRMCTEDLPFPPAASCDSF KNQLVTREGNELYHCVIYLAPGDYHCFHSPDTWTVSHRRHFPG SLMSVNPGMARWIKELFCHNERVVLTDGDKHGFPSLTAVGAT\ NWGSIRIYFDRDLHTNSPRHSKGSYNDFSFTHTNREGVPMAL RGEHLG/QSFNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALG SL
546	1285	185	3057	AELGLFGSLRFSSLLHFPFPRSPASACGPGEGRMERGLPLLC AVLALVLAPAGAFRNDKCGDTIKIESPGYLTSPGYPHSYHPSE KCEWLIQAPDPYQIRIMINFNPFDLEDRCYDYVEVFDGENE NGHFRGKFCGKIAPPPVSSGPFLLFIKFVSDYETHGAGFSIRY EIFKRGPECSQNYTTTPSGVIKSPGFPEKYPNSLECTYI\VFAP KMSEIIL\DFESFDLEPDSNPPGGMFCRYDRLEIWDGFPDVG HIGRYCGQKTPGRIRSSSGILSMVFYTD SAIKEGFSANYSVL QSSVSEDFKCM EALGMESGEIHS DQITASSQYSTNWSAERSRL NYPENGWTPGEDSYREWIQVDLGLLRFTAVGTQGAISKETKK KYYVKTYKIDVSSNGEDWITIKEGNKPVL FQGNTPD VVVAV FPKPLITRFVRIK PATWETGISMRFEVYGCKITDYPCSGMLGM VSGLISDSQITSSNQGDRNWPENIRLVT SRSGWALPPAPHSY INEWLQIDLGE EKIVRGII IQGKHKRENKVFMRFKIGYSNNG SDWK MIMDDSKRKAKSFE GNNNYDTPELRTFPALSTRFIRIYP ERATHGGLGLRMELLGCEVEAPT AGPTTPNGNLVDECD DDQAN CHSGTGDDFQLTGGTTVLATEKPTVIDSTIQSEFPTYGFNCEF GWGSHKTFCHWEHDNHVQLKWSVLTSKTGPIQDHTGDGNFIYS QADENQKGKVARLVSPVVYSQNSAHCMTFWYHMSGSHVGT LRV KLRYQKPEEYDQLVWMAIGHQGDHWKEGRVLLHKS LKLYQVIF EBEIGKGNLGGIAVDDISINNHSQEDCAKPADLDKKNPEIKI DETGSTPGYEGEGEGDKNISRKPGNVLKTLEPILITIIAMSAL GVLLGAVCGVVLYCACWHNGMSERNLSALENYNFELVDGVK LK KDKLNTQSTYSEA
547	1286	3	521	HEGSALTWASHYQERLNSEQSCLNEW TAMADLES LRPPSAEPG GSVCGGEG LGGGEGRIMQWGA WWRGERAP*LRGSAPRSSEQEQ MEQAIRAELWKVLDVSDLESVTSKEIRQALELRLGLPLQ/PVP *LHRQPDAAAGGTAGPSLPHLPPPLPGLRVERSKPGGAEEQV GL
548	1287	1742	1200	MAALDLRAELDSLVLQLLGDLEELGKRTVLNARVEEGWLSLA KARYAMGAKSVGPLQYASHMEPQVCLHASEAQEGLQKFVVR A GVHAPEEVGP REAGLRRRKGP TKTPEPESSEAPQDPLNWF GIL VPHSLRQAQASFRDGLQLAADIASLQNRIDWGRS QLRGLQEK L KQLEPGAA*

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549	1288	1	649	HSDVGAATAVLPLLTAVLGVTVVTRRDTEGPGRAALVHLTGSP RQKVGTSGREGLPGLGASCAESELERETQEPRSRGRCIFGAAR WRQVPLASPQRPFLLSPGPRLRHMGFLPVSWAPPALWVLGCCAL LLSLWALCTACRRPEDAVAPRKRARRQRARLQGSATAAEAVSA KLSRGPGWGPQGTDPSSPPVPTEADPPLLQQVGHQTARAAP G
550	1289	433	632	LTGPGQRLAGTTEGPRRCRGSSQAPTPTWKLVDTRLCAAAPWL ASRAPGHYSQMLLVN*PCRKDWLVSKWMRTPVCGQSPAMTDRP RSEAGRDRHRAKALPGLIPGSNPNLEACGHQALCSSVASVQG PWPLLPNASSPPTPGQPQP
551	1290	102	612	KHRLCSLEQLMTLISAAREYEIEFIYAISPGLDITFSNPKEVS TLKRKLDQVSQFGCRSFALLFDDIDHNMCAADKEVFSSFAHAQ VSIITNEIYQYLGEPEFTFLFCPT/EYCI*WLYI*LVFLEYITYK GPWAPFSLHFPPPLVCKSRNLFLEDIFQDPKLEKF*ELINDN
552	1291	269	565	TSALTQGLERIPDQLGYLVLSEGAVALASSGDLLENDEQAASIS ELVSTACGFRHLRGMNVPFKRLSVVFGEHTLLVTVSGQRVVFV KRQNRGEPIDV
553	1292	660	233	AKRAERTSRLQGLQHPSPPYPATLGVTGQDRTLQQLQHCPA GRKSRKKKSKATQLSPEDRVEDALPPSKAPSRTRRAKRDLPKR TATQRPEGTSLQDPEAPTVPKKGRRKGRQAASGHCRPRKVK DIPSLEPEGTSAS
554	1293	590	323	RKSSWLGAVAHACNPSSLGGPGRQITRSGVRDQPGQYGETPSL LKIQTLAGRGGACL*SHILRRLRQKNRLNLGGRGCSLRSRHC APA
555	1294	1	242	AWNSARGAVSPLWVPGCFLLSVTWIGAAPLILSRIVGGWECE KHSQPWQVLVASRGRAVCGGVLVHPQWVLTAAHCIRK
556	1295	1074	230	AEMADDLGDEWWENQPTGAGSSPEASDGEGEDTEVMQQETVP VPVPSEKTKQPKCEFLIQPKERKENTTKTRKRRKKKITDVLAK SEPKPGLPEDLQKLMKDYSSRRLVIELEELNLPDSCFLKAND LTHSLSSYLKEICPKWVKLRKNHSEKKSVMMLIICSSAVRALE LIRSMTAFRGDGKVIKLFKHIKVAQVKLLEKRVVHLGVGTP GRIKELVKQGGNLNLSPLKFLVFDWNWRDQKLRRMMDIPEIRKE VFELLEMGVLSLCKSESILKGLF
557	1296	929	289	RPGTAIWVVECEHGRPIAESEGEGRGHSPPGPCSVAGFLRGR LGRNLEIMGSTWGS PGWVRLALCLTGLVLSLYALHVKAARARD RDYRALCDVGTAISSRVFSSRWGRGFGFLVEHVLGQDSILNQS NSIFGCIFYTLQLLGLRTRWASVIMLLSSLSVLAGSVYLAW ILFFVLVDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRH

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558	1297	2	1063	ESPAPPAPFRPAMAVALMPPPLLLLLLLASPPAASAPSARDPF APQLGDTQNCQLRCRDRDLGPQPSQAGLEGASESPYDRAVLIS ACERGCRLFSICRFVARSSKPNATQTECEAACVEAYVKEAEQQ ACSHGCWSQPAEPEPEQKRKVLAPSGALSLDLFSTLCNDLV NSAQGFVSSWTYYLQTDNGKVVVFQTPQIVESLGFQGGRLQR VEVTWRGSHPEALEVHVDVPGPLDKVRKAKIRVKTSSKAKVES EEPQDNDFLSCMSRRSGLPRWILACCLFSLVLMWLWSCSTLV TAPGQHLKFQPLTLEQHKGFMMEPDWPLYPPPSHACEDSLPPY KLKLDLTKL
559	1298	2	485	FPELGTSLSAMRFLAATFLLLALSTAAQAEPVQFKDCGSVDGV IKEVNVSPCPTQPCQLSKGQSYSVNVTFTSNIQSKSSKAVVHG ILMGVPVPFPIPEPDGCKSGINCPIQDKTYSYLNKLPVKSEY PSIKLVVEWQLQDDKNQSLFCWEIPVQIVSHL
560	1299	1304	919	APETFRCVWRLOGLTFIAFTELQAKVIDTQQVKLADIQIEQL NRTKKHAHLTDTEIMTLVDETNMYEGVGRMFILQSKAHSQ LEKQKIAEEKIKELEQKKSYLERSVKEAEDNIREMLMARRAQ
561	1300	3	799	HSLLLGRTRVDASSKIQGEYTLTLRKGGNNKLSRVFHRDGHY FSEPLTFCSVVDLINHYRHESLAQYNAKLDTRLLYPVSKYQQV RAGLGAREGSTWLAPGLSFLGRPDQAMHLPFRHVSP\DQIVK EDSVEAVGAQLKVYHQYQDKSREYDQLYEYTRTSQELQMKR TAIEAFNETIKIFEEQQTQEKCSKEYLERFRREGN/QTKEMQ RILLNSERLKSRIA\EIHESPHRSWEQQLLVPRASDNKRD/ID KPH*TSLKPD
562	1301	1772	301	AAAAAGRGRSSGRRRRRRPGALFASLGVLGPRPPPGIPRTRA CSMGVGEGPGREGPAQPGAPLPTFCWEQIRAHQPGDKWLVI ERRVYDISRWAQRHPGGSRLIGHHGAEDATDAFRAFQDLNFV RKFLQPLLLIGELAPEEPSQDGPLNAQLVEDFRALHQAEDMKL FDASPTFFAFLGHILAMEVLAWLLIYLLGPGWVPSALAAFIL AISQAQSWCLQHDLGHASIFKKSWWNHVAQKFVMGQLKGFSAH WWNFRHFQHHAKPNI FHKDPDVTVPVFLGESSVEYGGKKRR YLPYNQQLHYFFLIGPPLLTLVNFEVENLAYMLVCMQWADLLW AASFYARFFLSYLPFYGVPGVLLFFVAVRVLESHWFVWITQMN HIPKEIGHEKHRDWSSQLAATCNVEPSLFTNWFSGHLNFQIE HHLFPRMPRHNYSRVAPLVKSLCAKHGLSYEVKPFALTALVDIV RSLKKSGDIWLDAYLHQ
563	1302	424	93	KSRATRLRESAEMTGFLLPASRGTRRSCSRSRKRQTRRRRN SSFVASCPTLLPFACVPGASPTTLAFPPVVLTPGPDGIPFAL SLQRVPFVLPSQVASLPLGHSRG
564	1303	1	414	IQYRSDELHLSITMKKSGVLFLLGIILLVLIGVQGTVPVRKGR CSCISTNQGTIHLQSLKDLKQFAPSPSCEKIEIIATLKNVQT CLNPDSADVKELIKKEKQVSQKKKQKNGKKHQQKKVLRKS QRSRQKTT

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565	1304	7	3007	IPGSTISCRGCCGKWPVQEADPPRAALRGRFPALLTRHCPSPR AEKEKRSLLRRCGRPLLVELAGPAGQAVEVLPHFESLGKQEKI PNKMSAFRNHCPHLDSVGEITKEDLIQKSLGTCQDCKVQGPNL WACLENRCSYVGCGESQVDHSTIHSQETKHYLTVNLTTLRVWC YACSKFVFLDRKLGTPSLPHVRQPHQIQENSVDQFKIPSNTT LKTPLVAVFDDLDIEADEEDELARGLTGLKNIGNTCYMNAAAL QALSNCPLTQFFLDCCGLARTDKKPAICKSYLKLMTLWYKS RPGSVVPTTLFQGIKTVNPTFRGYSQQDAQEFLRCLMDLLHEE LKEQVMEVEEDPQTITTEETMEEDKSQSDVDFQSCSCSNDR AENENGSRCFSEDNNETTMLIQDDENNSEMSKDQWQKEMCNKI NKVNSEGEFDKDRDSISETVDLNNQETVKVQIHSRASEYITDV HSNDLSTPQILPSNEGVNPRLSASPPKSGNLWPLAPPKKAQ SASPKRKKQHKYRSVISDIFDGTIISSVQCLTCDRVSVTLET FQDLSLPIPGKEDLAKLHSSSHPTSIVKAGSCGEAYAPQGWIA FFMEYVKRFVWSCVPSWFWGPPVVTLDCLAAFFARDELKGDNM YSCEKCKKLRLNGVKFKCVQNFPEILCIHLKRFHELMFSTKIS THVSFPLEGLDLQPFLLAKDSPAQIVTYDLSVICHHGTASSGH YIAYCRNNLNNLWYEFDDQSVTEVSESTVQNAEAYVLFYRKSS EEAQKERRRISNLLNIMEPSLLQFYISRQWLNKFKTFAEPGPI SNNDFLCIHGGVPPRKAGYIEDLVLMPLQNIWDNLYSRYGSGP AVNHLYICHTCQIEAEKIEKRRKTELEIFIRLNRAFQKEDSPA TFYCISMQWFREWESFVKGKGDGPPGPIDNTKIAVTKCGNVML RQGADSGQISEETWNFLQSIYGGGPEVILRPPVHVDPDILQA EEKIEVETRSL
566	1305	28	450	SPSAAGGLAWVSLALGSGSRGRDHS GSGVGTAMAGALVRKAAD YVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKKSPEIISGR MTFALCCYSLTFMRFAVKVQPRNWLLFACHATNEVAQLIQGGR LIKHEMTKTASA
567	1306	133	1292	LGSRQAAGTMRGQSRLLGPARLCLRLLLLLGYRRRCPPLLRG LVQRWRYGKVCRLRSLLYNSFGGSDTAVDAAFEPPVYWLVDNVIR WFGVVVVLVIVLTGSIVAIAYLCVLPILRTYSVPRLCWHFF YSHWNLILIVFHYQAITTPPGYPPQGRNDIATVSIKKCIYP KPARTHHCSICNRCVLKMDHCPWLNNCVGHYNHRYFFSFCFF MTLGCVCYSYGSWDLFREAYAAIEKMKQLDKNKLQAVANQTYH QTPPTFSFRERMTHKSLVYLWFLCSSVALALGALTVWHAVLI SRGETSIERHINKKERRRLQAKGRVFRNPYNYGCLDNWKVFLG VDTGRHWLTRVLLPSSHLPHGNGMSWEPPPWVTAHSASVMAV
568	1307	66	962	ATRRRAAEAGMAAVLQVRVERLSNRVVRVLGCNPGPMTLQGTNT YLVGTGPRRILIDTGEPAIPEYISCLKQALTEFNTAIQEIVVT HWRDHSGGIGDICKSINNDTTYCIKKLPRNPQREEIIGNGEQ QYVYLKGDVIKTEGATLRVLYTPGHTDDHMAALLLEENAI FS GDCILGEGTTFEDLDYDMNSLKELLKIKADIIYPGHGPIVHN ABAKIQQYISHRNIREQQILTLFRENFEKSFTVMELVKI IYKN TPENLHEMAKHNNLLHLKKLEKEGKIFSNTDPDKKWKHAHL

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569	1308	96	1017	ELHRAGQVAGGARRSRRESMELERIVSAALLAFVQTHLPEADL SGLDEVIFSYVLGVLEDLGPSPSEENFDM EAFTEMMEAYVPG FAHIPRGITIGDMMQKLSGQLSDARNKENLQ PQSSGVQGVPI S PEPLQRP EMLKEETRSSAAAAADTQDEATGAE EELLPGVDVLL EVFPTCSVEQAQWVLAKARGDLEEAVQMLVEGKEEGPAWEGP NQDLPRRLRGPQKDELKSFILQKYMVDSAEDQK IHRP MAPKE APKKLIRYIDNQVVSTKGERFKDVRNPEAEEMKATYINLKPAR KYRFH
570	1309	3	526	FITGKGIVAILRCLQFNETLT E LRFHNQRHMLGHHAE MEIARL LKANNTLLKMGYHFELPGPRMVVTNLLTRNQDKQRQKRQEEQK QQQLKEQKKLIAMLENGLGLPPGMWELLGGPKPDSRMQEFFQP PPPRPPNPQNVFQSQRSEMMKKPSQAPKYRTDPDSFRVVKLKR IQ
571	1310	3	1858	GGRAGTQCCWRAGARLRGISPSPALPEAPGLCRVRAGLGAGAL GRSPAGRRRRRGRPVSSSPAPHPRRVLCRCLLFFFSCHDRRGD SQPYQALKYSSKSHPSGDRHEKMRDAGDPSPPNKMLRRSDS PENKYS DSTGHSKAKNVHTHRVRERDGGTSYSPQENSHNHSAL HSSNFTFFLIPSN*PQGKTFRIAPYDS\ADDW/SLEHISSSGE KYYNCRTEVSQWGKTPKSGLERGQKQKEANKMAVNSFPKDRD YRREVMQATATSGFASGKSTSGDKPVSHSCTTPSTSSASGLNP TSAPPTSASA\VPVSP\VPQ\SPIPPLLQDPNLLRQLL\PALE ATLQLNNSNVDI\SIINEVLTGDVTQASLQTIHKCLTAGPSV FKITSLISQAAQLSTQAQASNQSPMSLTSDASSPR\SYVSPRN KAHLKLNTVPIQTFGFSTPPVSSQPKVSTPVVKQGPVSQSATQ QPVTADKQQGHEPVSPRSLQRSSSQRSPPGPNHTSNSSNASN ATVVPQNSSARSTCSLTPALAAHFSENLIKHVQGW PADHAEKQ ASRLREEAHNMGTIHMSEICTELKNLRLSLVRVCEIQATLREQR ILFLRQQIKELEKLNQNSFMV
572	1311	2	1165	VAPECRGAYPFRAMMPGTALKAVLLAVLLVGLQTATGRLLSGQ PVCRRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI ESEDEQK LIEKF IENLLPSDGD F WIGLRRREEKQSNSTACQDL YAWTDGSI SQFRNWYVDEPSCGSEVCVMYHQPSAPAGIGGPY MFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGETELTPVL PEETQEEDAKKTFKESREALNLAYILIPSIPLLLLLLVVTTVV CWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIR KQSEADLAETRPDLKNISFRVCSGEATPDDMSCDYDNMAVNPS ESGFVTLVSVESGFVTNDIYEFSPDQMGRSKESGWVENEIYGY

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573	1312	3	1416	TEWGLSGSCPGCSPLEPGSRGRGAAAWRIILRCRRLPEPSPFLT QPNLAQSQPPAPVPVTDPSVTMHPAVFLSLPDLRCSLLLLVTW VFTPVTTTEITSLDTENIDEILNNADVALVNFYADWCRFSQMLH PIFEEASDVKEEFPNENQVVFARVDCDQHSIDIAQRYRISKYP TLKLFNRNGMMMKREYRGQRSVKALADYIRQKQSDPIQEI RDLA EITTLDRSKRNIIGYFEQKSDNYRVFERVANILHDDCAFLSA FGDVSKPERYSQDNIIYKPPGHSAPDMVYLGAMTNFVDVTYNWI QDKCVPLVREITFENGEEELTEEGLPFLILFHMKEDTESLEIFQ NEVARQLISEKGTINFLHADCDKFRHPLLHIQKTPADCPVIAI DSFRHMYVFGDFKDVLPGLKQKFVFDLHSGKLHREFHHGPD TDTAPGEQAQDVASSPPESSFQKLAPSEYRYTLRLDRDEL
574	1313	928	142	LTPSVGPVFPGRPTRPLASPPFVPLHRCAGSQPPGPVPEGLI RIYSMRFCPYSHRTRLVLKAKDIRHEVVNINLRNKPWYYTKH PFGHIPVLETSQCQLIYESVIACEYLDAYPGRKLEFPYDPYER ARQKMLLELFCKVPHLTKECLVALRCGRECTNLKAALRQEFNS LEEILEYQNTTFFGGTCISMIDYLLWPWFERLDVYGILDCVSH TPALRLWISAMKWDPTVCALLMDKSI FQGFNLNLYFQNNPNAFD FGLC
575	1314	884	363	NTATNMTQPNAGTRKYSVPAISVHTSSSSFAYDREFLRTLPGF LIVAEIVLGLLVWTLIAGTEYFRVPAFGWVMFVAVFYWVLTVF FLIIYITMTYTRIPQVPWTTVGLCFNGSAFVLYLSAAVVDASS VSPERDSHNFNSWAASSFFAFLVTICYAGNTYFSFIAWRSRTI Q
576	1315	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQEKDSPSTSRSGG SSRLSSRSRSRSFSRSSHRSRVSSRFSSRSRSRSRSRSRRR HQRKYRRYSRSYSRSRSRSRRYRERRYGFTRRYRSPSRYSR SRSRSRSRSGRSYCGRAYAIARGQRYYGFGRTVYPEEHSRWR DRSRTSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDL ASLRTVPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQ I

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577	1316	265	2300	AEGSTMDLTCKMGMILQNPNHPTGLLCKANQMRLAGTLCDEVVI MVDSQEFHAHRTVLACTSKMFEILFHRNSQHYTLDFLSPKTFQ QILEYAYTATLQAKAEDLDDLLYAAEILEIEYLEEQCLKMLET IQASDDNDTEATMADGGAEKKDRKARYLKNIFISKHSSEESG YASVAGQSLPGPMVDQSPSVSTSFGLSAMSPTKAAVDSLMTIG QSLQGTLPAGPEEPTLAGGGRHPGVAEVKTEMMQVDEVP QDSPGAESSISGGMGDKVEERGKEGPGTPTRSSVITSARELH YGREESAQVPPPAEAGQAPTGRPEHPAPPPEKHLGIYSVLPN HKADAVLSMPSSVTSGLHVQPALAVSMDFTYGGLLPQGFQIR ELFSKLGELAVGMKSESRTIGEQCSCVCGVELPDNEAVEQHRKL HSGMKTGCELCKGRFLDSLRLRMHLLAHSAGAKAFVCDQCGA QFSKEDALETHRQTHGTDMAVFCLLCKGRFQAQSAQQHMEV HAGVRSYICSECNRTFPSHTALKRHLRSHTGDHPYECFECGSC FRDESTLKSHKRIHTGEKPYECNCGCKKFSLKHQLETHYRVHT GEKPFECKLCHQRSRDYSAMIKHLRTHNGASPYQCTICTEYCP SLSSMQKHMKGHKPEEIPDWRIEKTYLYLCYV
578	1317	686	908	IWEAPTLIFTLAGGRALGHPPMQKGSQGCALPHPLPGASLPAQ PGPADHRGWECRIGGEASVFTHLFCPLPHSPT
579	1318	150	1204	ASGSPAPSSSSAMAAACGPGAAGYCLLLGLHLFLLTAGPALGW NDPDRMLLRDVKALTLYHDYTTSRRLDPIQLKCVGGTAGCD SYTPKVIQCQNKGWGDYDVQWECKTDLDIAYKFGKTVVSCGY ESSEDQYVLRGSCGLEYNLDYTELGQLKESGKHGFASFSD YYYKWSSADSCNMSGLITIVLLGIAFVVYKLFSLDGQYSPPP YSEYPPFSHRYQRFNTSAGPPPPGFKSEFTGPQNTGHGATSGF GSAFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDS WYYPSPPSYPGTWNRAYSPLHGGSGSYSVCSNSDTKTRTASG YGGTRRR
580	1319	1208	276	GRCGAMAAGLARLLLLLGLSAGGPAPAGAAKMKVVEEPNAGV NNPFLPQASRLQAKRDPSPVSGPVHLFRLSGKCFSLVESTYKY EFCPFHNVTQHEQTFRWNAYSGILGIWHEWEIANNTFTGMWMR DGDACRSRSRQSKVELACGKSNRLAHVSEPSTCVYALTFTETPL VCHPHALLVYPTLPEALQRQWDQVEQDLADELITPQGHEKLLR TLFEDAGYLKTPENEPTQLEGGPDSLGFETLENCRAHKELS KEIKRLKGLLTQHGIPYTRPTETSNLEHLGHETPRAKSPEQLR GDPGLRGS
581	1320	1074	132	NSFWSVFLVQEETEVARCNAQHRLRQSRDSKPDPSFRSQPID SSISFAGSDIQPLFSFASVDGTQVGEAEWAGPWAEATLLPGP GNRWPPRAGLSGNWLEEDGDWPSLPEVVGVSERELFRDALGA GCRILLICEMQLTHQLDLFPECRTVLLLFKDVKNAGDLRRKAM EGTIDGSLINPTVIVDPFQILVAANKAVHLYKLGKMKTRTLST EIIIFNLSPNNNISEALKKFGISANDTSILIVYIEEGEKQINQE YLISQVEGHQVSLKNLPEIMNITEVKKIYKLSSQEESIGTLLD AIICRMSTKDV

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582	1321	5021	7694	QRSWAGPGAGPEAGTRPPARGRRRQPGNVDPRRRAPQLRSQM VAMARATTATGNRLWPGLLIMLGSCLHRGSPCGLSTHIEIGH ALEFLQLHNGRVNYRELLLEHQDAYQAGIVFPDCFYPSICKGG KFHDVSESTHWTPFLNASVHYIRENYPLWEKDEKLVAFLFG ITSHMAADVSWHSLGLEQGFRLTMGAIDFHGSYSEAHSAAGDFG GDVLSQFEFNFNYLARRWYVPVKDLLGIYEKLYGRKVITENVI VDCSHIQFLEMVGEMLAVSKLYPTYSTKS PFLVEQFQEYFLGG LDDMAFWSTNIYHLTIFMLENGTSDCNLPENPLFIACGGQQNH TQGSKMQKNDFHRNLTTSLTESVDRNINYTERGVFFSVNSWTP DSMSFIYKALERNIRTMFIGGSQLSQKHVSPLASYFLSFPYA RLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIYGN DLGLPPVDLDLDKEAHRILEGFQPSGRFGSALAVLDFNVDGVP DLAVGAPSVGSEQLTYKGAVYVYFGSKQGGMSSSPNITISCQD IYCNLGWTLAADVNGDSEPDLVIGSPFAPGGGKQKGIVAAFY SGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTL LLVGSPTWKNASRLGHLLHIRDEKKS LGRVYGYFPPNGQSWFT ISGDKAMGKLGTSLSSGHVLMNGTLKQVLLVGAPTYDDVSKVA FLTIVTLHQGGATRMALYALTSDAQPLLLSTFSGDRRFRSFGGV LSDLDLDDGLDEI IMAAPLRIADVTSGLIGGEDGRVYVYNGKET TLGDMTGKCKSWITPCPEEKAQYVLISPEASSRFGSSSLITVRS KAKNQVVIAGRSSSLGARLSGALHVYSLGSD
583	1322	1	357	SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASS QLKEHFAQFGHVRRRCILPFDKETGFHRGLGWVQFSSEEGLRNA LQQENHIIDGVKVQVHTRRPKLPQTSDDDEKKDF
584	1323	1205	433	GSSNIHSASTHGFCHWFSSPSTLKRQKQAIRFQKIRRQMEAPG APPRTLWEAMEQIRYLHEEFPEWSVPRLAEGFDVSTDVIRR VLKSKFLPTLEQKLKQDKVLKKAGLAHSLQHLRGSGNTSKLL PAGHSVSGSLMPGHEASSKDPNHSTALKVIESDTHRTNTPRR RKGRNKEIQDLEESFVPVAAPLGHPRELQKYSSDSES PRGTGS GALPSGQKLEELKAEEDPNFSSKVVQGREFFDSNGNFLYRI
585	1324	134	954	ETRVKTSLELLRTQLEPTGTVGNTIMTSQPVPNETIIVLPSNV INFSQAEKPEPTNQGD SLKKHLHAEIKVIGTIQILCGMMVLS LGIILASASFPNFTQVTSTLLNSAYPFIGPFFFIISGSLSIA TEKRLTKLLVHSSLVGSILSALSALVGFIILSVKQATLNPASL QCELDKNNIPTRSYVSFYHDSLYTTDCYTAKASLAGTSLML ICTLLEFCLAVLTAVLRWKQAYSDFPGSVLFLPHSYIGNSGMS SKMTHDCGYEELLTS

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586	1325	106	1537	EMVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGSGQP LFLTPYIEAGKIQKGRELSLVGPFPGGLNMKSYAGFLT VNKTYN SNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGPYV VTSNMTLRDRDFPWTTLTSLMLYIDNPVGTGFSFTDDTHGYAVN EDDVARDLYSALIQQFFQIFPEYKNDFYVTGESYAGKYVPAIA HLIHSNPNVREVKINLNGIAIGDGYSDPESIGGYAEFLYQIG LLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTS DPSYFQNVTCGSNYNFLRCTEPEDQLYYVKFSLPEVRQAIH VGNQTFNDGTIVEKYLREDTVQSVKPWLTEIMNNYKVLIIYNGQ LDIIVAAALTEERSLMGMDWKGSQYKKAEEKVWKIFKSDSEVA GYIRQAGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWD PYVG
587	1326	883	541	RDERAKVPFRSTEG\GRRRRRMEAVVFVFSLLDCCALIFLSV YFIITLSDLECDYINARSCCKLNKWIPELIGHTIVTVLLLM SLHWFIFLLNLPVATWNIYRYIMVPSGNMGVFDPTIEHNRGQL KSHMKEAMIKLGFHLLCFFMYLYSMILALIND
588	1327	1126	732	QSPGHGAPCQLSSSHSRNRLSPMARATLSAAPSNPRLLRVA LLLLLLVAASRRAGAPLATELRQCQLQTLQGIHLKNIQSVKV KSPGPHCAQTEVIATLKNGQKACLNPASPMVKKII EKMLKNGK SN
589	1328	197	330	HPLSLVFLALNTGKEKSHPGGGGERPGLAGQGEPDHPAGARDG R
590	1329	1	1575	CTPVARSMATTATCTRFTDDYQLFEELGKGAFSVVRRVCVKTS TQEYAAKIINTKKLSARDHQKLREARICRLKHPNIVRLHDS ISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQILE SVNHIHQHDIVHRDLKPENLLASKCKGA AVKLADFGLAIEVQ GEQQAWFGFAGTPGYLSPEVLRKDPYGKPVDIWACGVILYILL VGYPFPWDEDQHKLYQQIKAGAYDFPSPEWDTVTPEAKNLINQ MLTINPAKRITADQALKHPWVCQRSTVASMHRQETVECLRKF NARRKLKGAILTTMLVSRNFSAAKSLNKKSDGGVKPQSNKN SLVSPAQEPAPLQTAMEPQTTVVHNATDGIKGSTESCTTTED EDLKVRKQEI IKITEQLIEAINNGDFEAYTKICDPGLTSFEPE ALGNLVEGMDFHKFYFENLLSKNSKPIHTTILNPHVHVIGEDA ACIAYIRLTQYIDGQGRPRTSQSEETRVWHRD GKWLVNHYHC SGAPAAPLQ
591	1330	17	636	NRRTVKMLLELSEEHKEHLAFLPQVDSAVVAEFGRIVAEFLRR GANPKIYEGAARKLNVSSTVQHGVGLTYLLTSSKLMISEL DFQDSVFLGFSEELNKKLLQLYLDNRKEIRTI LSEL\APSLP SYHNLEWRDLVQLASRSLRQQIKPAVTIKLHLNQNGDHNTKVL QTD PATLLHLVQOLEQALEEMKTNHCRRVVRNIK
592	1331	1	237	GTSIYLAHRVA\RAWELAQFIHHTSKKADVVLACGDSIVHPED LICCLTGRSCLCDVHLLSSLLARLGRGYAVSLTNL

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593	1332	2506	1684	RGCGSCGYKPSAGPAWRPRPPPAVSPLRHPEPAKVLSSFSSCPL PALGRTGPSRAARAQSLTMASLFKKKTVDVVIKEQNRELRGTO RAIIRDRAALEKQEQLELEIKKMAKIGNKEACKVLAKQLVHL RKQKTRTFVSSKVTSMSTQTKVMNSQMKMAGAMSTTAKTMQA VNKKMDPQKTLQTMQNFQKENMKMEMTEEMINDTLDDIFDGSD DEEESQDIVNQVLDEIGIEISGKMAKAPSAARSLSASTSKAT ISDEEIERQLKALGVD
594	1333	905	432	STDGNGAERLFAELRKMNARGLGSELKDSIPVTELSASGPFES HDLLRKGFSCVKNELLPSHPLELSEKNFQLNQDKMNFSTLRNI QGLFAPLKLQMEFKAVQQVQRLPFLSSSNLSLDVLRGNDDETIG FEDILNDPSQSEVMGEPHLMVEYKLGLL
595	1334	111	117	RNMKLHYVAVLTLAILMFLTWLPESLSCNKALCASDVSKCLIQ ELCQCRPGEGNCSCCKECLGALWDECCDCVGMCPNPNYS DTPPTSKSTVEELHEPIPSLFRALTEGDTQLNWNIVSFPVAEEL SHHENLVSFLETVNQPHHQNVSPSNNVHAPYSSDK/E*LPTV DFFHSAPSCGLSM*SIIFFEET
596	1335	817	278	VGGVPTWLEGCGSGNPSRSGGGPGARLTLPALQMTVHNLYLF DRNGVCLHYSEWHRKKQAGIPKEEYKLMYGM LFSIRSFVSKM SPLDMKDGFLAFQTSRYKLHYETPTGIKVMNTDLGVGPIRD VLHHIYSALYVELVVKNPCLPLGQTVQSELFRSLDSYVRS LP FFSARAG
597	1336	171	881	PGLSQEPGSGMETVVIVAIGVLATIFLASFAALVLVCRQRYCR PRDLLQRYDSKPIVDLIGAMETQSEPSELELDDVVITNPHIEA ILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKM KTSASVSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTAL LLSVSHLVLVTRNACHLTGGLDWIDQSLSAABEHLEVLREAAL ASEPDKGLPGPEGFLQEQSAI
598	1337	1078	594	VGMELPAVN LKVILLGHWLLTTWGCIVFSGSYAWANFTILALG VWAVAQRDSIDAISMFLGGLLATIFLDIVHISIFYPRVSLTDT GRFGVGMAILSLLLKPLSCCFVYHMYRERGELLVHTGFLGSS QDRSAYQTIDSAEAPADPFAVPEGRSQDARGY
599	1338	717	116	PASRPLGPDGTGSVANIFKGLVILPEMSLVIRNLQRVIPIRRA PLRSKIEIVRRILGVQKFDLGIICVDNKNIQHINRIYDRNVP TDVLSFPFHEHLKAGEFPQPDFDDYNLGDIFLGVEYIFHQCK ENEDYNDVLTVTATHGLCHLLGFTHGTEAEWQQMFQKEKAVLD ELGRRTGTRLQPLTPGPLPEGAEGRVFF
600	1339	1	804	LRNALDVLHREVPRVLVNLVDFLNPTIMRQVFLGNPDKCPVQQ A/MLEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYP IKPAIENWGSDFLCTEWKASNSVPTS VHQLRPADIKVVAALGD SLTTAVGARPNSSDLPTSWRGLSWSIGDGNLETHHTLPNIL KKFNPYLLGFSTSTWEGTAGLNVAEGARARMPAQAWDLVER MKNSPDINLEKDWKLVTLFIGGNDLCHYCENPEAHATEYVQH IQQALDILSE

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601	1340	1	860	VVEFLWSRRPSGSSDPRRRPASKCQMMEERANLMHMMKLSIK VLLQSALSGLRSLDADHAPLQQFFVMEHCLKHGLKVKSFIG QNKSFPGPLELVEKLCPEASDIATSVRNLPKLTAVGRGRAWL YLALMQKKLADYLVKVLIDNKHLLSEFYEPALMMEEGMVIVG LLVGLNVLDANL\CLKGEDLDSQVGVIDFSLYLKDVQDLGGK EHERITDVLQKNYVEELNRHLSCTVGDLTQTKIDGLEKTNSKL QERVSAATDRICSLQEEQQQLREQNELIR
602	1341	60	762	KPEGARRVQFVMGLFGKTQEKPPKELVNEWSLKIRKEMRVVDR QIRDIQREEEKVKRSVKDAAKKGQKDVCIVLAKEMIRSRKAVS KLYASKAHMNSVLMGMKNQLAVLRVAGSLQKSTEVKAMQSLV KIPEIQATMRELSKEMMKAGIIEMLEDTFESMDDQEEMEEEA EMEIDRILFEITAGALGKAPSKVTDALPEPEPPGAMAASEDEE EEEEALEAMQSRLATLRS
603	1342	3	456	RWNSIMELALLCGLVVMAGVPIPIQGGIILNLNMVKQVTGKMPI LSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGGCI YKDYRYNFSQGNIHCSDKGSWCEQQLCACDKVAFCLKRNL TYQKRLRFYWRPHCRGQTPGC
604	1343	249	632	KTVAEEASVGNPEGAFMKMLQARKQHMSTELTIESEAPSDSSG INLSGFGSEQLDTNDES DVSSALSYILPYLSLNLGAESILLP FTEQLFSNVQDGDRLLSILKNNRKSPSQSSLLGNKFKNKIF
605	1344	2	382	LPLTLLLAAPFAHLLLP PGHDQSPCWHPGPALSPGTLGLPLSWA MANSGQLLLGYFLALGGWVGIIASTALPQWKQSSYAGDASIQL RSKVVFLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
606	1345	2	987	DPRVRPPLLQPPPLLPRVLILKMAPLDDKYVEIARLCKYLP ENDLKRCLDYVCDLLEESNVQPVSTPVTVCGDINHGFYDLCE LERTGGQVPDTNYIFMGDFVDRGYYSLETFTYLLALKAKWPDR ITLLRGNHESRQITQVYGFYDECQTKYGNANAWRYCTKVFDML TVAALIDEQILCVHGGLSPDIKTLQIRTIERNQEI PHKGAF DLVWSDPEDVDTWAI SPRGAGWLF GAKVTNEFVHINNLKLCR AHQLVHEGYKFMFDEKLVTVWSAPNYCYRCGNIASIMVFKDVN TREPKLFRAPDSERVIPRRTTTPYFL
607	1346	10	768	SFAGAAARPSTPPASGRGAAPGRPGPSPMDLRAGDSWGLACL CTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQRLSLA GTYLNYLGPPFNEDFNPPRLGAETLPRATVDLEVWRSNDKL RLTQNYEAYSHLLCYLRGLNRQAATAELRRSLAHFCTSLQGLL GSIAGVMAALGYPLPQPLPGTEPTWTTPGPAHSDFLQKMDDFWL LKEIQTWLWRS AKDFNRLKKKMQPPAAVTLHLGAHGF
608	1347	114	700	IKISLKKRSMGSGCPFFLWGLLALLGLALVTSILFNISHYV EKQRQDKMYSYSSDHTRVDEYYIEDTPIYGNLDDMISEPMDEN CYEQMKARPEKSVNKMQEATPSAQATNETQMCYASLDHSVKGK RRKPRKQNTHFSDKDGDEQLHAIDASVSKTTLVDSFSPESQAV EENIHDDPIRLFGLIRAKREPIN

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609	1348	2	807	VEFHPQRRARAGARAPSMGVLLTQRTLLSLVLALLFPSMASMAA IGSCSKEYRVLLGQLOKQTDLMQDTSRLLDPIRIQGLDVPKL REHCRERPGAFPSEETLRGLGRRCFLOTLNATLGCVLHRLADL EORLPKAQDLERSGLNIEDLEKLQMARPNILGLRNNIYCMAQL LDNSDTAEPTKAGRGASQPPTPTPASDAFQKLEGCRFLHGYH RFMHSVGRVFSKWGESPNRSRRHSPHQALRKGVRRTRPSRKGG RLMTRGQLPR
610	1349	2	418	DFPGRFRFLVWLLVLRPLPWRVPGQLDPTTGRRFSEHKLCADDE CSMLMYRGEALEDFTGPD CRFVNFKKGD PVYVYK LARGWPEV WAGSVGRTFGYFPKDLIQVVHEYTKHEELQVPTNETDFVCFDGG RDDFHNYNV
611	1350	823	115	SPLGKEGQEEVRVKIKDLNEHIVCCLCAGYFVDATTITECLHT FCKSCIVKYLQTSKYCPMCNIKI HETQPLNLKLDRVMQDIVY KLVPGLQDSEKRIREFYQSRGLDRVTQPTGEEPALS NLGLPF SSFHDKAHYYRYDEQLNLCLERLSSGKDKNKS VLQNKYVRCS VRAEVRHLRRVLCHRLMLNPQH VQLLFDNEVLPDHTMKQIWL SRWFGKPSPLLQYSVKEKRR
612	1351	9	545	LWWYSAHA AVDAMDVFGVGFPSKVPWKMSAEELNQYCPSR WVVR LGAEALRTYSQIGIEATTRARATRKSLLHVPYGDGEGE KVDIYFPDESSEATTRARATRKSLLHVPYGDGEGEKVDIYFPD ESSEALPFFLFFHGGYWQSGRHPGPHGRPGDPQRCVCPEAVSK QQAFSW
613	1352	49	902	GVRMASRGRRPEHGGPPELFYDETEARKYVRNSRMIDIQTRMA GRALELLYLPENKPCYLLDIGCGTGLSGSYLSDEGHYWGVDI SPAMLDEAVDREIEGDL LLDGDMGQGI PFKPGTFDGCISISAVQ WLCNANKKSENPAKRLYCFASLFSVLVRGSRAVLQLYPENSE QLELIT TQATKAGFSGGMVVDYPNSAKAKFYLC LFSGPSTFI PEGLSENQDEVEPRESVFTNERFPLRMSRRGMVRKSRAWVLEK KERHRRQGREVRPDTQYTGRKRKPRF
614	1353	1960	871	TLICRMAGCGEIDHSINMLPTNRKANESCSNTAPSLTVPECAI CLQTCVHPVSLPCKHVFCYLCVKGASWL GKRCALCRQEIPEDF LDKPTLLSPEELKAASRGNGEYAWYEGRNWWQYDERTSREL EDAFSGKKNTEMLIAGFLYVADLENMVQYRRNEHGRRRKIKR DIIDIPKKG VAGLRLCDANTVNLARESSADGADSVSAQSGAS VQPLVSSVRPLTSVDGQLTSPATPSPDASTSLED SFAHLQLSG DNTAERSHRGEGEEDHESPSSGRVPAPDTSIEETESDASSDSE DVSAVVAQHSLTQQRLLVSNANQTVPDRSDRSRGTDRSVAGGGT VSVSVRSRRPDGQCTVTEV

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615	1354	5653	4549	GATPLGSGVGGRTGKMDAATLT YD T L R F A E F E D F P E T S E P V W I L GRKYSIFTEKDEILSDVASRLWFTYRKNFFAIGGTGPTSDTGW GCMLRCGQMIFAQALVCRHLGRDWRWTQQRKQPD SYFSVLNAF IDRKDSYYSIHQIAQMGVGEKSGSIGQWYGPN T V A Q V L K K L A V F DTWSSLAVHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDR HCNGFPAGAEVTNRPS PWRPLVLLIPLRLGLTDINEAYVETLK HCFMMPQSLGVIGGKPN SAHYFIGYVGEELIYLDPHTTQPAVE PTDGC FIPDES FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAF GAECCLGMTRKTFGFLRFFFSMLG
616	1355	416	65	PTTSNRAITLTAWPKIPFLGICEAKNPRSENMRLATILEVACH HLGSGPPPSWELWEQGP PGNSSRYIEFLNKHTYIKGTLRVYTK KFCMLVIKSFESKSCVCVYDFDSKSSVNVTV
617	1356	2	382	PRVRFRLLHVT S I R S A W I L C G I I W I L I M A S S I M L L D S G S E Q N G SVTSCLELNLYKIAKLQTVNYIALVVGCLLPFFTL S I C Y L L I I RVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLPYHT
618	1357	3	672	GRHWLGSAQLTDGGSARKPKMAVPAALILRESPMKKAVSLIN AIDTGRFPRLLTRILQKLHLKAESSFSEEEEEKLQAASFLEKQ DLHLVLETISFILEQAVYHNVKPAALQQOLENIHLRQDKAEAF VNTWSSMGQETVEKFRQRILAPCKLETVGWQLNLQMAHSAQAK LKSPQAVLQLGVNNEDSKSLEKVLVEFSHKELDFYNKLETIQ AQLDSL T
619	1358	557	208	EASSAKTRKKEEKGP KAKMKMLVLF T I G L T L L L G V Q A M P A N R LSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDGKGCEMI CYCNFSELLCCPKDVFFGPKISFVIPCNNQ
620	1359	335	1735	KMAEAVFHAPKRKR R R V Y E T Y E S P L P I P F G Q D H G P L K E F K I F R A EMINNNVIVRNAEDIEQLYGKGYFGKGILSRSRPSFTISDPKL VAKWKDMKTNP I I T S K R Y Q H S V E W A A E L M R R Q G Q D E S T V R R I LKDYTKPLEHPPVKRNEEAQVHDKLNSGMVSNMEGTAGGERPS VVNGDSGKSGGVGDPREPLGCLQEGSGCHPTTESFEKSVREDA SPLPHVCCCKQDALILQRLHHEDGSQHIGLLHPGDRGPDHEY VLVEEAECAMSEREAAPNEELVQRNRLICRRNPYRIFEYLQLS LEEAF FLVYALGCLSIYYEKEPLTIVKLWKAFTVVQPTFRTTY MAYHYFRSGKWVPKVGLKYGTDLLLYRKGPFPYHASYSV I I E L VDDHFEGLRRPLSWKSLAALSRVSVNVSKELMLCYLIKPMSTM TDKEMESPECMKRIKVQEVILSRWVSSRERSDQDDL

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621	1360	5693	4435	RDIWTMNLQRYWGEIPISSSQTNRSSFDLLPREFRLVEVHDPPLHQPSSANKPKPPTMLDIPSEPCSLTIHTIQLIQHNRRRLRNLIATAQAQNOQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPNAFFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLKFTKLLRFVADREARLGQTPFPDVMEOQVFHEVGIGSVLSLQKFWQHRIDYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELADLASGDQSLPMGVLGAQSERFPSNLEVEASPOASSAEVNASPLWNLAHVKMEPQSEEGNVSGHGVLSGSDVFEEPMSEAGIPQSPDSDSSSYGSHSTDSLMGSSPVFNQRCCKMRKI
622	1361	15	678	REQILFIEIRD TAKGGETEQPPSLSLHGGMRPEMGEIGIQLSARETQSHRGRRGWDATWVTRCRESLNRGGAGAGKRAGALAHVFLALIEPNLAEREASEEEVKACSDETVVADLLVKVVYVLGAILKIFLREGNVNLQHSGMDIEKYSEHYQHDHSPGAEDDAAGQLRPTAQERRHKEGSRGSPRCKRARKAVGESPGCPRPRVRPRVRPRVRPRV
623	1362	1080	835	GTRGCCREGTAYAKAYQFMASHLSLGKPVSTGSI PRFNKALFNKQAKCKPNHYSFIGLSMLSPENFSGCKYSVWFSETKGF
624	1363	872	441	GAQGVVRVGIGEVGRVQAPRVSLLSHSGQVPRGGTGEAVKEEGRGSSLHPPPLPPQGLGEYACQSHAFMKGVFTFTVTGTGMAFGLQMF IQRKFPYPLQWSLLVAVVAGSVVSYGVTRVESEKCNNLWLFLETGQLPKDRSTDQRS
625	1364	1	585	GTSELLCIQRWNWGPAPPPRGLALAPTLQLLVEMGSAKSVPTPARPPPHNKLARVADPRSPSAGILRTPIQVESSPQGLPAG EQLEGLKHAQSDPRSPLGKN*GHGWQVGQSDLGSPQPLPPSASHL/YSSRASRCSQPPCLSLPWFGVRSSPANTYHVPVTS LCPSPALHYTALQAGIISTSQARAPR
626	1365	36	381	PLLLPRFIDIPCLLCYLTQVTPDDMYAKAFLIKPN TAITGTDR RKL\RADETTDFP\TLGTDQIYELLPGKDELNIVKSNAHKRDA *TAYVSGENHILSEP*KNLYPAVNTLSSYP
627	1366	763	1003	SRQPPPLLTVMFLLEFLVFFPGCVNQLLSYPWQGGQGTSLWSSLSFHWLLPQEDSSRLSIFPLRAGSPPPQPAQAPQRI
628	1367	296	1199	KSREQSSLFAADAERSWGGKSCCLLRWRFGKASHFPRLLPLPGEERPETKERAWKMEQTWTRDYFAEDDGEMVPRTSHTA/ASVSLTAFSLSDTKDRGPPVQSQIWRSGEKVPFVQTYSLRAFEKPPQVQTQALRDFEKLHNDLKKENFSLKLLIYFLEERMQQKYEASREDIYKRNTTELKVEVESLKRELQDKKQHLDKTWADVENLNSQNEAELRRQFEERQQEMEHVYELLENKMQLLQEE SRLAKNEAARMAALVEAEKECNLELSEKLGVTKNWEDVPGDQVKPDQYTEALAQRD K

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629	1368	191	1116	TRRRGTTWRSRPRRASTRPSTRPRGVASWPWETAGTATTGP GPSARTRRRAARRRRSRPRRAHGGLSQPAGWQSLLSFTILFL AWLAGFSSRLFAVIRFESI IHEFDPWFNYRSTHHLASHGFYEF LWNFDERAWYPLGRIVGGTVYPGLMITAGLIHWILNTLNTVH IRDVCVFLAPTFSGLTSISTFLLTRELWNQAGLLAACFIAIV PGYISRSVAGSFDNEGIAIFALQFTYYLWVKSVKTSVFWTMC CCLSYFYMVSAWGGYVFIINLIPLHAFVLVLM/Q/RYSKRVI *YSTFYIVG
630	1369	852	214	RRLIVVLSDAFLSRAWCSHSF/RVGPARGWVGPSVAPTPLTVP PRREGLCRLELTRRPIFITFEGQRRDPAHPALRLLRQHRHLV TLLLWRPGSVTPSSDFWKEVQLALPRKVRYRPVEGDPQTQLQD DKDPMILRGRVPEGRALDSEVDPDPEGDLGVRGPVFGEPSAP PHTSGVSLGESRSSEVDVSDLGSRNYSARTDFYCLVSKDDM
631	1370	246	1091	LSHEGWRRGREGERINSSVASLAPLCILPDLPSNMHLARLVGS CSLLLLLALSGWAASDDPIEKVIEGINRGLSNAEREVGKALD GINSGITAGREVEKVFNGLSNMGSHTGKELDKGVQGLNHGMD KVAHEINHIGIQAGKEAEKLGHGNNAAAGQAGKEADKAVQGFH TGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAG KELQNAHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLAS GASVNTFPFNLPALWRSVANIMP
632	1371	3150	2792	SASGGLGMTVEGPEGSEREHRPPEKPPRPPRPLHLSDRSFRRK KDSVESHPWDDTRIDADAIVEKIVQSQDFTDGSNTEDSNLR LFVSRDGSATLSGIQLATRVSSGVYEPVVIESH
633	1372	667	993	ERSGWQPPEGTVTAQGPLEWERLSGAVTVSSGYKADMWPSFPQ \VRVGSFLFGILFFSFGSSSLPPGLPPPASLLCCAVQWGARAL FLPCLKERALGMEMRNNTLSFRQ
634	1373	636	2	SSSNLRLSFLINENILGKCFRSGPSCAGPRISPLAAQYECPRP SLLIMASVPKTNKIEPRSYSIIPSCGI\RLGPALNTLIF\QS KRFQPRG\HSAKSIEGAPRGKGRGRAVARLAADRPPAPKIQLR AF*LQQL*YTLLELELPRLAPDLPSNGSSSLKDLKWTSHSNYRA SKESCIVIF\VTTSPPGREWVICALAFLGCGS\LSQAPSPES
635	1374	61	519	LRIINTYFCFKFLIVNYIHGTTKARKPHVLGESLISAMSRQEP KMFVLLYVTSFAICASGQPRGNQLKGENYSPRYICSIPGLPGP PGPPGANGSPGPHGRIGLPGRDGRDGRKGEKGEKGTAGLRGKT GPLGLAGEKGDQGETGKKGP IGPE
636	1375	129	579	FASAMLGSRVDRPKLSVAPSVVLEEDQVLVSPAVDLEAGCRLR DFTEKIMNVKGVILSMLVVSTVIIVFWEFINSTEGSFLWIYH SKNPEVDDSSAQKGWFLSWFNNGIHNYYQQGEEDIDKEKGREE TKGRKMTQQSFGYGTGLIQT

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637	1376	127	1376	GSHRFSLASPLDPEVGPYCDTPTMRTLFLNLLWLALACSPVHTT LSKSDAKKAASKTLLKESQFSQDKPVQDRGLVVTDLKAESVLE HRSYCSAKARDRHFAQDVLGYVTPWNHSHGYDVTKVFGSKFTQI SPVWLQLKRRGEMFEVTGLHDVDQGWMAVRKHAAGLHIVPR LLFEDWTYDDFRNVLDSEDEIEELSKTVVQVAKNQHFDFGVVE VWNQLLSQKRVLHMLTHLAEALHQAARLLALLVIPPATPGT DQLGMFTHKFEFEQLAPVLDGFSIMTYDYSTAHPGPNAPLSWV RACVQVLDPKSKWRSKILLGLNFYGM DYATSKDAREPVVGARY IQTLKDHPRMVWDSQVSEHFFYKKSRSRGRHVVFYPTLKSLO VRLELARELGVGVS IWE LGQGLDYFYDLL
638	1377	998	48	GREGTGWGPAMSEVTRSLQRWGASFRGADFDSDWGQVLEAID EYQILARHLQKEAQAQHNNSEFTEEQKKTIGKIATCLELRSAA LQSTQSQEEFKLEDLKKLEPILKNILTYNKEFPFDVQVPVLR ILAPGEEENLEFEDEEEEGGAGAGSPDSFPARVPGTLLPRLPS EPGMTLLTIRIEKIGLDAGQCINPYITVSVKDLNGIDLTPVQ DTPVASRKEDTYVHFNVDI ELQKHVEKLTGAAIFFEFKHYKP KKRFTSTKCF AFMEMDEIKLGPIVIELYKKPTDFKRKQLQLLT KKPLYLHLHQTLHKE
639	1378	1298	1569	GSITSEPSLDSLQPLPPGFKRFSCLSLPSSWDYRRPPPGLAYF CIFSRDEVSPCWPGCSPSPDLMLRPRPPSVGITGVSHRAWPT IDNF
640	1379	196	1197	KMPVPWFLLSLALGRSPVVLSELRVGPQDATHCSPGLSCRLW DSDILCLPGDIVPAPGPVLAPTHLQTELVLRCQKETDCDLCLR VAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVL FQAYPTARCVLLEVQVPAALVQFGQSVGSSVYDCFEAALGSEV RIWSYTQPRYEKELNHTQQLPDCRGLEVWNSIPSCWALPWLNV SADGDNVHLVLNVSEEQHFGLSLYWNQVQGP KPRWHKNLVRP PPSQVHSHCRP\CLCK\DAVPYQRGSLKRTHPKQKIGGTS AFLVSLTLASSSSSLSSPTSFLYLFHRLDRSLP
641	1380	756	1110	LRLWNRNQMMHNIIVKELIVTFFLGITVVQMLISVTGLKGVEA QNGSESEVFVGKYETLVFYWPSLLCLAFLLGRFLHMFVKALRV HLGWELQVEEKSVLEVHQGEHVQQLLRIPRP
642	1381	631	1278	KVNRKLRKKGKISHDKRKKSRKAIGSDTSDIVHIWCPEGMKT SDIKELNIVLPEFEKTHLEHQRIESKVCKAAIATFYVNVKEQ FIKMLKESQMLTNLKRKNAMISDIEKKRQRMIEVQDELLRLE PQLKQLQTKYDELKERKSSLRNAAYFLSNLQQLYQDYSDVQAQ EPNVKETYDSSSLPALLFKARTLLGAESHLRNINHQLEKLLDQ G
643	1382	1167	755	VWAMEEPPVREEE*EEGEDEERDEVGPEGALGKSPFQLTAE DVYDISYLLGRELMAIGSDPRVTQLQFKVVRVLEMLEALVNEG SLALEELKMERDHLRKEVEGLRRQSPASGEWPDSTKRRPRRK KRKRCCGY

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644	1383	1	271	PRNDHRLTQSRDSSSKTRAFVPRFLPAHAGVTSEERTAMKR EGGAAHLCSDSLPESSQQQDGNHAPNFSSSHGSCRRRRQRRRHDKA LHAR
645	1384	1	499	THASEKSRATMSSWSRQRPKSPGGIQPHVSRTFLLLLLLAASA WGVTLSPKDCQVFRSDHGSSISCQPPAEIPGYLPADTVHLAVE FFNLTHLPANLLQGASKLQELHLSSNGLESLSPEFLRPVQRLR VLDLTRNALTGLPPGLFQASATLDTLVLENQLEVE
646	1385	178	675	ERPRIMDLAGLLKSQFLCHLVFCYVFIASGLIINTIQFLTLL WPINKQLFRKINCRLSYCISSQLVMLLEWWSGTECTIFTDPRA YLKYKGENAIVVLNHKF\EI\DFLCGWSLSERFGLLGVSQKCI PPCLTHFFGSAPPLVFLLLVIQNLQKNQSSFYLMKWS
647	1386	630	1499	MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNS CICRDDSGTDDSDVTQQQQAENS AVPTADTRSQPRDPVRPPRR GRGPHEPRRKQNV DGLVLDTLAVIRTLVDNDQEPYSMITLH EMAETDEGWLDVVQSLIRVIPLEDPLGPAVITLLLLDECPLPTK DALQKLTEILNLNGEVACQDSSHPAKHRNTSAVLGCLAELKLAG PASIGLLSPGILEYLLQCLLQSHPTVMLFALIALEKFAQTSN KLTISESSISDRL\VTLESW\ANDPDYLRQVG
648	1387	1	962	RFGTRGLAKSKGVVLMALCALTRALRSLNAPPTVAAPAPSLF PAAQMMNNGLLQPPSALMLLPCRPLVTSVALNANFVSWKSRTK YTITPVKMRKSGGRDHTGRIRVHGIGGGHKQRYRMIDFLRFRP EETKSGPFEEKVIQVRYDPCRSADIALVAGGSRKRWIIATENM QAGDTILNSNHIGRMAVAAREGDAHPLGALPVGTILNNVESEP GRGAQYIRAAGTCGVLLRKVNGTAIIQLPSKRQMQVLETCTVAT VGRVSNVDHNKRVIKAGRNRWLGRPNSGRWHKGGWAGRKI RPLPPMKSYVKLPSASAQS
649	1388	291	714	PVQGARCWLDARRNVRFSGVCCGCGIHGYWAEPCGGCGAMEG LRSSVELDPELTPGKLDEEMVGLPPHDASPVTFHSLDGKTVV CPHFMGLLGLLLLTLSVRNQLCVRGERQLAETLHSQVKEKS QLIGKKTDCRD
650	1389	874	2220	GARGRPLAETWPFLTAPVLPGLQITEPTMAEKGDCIASVYGY DLGGRFVDFQPLGFGVNGLVLSAVDSRACRKVAVKKIALSDAR SMKHALREIKIIRRLDHDNIVKVYEVLPKPGTDLQGELEKFSV AYIVQEYMETDLARLLEQGTLAEEHAKLFMYQLLRGLKYIHS NVLHRDLKPANIFISTEDLVKIGDFGLARIVDQHYSHKGYL SEGLVTWKYRSPRLLLSPNNYTKAIDMWAAGCILAEMLTGRML FAGAHELEQMLILETIPVIREEDKDELLRVMPFSVSSTWEVK RPLRKLLEPVNSEAIDFLEKILTFNPMDRILTAEMGLQHPYMS YSCPEDEPTSQHPFRIEDEIDDIVLMAANQSQSLSNWDTCSRY PVSLSDDLWRPDRCDASEVQDRPRAGSAPLAENVQVDPKRD SHSSSASCQAGRNGVSRYQ

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651	1390	1	2451	MRTLGTCLATLAGLLLTAAGETFSGGCLFDEPYSTCGYSQSEGG DDFNWEQVNTLTTKPTSDPWPMPGSGFMLVNASGRPEGQRAHLLLPQLKENDTHCIDFHYFVSSKSNSPPGLLNIVYVKVNNGPLGNPIWNISGDPTRTWNRAELAISTFWPNFYQVIFEVITSGHQGYLAIDEVKVLGHPCTRTPHFLRIQNVEVNAGQFATFQCSAIGRTVAGDRLWLQGIDVDRDAPLKEIKVTSSRRFIASFNVNTTKRDAGKYRCMI\RTEGGVGISNYAEL\VVKEPPVPIAPPQLASVGATYLV IQLNANSINGDGPVAREVEYCTASGSWNRQPV DSTSYKIGH LDPDTEYEISVLLTRPGEGGTGSPGALRTRTKCADPMRGPRK LEVVEVKSRQITIRWEPFGYNVTRCHSYNLTVHYCYQVGGQEQ VREEVSWDTENSHPQHTITNLSPTYTNVSVKLILMNPEGRKESQ ELIVQTDDELPGAVPTESIQQSTFEEKIFLQWREPTQTYGVIT LYEITYKAVSSFDPEDIDLSNQSGRVSKLGNETHFLFFGLYPGT TYSFTIRASTAKGFGPPATNQFTTKISAPSMPAYELETPLNQTDNTVTVMKPAHSRGAPVSVYQIVVEEERPRRTKKTTEILKCY PVP IHFQNASLLNSQYYFAAEFPADSLQAAQPFITGDNKTYNG YWNTPLLPYKSYRIYFQAASRANGETKIDCVQVATKGAATPKP VPEPEKQTDHTVKIAGVIAGILLFVIIIFLGVLVLMKKRLYKHG ASICSASGEASGSFQSWRKAKHKQACPMARAGARERAGGCLKL
652	1391	30	459	GIRQLQLSRASMAARKSWTALRLCATVVVLDMVVCKGFVQDL DESFKENRNDIWL VHFYAPWCGHCKKLEPIWNEAGLEMKSIG SPVKAGKMDATSYSSIASSEFGVRYPTIKLALIRPLPSQQMFE HMHKRHRVFFVYV
653	1392	168	1016	GLVIVISHFSPSPGLLPATQSPAMSDPITLNVGGKLYTTSLAT LTSFPDSMLGAMFSGKMPTKRDSQGNCFIDRDGKVFRYILNFL RTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQEKEVELSKA EKNAMLNITLNRVQTVHFTVREAPQIYSLSSSSMEVFANIF STSCLFLKLLGSKLFYCSNGLSSITSHLQDPNHLTLDWVANV EGLPEEEYTKQNLKRLWVVPANKQINSFQVFVEEVLKIALSDG FCIDSSHPhALDFMNNKIIRLIRY
654	1393	3	927	SCADNLVAASGGCWFVLGERRAGSLLSASYGT FAMPGMVLFGR RWAIASDDLVPFGFFELVVRVLWWIGILTLYLMHRGKLD CAGG ALLSSYLIVLMILLAVVICTVSAIMCVSMRG TICNPGPRKSMS KLLYIRLALFFPEMVWASLGAAWVADGVQCDRTVNGIIATVV VSWIIIAATVVSIIIVFDPLGGKMAPYSSAGPSHLDSDHSSQL LNGLKTAATSVWETRIKLLCCCGKDDHTRVAFSSSTAELFSTY FSDTDLVPSDIAAGLALLHQQDNIRNNQ\DLPRWSAMPQAGAP RKLIWMQN
655	1394	1	716	FRAATAAAGNGGGGGRAGAGDASGTRKKKGPGPLATAYLVII NVVMTAGWLVIAGVLVRLAYLAKGSYHSLYYSIEKPLKFFQTGA LLEILHCAIGIVPSSVVLTSFQVMSRVFLIWA VTHSVKEVQSE DSVL\FVIAWTITEIIRYSFYTFSLNHLPYLIKRARYTLFIV LYPMGVSGELLTIYAALPFVRQAGLYSISLPNSTKKIFLISQV WWHMLAVSADAKAEMPAVLKPGP

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656	1395	72	766	MLTGVGCLVSSSESLSCVQCNSWEKSCVNSIASECPSHANTSCI SSSASSSLETVPRLYQNMFCSAENCSEETHITAFTVHVSAEEH FHFVSQCCEGKECSNTSDALDPPLKNVSSNAECPACYESNGTS CRGKPWKCYEBEQCVFLVAELKNDIESKSLVLKGCNSVSNATC QFLSGENKTLGGVIFRKFEKANVNSLTPTSAPTTSNVGSKAS LYLLALASLLLRGLLP
657	1396	97	746	VPARRRAMEIGTEISRKIRSAIKGKLQELGAYVDEELPDYIMV MVANKKSQDQMTEDLSLFLGNNTIRFTVWLHGVLDKLRSVTTE PSSLKSSDTNIFDSNVPSNKS NF SRGDERRHEAAVPPL\AIPS ARPEKRDSRVSTSSQESKTTNVRQTYDDGAATRLMSTV/KPLR EPAPSEDVIDIKPEPDDLIDEDLN FVQEKPLS QK KPTVTLTYG SSR
658	1397	155	560	ASRVLAAVMGLPWGQPHLGLQMLLLALNWLRLPSLSLELVPYTP QITAWDLEGKVTATTFSLEQPRCVFDGLASASDTVWLVVAFSN ASRGFQNPETLADIPASPQLLTDGHYMTLPLSPDQLPCGDPMA GSGSAP
659	1398	416	539	NSLNNFFETESCCVAQAGVQWRDLGSLQAPPPGFKRFSC
660	1399	281	736	KSLPLQKHPKPSQEDQGLGRGSLSGHSPLTLLTFLTSCALGD QQLLPRTSGSLCQESMSEQSCQMSELRLLLLGKCRSGKSATG NAILGKHVFKSKFSDQTVIKMCQRESWVLRERKVVVIDTPDLF SSIACAEDKQRNIQHLELSAP
661	1400	2	974	FVETTVSVQSAESSDALSWRLPRALASVGPEEARS GAPVGGG RWQLSDRVEGGSPTLGLLGGSPSAQPGTGNVEAGIPSGRMLEP LPCWDAADLKEPQCPPGDRVGVQPGNSRVWQGTMEKAGLAWT RGTGVQSEG TWESQRQDS DALPSP ELLPQDQDKPFLRKACSPS NIPAVIITDMGTQEDGALEETQGS PRGNLPLRKLSSSSASSTG FSSSYEDSEEDISSDPERTLDPNSAFLHTLDQKPRVVESRSV TQAGVQWHDIGSLQPLPP/WIQAIL/HASAFRIAGTTGACHHA RIIFGFLVERGFHHVGDGLYLLIL
662	1401	232	3	KICSSYFLRIICILQKEAQEASNLYTSCDFFSPA FYFVIYRLY NFKIHWPGAVAHTYSPSTLGGRGRWVT*GREFM
663	1402	250	556	LILSLPLLYGHLKSYTFPSEHYLHLLQTFATFNKYLNVCVLIF IHHKPVVPAIQGTNVGGSLEPRRLRLQQAMIVPLHFG LGNRVR PCLKKQQQQQQQQQK
664	1403	1	373	RMETKPVITCLKTLIIYSFVFWITGVILLAAGVWGKLTGSGY ISLIAENSTYAPYVLIVTGTTIVAYPLV*FFFSYSSGFSYILA VRLIAGIALVYNYIPRSSRALVRLVLLRFLLSRHPS
665	1404	3	413	NAEHPGMDRDLQCQAKLAEHAERDDMAACMKTVDQGAELS NEERNLLSDAHTNAV*ARRSSWMGA*RIEQKTEGADTQQQMAP DCREIFATELRDICDDVLSLLEKLLIPNASHA*SLVYYLHMIG DYRYRWL
666	1405	2	334	GGGPLGKMPRAQLADPWQMMAVESPSDCADNGQQIMDEPMGED EISPQTE*VSIKEVAVTHCVKEGHDKADPSQIELLRVLRQGS GKVYL GK KVS GSDAKQLYAMKVLT

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667	1406	2	332	DAAGIRHEAHFGKLECLVQLVRAGA\SLFVSTTRYAQTTPA\HIAAFGGHPQCLVWLIQAGANINKPDCEGETPIHKAARSGSLECI SALVANGAHVDNPKKGIRVLEWLFE
668	1407	242	1157	LLKLMFLAELGDYDLAEHSPELVSEFRFVPIQTEEMELAI FEK WKEYRGQTPAQAE TNYLNKAKWLEMYGVD MHVVKARDGNDYSL GLTPTGVLVFE GDTKIGLFFWPKITRLDFKKNKLTLVVVEDDD QGKEQEHTFVFR LDHPKACKHLWKCAVEHHAFFRLRGPVQKSS HRS GFIRLGS RFRYS GKTEYQTTKTNKARRSTSFERRPSK RYS RRTLQMKACATKPEELS VHN NVSTQSN GSQAWGMRSALPVSP S ISSAPVPVEIENLPQSPGTDQH DRKWLSAASDCCQ RGGNQWN TRAL
669	1408	278	1	ATAPGLFNFF*FLFQCREEHKKKNPEVPVNF AEFSKKCSGRWK TMSSKEKFKFGEMAKADEVCYDREMKDYGPAKGGKKKDPNAPK RPPSGF
670	1409	139	646	AEGLGSWAVWAGLGWAGRMEAGGATGALGVGSKLPSAFCFPG SSVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDL *VLGRPLSYPPWAITTWALPDPPPLSWSPRLTPLGAAQQPLPV LSPVHCLLTSLCRGPD CGVWMT CQGAQVSIAGALVILWG
671	1410	3	442	LCVSVLCSFSYLQNGWTASDPVHGYWFR\AGDHVSRNIPVATN NPVRAVQEETRDRFHLLGDPQNKDCTLSIRD TRES DAGTYVFC VERGNMKWNYKYDQLSVNVTASQDLLSRYRLEVPE SVTVQEGL CVSVP/WQCPLPPLQLDCL
672	1411	84	836	QLQLCQNCTKRGECHCVPFD TYIKTKKEKKRLSVLPPTRLMEA RFSPINQILPWC RQDLAISISK AINTQEAPVKEKHARRI ILGT HHEKGAFTFWSYAIGLPLPSSSILSWKFCHVLHKVLRDGHPNV LHDCQRYRSNIREIGDLWGH LHDRYGQLVNVYTKLLLT KISFH LKHPQFPAGLEV TDEVLEKAAGTDVNNM*VTLHG YMASSPRLP HSFLPRLTPRRPHGAVGLNESVALLVDAHAPRDRG
673	1412	307	664	AAPHRMPRAPHFMP LLLLLLLLLSLPHTQA AAFPQDPLPLLISDL QGTSPLSWLPSLEDDAVAA*LGLDFQRFLT LNRTL LVAARDHV F SFDLQAE EEEGGLVPNKYLTWRSQDV ENCAVR*KLT LNRTL LVAARDHVFSFDLQAE EEEGGLVPNKYLTWRSQDV ENCAVR
674	1413	24	420	HLVPKTRGRGTPSGDQSPVLTLP*GDPPTILGPQTNPKEHL TNFKSGKRSFHSLLQPL LLLLHPSIS PFLNFGSFPFLVETEET CFIHKLKTPALVTPDSLPLVFNHCGDACLI IHPHFRDVEFHHT GN

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675	1414	1	1101	CCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLK PAKGLMSYRIITDFPSLTRNLPSQELPQEDSLHGFQFSQAVTP LAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQL LAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTT SATPKPATLL\PTNASVTPSGTSQPQLA\TTAPPVTTVTSQPP TTLISTVFTRAAATLQAMATTAVLTTTTFQAPTDSKGSLETIPF TEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPG SSSQGSVPENQYGLPFKEKWLIGSLLFGVLFLVIGLVLLGRIL SES LRKRYSRLDYLINGIYVDI
676	1415	178	621	IFAGSGVMRLKISLLKEPKHQELVSCVGTTAELYSCSDDHH IVKWNLLTSETTQIVKLDDIYPIDFWFPKSLGVKKQTHAES FVLTSSDGKFHLISKLG RVEKSVEAHCGAVLAGRWNYEGTALV TVGEDGQI*IWSKTGMLIS
677	1416	1258	944	ARATTKRHFILLFLFLRRC\LFLSPRMECNGAILAHCNLHLP GSSSSSASAS*VAGITDVRHHAQLILFVFLVETGFHRVGGAGL KLLTSGDLLTSASQSAIIMGISHCAQPKKAF*TKTF
678	1417	876	1291	EAGSNDLAT*KTCGRARPSSRSRQFGSRVWNHRQGVRSPPGE GAGSRSPCRRRHRRKHRRNVQSP*RRRSRSCSRSSGRCSVALL GACPVAGHSRGKVVCRAHAITQRRRCGFDPMVHPKEHRG*R ERSRKWSRS
679	1418	262	539	ATAPGLFNFF*FLFQCREEHKKKNPEVPVNFAEFSKKCSGRWK TMSSKEKFKEFGEMAKADEVCYDREMKDYGPAKGKKKDPNAPK RPPSGF
680	1419	104	236	LTVNYVLVFSRDSGLRAIENLMQKKGKFDYILLETTGLADPGK K
681	1420	3	277	HEAALCRTRAVAAERHFLRVFLFFRPFRGVGTESGESGSSKA KEPRT PSSSYGTAQYRRWP IAEYKHCTAHNDTGTLCSELREP WRRPQ
682	1421	3	576	EGSSQANTLSRKENRNNLLACLESHVLR*QFTESHLCSLMGD NPFQPKSNSKMAELFMECEEELEPWQKKVKEVEDDDDEPIF VGEISSSKPAISNILNRVNPSYSRGLKNGALSRGITAAFKPT SQHYTNPTSNPVPASPINFHPESRSSDSSVIGQPFSKPVSVSK TIRPAQGSIGCCLSISTV
683	1422	6	627	CFSLEDILNFFLQGFSA GLFAFYHDKDGNPLTSRFADGLPPFN YSLGLYQWSDKVVRKVERLWDVRDNKIVRHTVYLLVTPRVVEE ARKHFDPCVLEGMELNQGQGVGTENLHWEKRLLENEAMTGSH QNRVLSRITLALMEDTGRQMLSPYCDTLRSNPLQLTCRQDQRA VAV\CNLQKFPPKPLPQEYQYFDELSGIPAECLPYG

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
684	1423	1	1272	AARRRRQLVSRRTAE\YPRRRRSSPSARPPDVPQQPKAAKS PSPVQGGKSPRLLCIEKVTDDKDPKEEKEEEDDSALPQEV ASRPSRGWRSSRTSVSRHRDTENTRSSRSKTGSLQLICKSEPN TDQLDYDVGEEHQSPGGISSEEEEEEEEEMLISEEIPFKDDP RDETYKPHLERETPKPRRKSGKVKEEKEKEIKVEVEVEVKEE ENEIREDEEPPRKRGRRRKDDKS PRLPKRRKKPIQYVRCME GCGTVLAHPRYLQHIIKYQHLLKKKYVCPHPSCGRFLRLQKQL LRHAKHHTDQRDYICEYCARAFKSSHNLA VHRMIHTGEKPLQC EICGFTCRQKASLNWHMKKHDADSFYQFSCNICGKKFEKSDSV VAHKAKSHPEVLIAEALANAGALITSTDILGTNPES
685	1424	56	526	MTANRLAESLLALSQQEELADLPKDYLLSESEDEGDNDGERKH QKLEAIISSLDGKNRRKLAERSEASLKVSEFNVSSSEGSGEKL LADLLEPVKTSSSLATVKKQLSRVKS KKTVELPLNKEEIERIH REVAFNKTAQVLSKWDPVVLKNRQAEQL*
686	1425	132	344	RIDFMFHSSAMVNSHRKPMFNIHRGFYCLTAILPQICICSQFS VPSSYHFTEDPGAFFVATNGERFPWQELRLPSVVIPLHYDLFV HPNLTSLDFVASEKIEVLVSNATQLIILHSDLEITNATLQSE EDSRYMKGKELKVLSPYPAHEQIALLVPEKLTPLHKYYVAMDF QAKLGDGFEGFYKSTYRTLGGETRILAVTDFEPTQARMAFFCF DEPLFKANFSIKIRRESRHIALSNMPKVKTIELEGGLLLEDHFE TTVKMSTYLVAYI/DL*FPLMGNDFLGRS
687	1426	3	678	RSKIPRSDPRVTPAPAEAEQKGSQCPSGSTAQSWSAMDILVP LLQLLVLLLTPLPLHMLLGCWQPLCKSYFPYLMVLTTPKSNR KMESKKRELFSQIKGLTGASGKVALLELGC GTGANFQFYPPGC RVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDMRQLAD GSM DVVCTLVLC SVQSPRKVLQEVRRVLRPGGVLF FWEHVAE PYGSWAFMW
688	1427	240	641	RLQNSSLMDPKLGRMAASLLAVLLLLLLERGMFSSPSPPALL EKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMM AVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSD PTKG
689	1428	1	116	FFFFEMESCSVTQAGVPWHDLSLQPPPPRFRKFSCLS
690	1429	75	511	DPKAQLPEPLRVLWTAHLVAMAPGSRTSLLAFALLCLPWLQE AGAVQTVPLSRLFDHAMLQAHRAHQLAIDTYQEFEETYIPKDQ KYSFLHDSQTSFCFSDSIPTPSNMEETQQKSNLELLRISLLLI ESWLEPVRI LMSIVPN

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
691	1430	2	1364	FVKLIKHHQAAMEKEAKVMSNEEKKFQQHIQAQQKKELNSFLE SQKREYKLRKEQLKEELNENQSTPKKEKQEWLSKQKENIQHFQ AEEANLLRRQRQYLELECRRFKRRMLLGRHNLEQDLVREELN KRQTQKDLEHAMLLRQHESMQELEFRHLNTIQKMRCELIRLQH QTELTNQLEYNKRERERELRRKHVMEVRQQPKSLKSKELQIKKQ FQDTCKIQTRQYKALRNHLLLETPPKSEHKAVLKRLKEEQTRKL AILAEQYDHSINEMLSQALRLDEAQAECQVLKMQLOQLELEL LNAYQSKI KMQAEAQHDRELRELEQRVSLRRALLEQKIEEEML ALQNERTERIRSLERQAREIEAFDSESMRLGFSNMVLSNLS EAFSHSYPGASGWSHNPTGGPGPHWGHMGGPPQAWGHMGGG PQPWGHPS\GPMQ\GVPR/GSSMGVR
692	1431	50	504	LAHGSFGVSDFFAPAAAPAHTLTSFSGSLSPQFRKPLGRAPAM PLVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYS KIVTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSV TSLHSFQVIESLYQKLHEGHGK
693	1432	130	1671	SSPSRELCFYGFWIASSWSRWVGSGLGPGILPSPPARGRFTAS VSRLPPPWSAGITLTPFLICQSGSVCPGLGAGFGVRSFHHFVA RSAVLLLPLAPAAAQDSTQASTPGSPLSPTEYERFFALLTPTW KAETTCRLRATHGCRNPTLVQLDQYENHGLVPDGAVCNSLPYA SWFESFCQFTHYRCSNHVYAKRVLCSQPVLSLSPNTLKEIEA SAEVSPTMTSPISPHTVTERQTFQPWPERLSNNVEELLQSS LSLGGQEQAPEHKQEQGVEHRQEPTEHKQEEGQKQEEQEEQ EEEGKQEEGQGTKEGREAVSQLQTDSEPKFHSESLSSNPSSFA PRVREVESTPMIMENIQELIRSAQEIEMNEIYDENSYWRNQN PGSLLQLPHTEALLVLCYSIVENTCIITPTAKAWKYMEEEEILG FGKSVCDLGRHRMSTCALCDFCSLKLEQCHSEASLQRQCDT SHKTPFVSPLLASQSLSIGNQVGSPESGRFYGLDLYGGLHM
694	1433	517	578	VSWVPSKGDGVEGARRPFTRLNTSLGPGLOEGRRTWLVPPIPG AVLPGRTQEQPRASPLY*PGAPPCQPQGLVAGPWAQ*AGLRSD GFGPWPW\RLVGTAGPREKKVQKSKCWHFRGCRHPARRSGWAG RHASLLATGRPCSSAPSQQPLGTAGDSRQELLRPPLV*VNGAQ SSAAGDWGSSPRTAQALARPHRLGHHPAAVAPAAARLRTQSGHS PRGPLCRSPGSPRRMGTWRGPAGHSHD
695	1434	249	632	KTVAEEASVGNPEGAFMKMLQARKQHMSTELTIESEAPSDSSG INLSGFGSEQLDTNDES DVSSALS YILPYLSLRNLGAESILLP FTEQLFSNVQDGRLLSILKNNRKS PSQSLLGNKFKNKIF
696	1435	333	881	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDP AIFPAVIVEH VPGADILNSYAGLACVEEPNDMITESSLDVAEEEEIDDDDDDI TLTVEASCHDGETIETIEAAEALLNMDS PGPMLDEKRINNNI FSSPEDDMVAPVTHSVTLTGIPVMEQTQQVQEKYADSPGAS SPEQPKRKKK

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
697	1436	3	466	HEASGVSRALLQSAPGTPATVGVISVGELWPFARCCSHSYVRSL RGLSVSTHLLCFTIYIMNPSMKQKQEEIKENIKTSSVPRRTLK MIQPSASGSLVGRENELSAGLSKRKHRNDHLTSTTSSPGVIVP ESSENKNLGGVTQESFDLMIKGMKK
698	1437	50	241	PLPARGKSTLPATFCSPSAPELASMSVVPPNRSQTGWPRGVTQ FGNKYIQQTKPLTLTLRTINL
699	1438	1	422	AEGEDVPPLPTSSGDGWEKDLEEALEAGGCDLETLRNIIQGRP LPADLRKAVWKIALNVAGKGDLSLAWDGIIDLPEQNTIHKDCL QFIDQLSVPEEKAAELLLDIESVITFYCKSRNIKYSTSLSWIH LLKPLVHLQLP
700	1439	161	413	ALPKFLTHGVKSNERVVVWLFPPSFRAATMVHMNVLPDALKSI NNAERRGKQPVLIRLCSKIIIWFLTMVKYGYIGKFEPTRP
701	1440	211	977	AMAYQGHPSPLGMAAREELYSKVTPRNRQQRPGTIKHGSALD VLLSMGFPRARAQKALASTGGRSVQAACDWLFSHVGDPFLDDP LPREYVLYLRPTGPLAQKLSDFWQQSKQICGKNKAHNIFPHIT LCQFFMCEDSKVDALGEALQTTVSRWKCKFSAPLPLELYTSSN FIGLFVKEDSAEVLKKFAADFAAEAASKTEVHVPEPHKKQLHVT LAYHFQASHLPTLEKLAQNIDVKLGCDWVATIFSRDIRFA
702	1441	3	408	QTRPASPRTARESVLGVSONMSFNLQSSKKLFIPLGKSLFSLI EAMIFALLPKPRKNVAGEIVLITGAGSGLGRLLALQFARLGSV LVLWDINKEGNEETCKMAREAGATRVHAYTCDSCSQKEGVYRVA DQVKK
703	1442	708	244	MVARKGQKSPRFRRTVTCFLRLGRSTLLELEPAGRPCSGRTRHR ALHRRLVACVTVSSRRHRKEAGRGRAESFIAVGMAAPSMKERO VCWGARDEYWKCLDENLEDASQCKLRSSFESSCPQQWIKYFD KRRDYLKFKFKFEAGQFEPSETTAKS
704	1443	3	475	PAPAARSRELLKELRNGQDMDTVVFEDVVVDFTLEEWALLNPA QRKLYRDVMLETFKHLASVDNEAQLKASGSISQQDTSGEKLSL KQKIEKFTRKNIWASLLGKNWEEHSVKDKHNTKERHLSRNPRV ERPCKSSKGNKRGRTRFRKTRNCNRHLRR
705	1444	276	437	CVCGFFVCFETKSCFVAQAGVQWHNLSSLQALPPGFKQFSCLS LLSSWHYRRV
706	1445	2	322	GTRLRRRREAVWFVNVNMDFSRLHMYSPQCVPENTGYTYALS SSYSSDALDFETEHKLDPVFDSRMSRRSLRLATTACTLGDE AVGADSGTSSAVSLKNRAAR
707	1446	123	410	DTMQAVVPLNKMTAISPEPQTLASTEQNEVPRVVTSGEQEAIL RGNAADAESFRQRFWFCYSEVAGPRKALSQWLWELCNQWLRPD IHTKE\QILE
708	1447	2	384	PICLFSRPTLRPSRSKVSLEGRGANMAARWRFWCVSVTMVVA LLIVCDVPSASAQRKKEMVLSEKVSQLMEWNTKRPVIRMNGDK FRRLVKAPPRNYSVIVMFTALQLHRQCVVCKYELQLRFXIK

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
709	1448	104	535	QMRVKDPTKALPEKAKRSKRPTVPHDEDESSDDIAVGLTCQHVS HAISVNHVKRAIAENLWSVCSECLKERRFYDQGLVLTSDIWL LKCGFQCGCKNSESQHSLKHFKSSRTEPHCIIINLSTWIIWWY EWDEKIFTPLNKKG
710	1449	116	479	AKERGEERQEGGGWLSGSRWPLVRSFVPPAPSSLILSMCLSP GIPEAAPDSPLTASATP*VMLLGDGTGVGKTCFLIQFKDGAFL SGTFIATVGIDFRVRWLQALASSREPGLWLRHGGV
711	1450	2	232	FYPRSSADLPFQTTTRCEFQTSVMELAHSLLLNEEALAQITEAK RPVFI FEWLRFLDKVLVAANKVWYCSFFPVALT
712	1451	105	393	MNMKQKSVYQQTAKLLCKNFLKKWRMKRESLLEWGLSILLGLC IALFSSSMRNVQFPFGMAPQNLGRVDFKNSSSLMVVYTPISNLT QQIMNKTAL
713	1452	2	525	SPQNGCPCDVTGDSVIRVPLTLLVHNLAGLTGLLHHCLSGPLP APSPPPAMSSSRKDH LGASSSEPLPVIIVGNGPSGICLSYLLS GYTPYTKPDIAHPHPLLQRKLTEAPGVSILDQDL DYLSEGLEG RSQSPVALLFDALLRPD TDFGGMKSVLTWKHRKEHAIPHVVL GR
714	1453	2	1557	NRRTRAQRCQRGRSCGAREEEVEPGTARPPPAASAMDASLEKI ADPTLAEMGKNLKEAVKMLED SQRRTEEENGKKLISGDIPGPL QGSGQDMVSI LQLVQNL MHGDEDEEPQSPRIQNIQE QGHMALL GHSLGAYISTLDKEKLRKLTTILSDTTLWLCRIFRYENG CAY FHEEEREGLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSA AARPG LGQYLCNQLGLFPFCLCRVPCNTVFGSQHQMDVAFLEK LIKDDIERGRLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIW LHVEGVN LATALGYVSSSVLAAAKCDSMTMTGPWGLPAVP AVTLYKHDDPALTLVAGLTSNKPTDKLRALPLWLSLQYLGLDG FVERIKHACQLSQR LQESLKKVNYIKILVEDELSSPVVFRFF QELPGSDPVFKAVPVPNMTPSGVGRERHSCDALNRWLGEQLKQ LVPASGLTVMDLEAEGTCLRFSP LMTAAGKPGLVDIPCFCSGA AG
715	1454	319	873	LCIMDTKEEKKERKQSYFARLKKKKQAKQNAETASAVATRHT GKEDNNTVVLEPDKCNIAVEEEYMTDEKKKRKSNQLKEIRRT LKRYYSIDDNQNKTHDKKEKKMVVQKPHGTMEYTAGNQDTLNS IALKFNITPNKLVELNKLFTHTIVPGQVLFVPDANSPPSSTLRL SSSSPGATVSPSS
716	1455	60	681	SAGGDS CRAVPMLRFPTCFPSFRVVGEKQLPQEIIFLVWSPKR DLIALANTAGEVLLHRLASFHRVWSFPPNENTGKEVTC LAWRP DGKLLAFALADTKIIVLCDVEKPESLHSFSVEAPVSCMHWMEV TVESSVLTSFYNAEDESNNLLPKLPTLPKNYSNTSIFSEENS DEI IKLLGDVRLNILVLGGSSGFIELYAYGMFKI
717	1456	357	658	PRDPVTDRARAMPRRGLVAGPDLEYFQRHYFTPAEVAQHNRPE DLWVSYLGRVYDLTSLAQEYKGNLLLP IVEVAGQDISHWFD KTRDVS YAGTWD CG

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718	1457	2	481	RIPGRRFRAAFVLGSANVASSVRLRCSFPLSLGGPSGPAAASV ALGPAGPGRSLGRTPDTGDWEMDSVSFEDVAVAFQTQEEWALLD PSQKNLYRDVMQEIFRNLASVGNKSEDQNIQDDFKNPGRNLS HVVERLFEIKEGSQYGETFSQDSNLNLNKI
719	1458	6	469	SLSLSVSPFLRLSLGRVGGMAEEMESSLEASFSSSGAVSGASG FLPPARSRIFKIIVIGDSNVGKTCLTYRFCAGRFDPDRTEATIG VDFRERAVEIDGERIKIQLWDTAGQERFRKSMVQHYRNVHAV VFVYDMTNMASFHSLSWIEECKQH
720	1459	82	490	RRSPGSIVIMAAESDVLHFQFEQQGDVVLQKMNLLRQONLFC DVSIIYINDTEFQGHKVLAAACSTFMRDQFLLTQSKHVRITILQ SAEVGRKLLSCYTGALVVKRCELLKYLTAASYLQMVHIAEKR TEAFVKF
721	1460	48	708	AEGLQSAAGIRIDTKAGPPEMLKPLWKAAPVPTWPCSMPPRRP WDRQAGTLQVLGALAVLWLGVALICLLWQVPRPPTWGQVQPK DVPRSEHGSSPAWEPLAEARQQRDSCQLVLVESIPQDLPSA AGSPSAQPLGQAWLQLLDTAQESVHVASYVWSLTGPDIGVND SSQLGEALLQKLQQLLGRNISLAVATSSPTLARTSTDQLVLA RGAAH
722	1461	436	677	RKKKMLPFGKLKLRTRYTVSSKSCLVARIQLLNNEFVEFTL SVESTGQESLEAVAQRLELREVTYFSLWYYNKQNR
723	1462	45	569	LQPLSSWESASEVTRSPVSPEDVKQATSNFENLQKQLARKMKL PIFIADAFTARAFRGNPAAVCLLENELDEDHMQKIAREMNLSE TAFIRKLHPTDNFAQSSCFGLRWFTTPASEVPLCGHATLASAAV LFHKIKMNSTLTFVTLSGELRARRAEDGIVLDLPLYPAPQD FHE*
724	1463	79	530	AADTMQSDDDVIWDTLGNKQFCSEFKIRTKTQSFRCNEYSLTGLC NRSSCPLANSQYATIKEKGQCYLYMKVIERAAPRRLWERVR LSKNYEKALEQIDENLIYWPRFIRHKCKQRFTKITQYLIRIRK LTLKRQRKLVLPLSKKVERREK
725	1464	2	261	FVERGLGDPALPTLMFEEPEWAEAPVAAGLGPVISRPPPAAS SQNKVSDSREQWELFQAAKRTLVDPSAVCIAGRDTCTGTVKGES
726	1465	1	860	VVEFLWSRRPSGSSDPRPRRPASKCQMMEEERANLMHMKLSIK VLLQSALSLGRSLDADHAPLQOFFVVMHCLKHGLKVKKSFIG QNKSFPGPLELVEKLCPEASDIATSVRNLPCLKTAVGRGRAWL YLALMQKKLADYLVKVLIDNKHLLSEFYEPALMMEEGMVIVG LLVGLNVLDANL\CLKGEDLDSQGVVIDFSLYLKDVQDLGGK EHERITDVLQKNYVEELNRHLSCTVGDLOTQKIDGLEKTNSKL QERVSAATDRICSLQEQQLREQNELIR
727	1466	69	452	GCYAPSPHLGGSITPRFFPNGVFHRRRLPRPRPPQPPSVSSAPT LRPLCAHFSGLKRLRVRKSAEVAPPRTTEKGWGSAPRHSRAP LGLQGLRMAASAQVSVTFEDVAVTFTQEEWGQLDAAQRTLY

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
728	1467	1	439	FRGSLSSPSSSLRGRRLLVTGQTSRGTWCLYPGFCRSVACAMPC CSHRSCREDPGTSESREMPVVFEDVAVNFTQEEWTLDDISQK NLFREVMLETFRNLTSIGKKWSDQNIIEYEQNPRRSFRSLIEE KVNEIKEDSHCGETFTQ
729	1468	103	236	LNFANSAAFAVTMPQNEYIELHRKRYGFRLDYHEKKRKKQSRE A
730	1469	213	809	SGDLSPAELMMLTIGDVIKQLIEAHEQKIDIDLNKVKTKTAAK YGLSAQPRLDVIAAVPPQYRKVLMPKLKAKPIRTASGIAVVA VMCKPHRCPHISFTGNICVYCPGGPDSDFEYSTQSYTGYPESTS MRAIRARYDPFLQTRHRIEQLKQLGHSVDKVEFIEMGGTFMAL PEEYRDYFIRNLHDALSGHTSNNIYE
731	1470	264	799	WESDVGEGLRPPPPPPPPGRRRTQEPRARDAATVIFACPAALL ETLIAYGSSSPSFCKHRAARPLIFLLHRLTAEATARCPICAL ARNPGRWGICASWPGMKTFFGKAAAGQRSRTGAGHGSVSVTMI KRKAHKKHRSRPTSQPRGNIVGCIIQHGWKDGDDEPLTQWKGT VLDQLL
732	1471	2	763	RDLGVALEAFQWARAGDCGSGAGRAGGEGVDAGRRVPERQHRG RGGGEPGRRQRGGRRQ\RSSRRSGGDGGDEVEGSGVGAGEG ETVQHFPPLARPKSLMQKLQCSFQTSWLKDFPWLRYSKDTGLMS CGWCQKTPADGGSDVLPVGHDELSRGTRNYKKTLLLRHHVST EHLHEANAQESEIPSEEGYCDFNSRPNENSICYQLLRQLNEQ RKKGILCDVSIIVVSGKIFKAHKNILVAGSRFFKTLYCFS
733	1472	82	523	SLRAAAAMADVARSLOQYKANSNLVLQADRSLIDRTRRDEP TGEVLSLVGKLEGTRMGDKAQRTKPMQEBERRAKRRKREDRH DINKMKGYTLLSEGIDEMVGIIYKPKTKETRETYEVLLSFIQA ALGDQPRDILCGAADEVL
734	1473	536	110	CNSAESRMDVLFVAIFAVPLILGQYEDEERLGEDEYYQVVYY YTVTPSYDDFSADFTIDYSIFESEDRNLRLDKDITEAIIETIS LETARADHPKPVTVKPVTTPEQSP\DL\NDAVSS\LRSPIPL\ LLS\CAFVQVGMVFM
735	1474	2	557	FVRGPGEEQAPAFRKPAPGAMGAQVRLPPGPEPCREGYVLSLVC PNSSQAWCEITNVSQLLASPVLYTDLNYSINNLSISANVENKY SLYVGLVLAVSSSIFIGSSFILKKKGLLQASKGFTRAGQGGH SYLKEWLWWVGLLSILSWNAREKVDL*NITF*PQTSCIFFTIT IEKSTFLSYFPTS
736	1475	127	401	ARGSCPTRPRPANGRMAETKDAAQMLVTFKDVAVTFTREEWRQ LDLAQRTLYREVMLETGGLLVSLGHRVPKPELVHLLKHGQELW IVKRG
737	1476	311	790	YTMLRGTMATAWRGMRPEVTIACLLLATAGCFADLNEVPQVTVQ PASTVQKPGGTVILGCVVEPPRMNVTVRLNGKELNGSDDALGV LITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLASE SAPLPCHGAVPPHLSHPEPTIHAASCYS

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
738	1477	2	421	WGRRRQLVSEAARAQGDPVCSTMSEEEAAQIPRSSVWEQDQQN VVQRVVALPLVRATCTAVCDVYSAAKDRHPLLGSACRLAENCV CGLTTRALDHAQPLLEHLQPQLATMNSLACRGLDKLEEKLPFL QQPSETVVT
739	1478	256	1250	AKAFTMAESPGCCSVWARCLHCLYSCHWRKCPRRMQTSKDC IWFGLLFLTFLLSLSWLYIGLVLLNDLHNFNEFLFRRWGHWM WSLAFLLVISLLGTYSLLLVLALLRLCRQPLHLHSLHKVLL LLIMLLVAAGLVGLDIQWQQRHSLRVSL/QDCR*L*TPAVRP *EESGEGHWRRALHTSSCPQATAPFLHIGAAAGIALLAWPVAD TFYRIHRREPKILLLLLFFGVVLVIYLAPLCISSPCIMEPRDL PPKPGLVGHARGAPMLAPENTLMSLRKTAECGATVFETDVMVSS DGVPFMLHDEHLSRTTNVASVFPTRITAHSS

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-739, a mature protein coding portion of SEQ ID NO:1-739, an active domain of SEQ ID NO: 1-739, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-739.
11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-739, a mature protein coding portion of SEQ ID NO: 1-739, an active domain of SEQ ID NO: 1-739, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-739, under conditions sufficient to express the polypeptide in said cell; and
- b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 740-1478, the mature protein portion thereof, or the active domain thereof.
21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-739.
23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

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tgcagcaatc	cctttgagtt	tccaagtcag	gatatgtgcc	tttcagcttt	aaagagaatt	480
gaagaagaga	agccagattg	ctccaaggcc	cgctgtgaag	tccagttctc	tccacgttgt	540
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<210> 15

<211> 693

<212> DNA

<213> Homo sapiens

<400> 15

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gagcagtcca	gaaagcggct	tatcgaaacag	agccgggagt	tcaagaagaa	cactccagag	180
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gtggggatgt	ggaaattgat	aggttgtctg	gaaatatgaa	agtcagagcc	aattccagggt	420
gcagatactg	gacaagcttg	gtctgttaaga	acacgtgggc	aggtgtgtgg	gtgtctcaaa	480
ccctcgagct	catcccagac	cctgtcccat	gtcagtttagc	aagccaccaa	agtccataag	540
ggatcctgtg	gggtggaagg	tccgcggggc	ctgcttccct	gttgctgggtg	caggcggagt	600
gtctgaaggc	tgacgcacgc	tgggcatagc	agtgcgccta	acgcttcttg	taaaacagac	660

atttcgcctg ctaagccttt taaatgcctc tet

693

<210> 16
 <211> 562
 <212> DNA
 <213> Homo sapiens

<400> 16
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 gaggggaccg cgcccgcctc atttgcgcct tgcagcactg ctggaccagg ttacaagatg 120
 ttcacctaag attgagacct agtgactaca ttctctacgg gaacaaataa atggtttttc 180
 atctcccgga gatacattac aaacaaatat ggtgctaaaa gaactcctta cttttctctg 240
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 tttggaccat gtgggaaata ta 562

<210> 17
 <211> 899
 <212> DNA
 <213> Homo sapiens

<400> 17
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<210> 18
 <211> 519
 <212> DNA

<213> Homo sapiens

<400> 18

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tgtccagctc	tgaagccgaa	gacgactttc	tggagccggc	cacgccgacg	gccacgcagg	180
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gaggggctca	cttcaactaca	cgcctgtcca	cactgcgggtg	ctacgaagac	accatgttgg	300
cagccatggt	cagtgggcgg	cactacatcc	ccacggactc	cgagggccgg	tacttcacgc	360
accgagatgg	cacacacttt	ggagatgtgc	tgaatttct	gcgctcaggg	gacctccac	420
ccagggagcg	tggtcgagct	gtgtacaaag	aggcccagta	ctatgccatc	gggcccctcc	480
tggagcagct	ggagaacatg	ccgccactga	aaggcgaga			519

<210> 19

<211> 460

<212> DNA

<213> Homo sapiens

<400> 19

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tgccgtaata	aaagaagcag	tcaaagctgc	aggaatacag	atgaatcaaa	ttgttgggtc	420
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<210> 20

<211> 731

<212> DNA

<213> Homo sapiens

<400> 20

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atgcaatttg	tgaagctgtg	gtgtggctgc	agtggagagt	tcccaacaag	gctacgcaga	180
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ggcccagagc	ctactagaaa	cgggtgtggac	ccccaccac	gggccagagc	tgccctctgtg	360
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gtggccatct	cagatgcaga	ggactgcgtg	cagctgaacc	agtacaagct	gcagagtgag	600

attggcaagg	gtgcctacgg	tgtggtgagg	ctggcctaca	acgaaagtga	agacagacac	660
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cctccccga	a					731

<210> 21
 <211> 519
 <212> DNA
 <213> Homo sapiens

<400> 21						
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cattgcattg	atattagcac	tggccattgg	tctgggcac	cacttcgact	gctcagggaa	360
gtacagatgt	cgctcatcct	ttaagtgtat	cgagctgata	gctcgatgtg	acggagtctc	420
ggattgcaaa	gacggggagg	acgagtaccg	ctgtgtccgg	gtgggtggtc	agaatgccgc	480
gctccagggtg	ttcacagctg	cttcgcggaa	gaccatgtg			519

<210> 22
 <211> 544
 <212> DNA
 <213> Homo sapiens

<400> 22						
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ctggggaccc	aaaattcccc	agcggcccagg	gctttcacct	gtcccaccct	ctgcagctaa	540
ggag						544

<210> 23
 <211> 749
 <212> DNA
 <213> Homo sapiens

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 caccgatgcc cggacccccct ctgtcttctg ctagacatgc tcttcctctc gtttcatgca 180
 ggctcttggg aaagctgggtg ctgctgctgc ctgattcccc cgcacagacc ttgggaccgg 240
 ggccaacact ggcagctgga gatggcggac acgagatccg tgcacgagac taggtttgag 300
 gcggcctgga aggtgatcca gagtttgccg aagaatgggt cattccagcc aacaaatgaa 360
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 aggcctggat tttgggatcc tattggaaga tataaatggg atgcttggag ttactgggt 480
 gatatgacca aagaggaagc catgattgca tatgttgaag aaatgaaaaa gattattgaa 540
 actatgccaa tgaactgagaa agttgaagaa ttgctgcgtg tcataggtcc attttatgaa 600
 attgtcgagg acaaaaagag tggcaggagt tctgatataa cctcagatct tggtaatgtt 660
 ctcaattcta ctccaaacgc caaaaccgtt aatggtaaag ctgaaagcag tgacagtgga 720
 gccgagtctg aggaagaaga ggcgtgtgt 749

<210> 24
 <211> 556
 <212> DNA
 <213> Homo sapiens

<400> 24
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 gggctcgttg tgggcgccat ttctcggcgt ctaccgagga gccgcccctt tctcagcctt 120
 gctcggctct tccccgctct ggtcgccggg gctgcgcgt cccagctca gtgacaaaaa 180
 tgctgagttt cttccgtaga aactagggc gtcggtctat gcgtaaacad gcagagaagg 240
 aacgactccg agaagcacia cgcgcgccca cacatattcc tgcagctgga gattctaagt 300
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 aaaaagccaa aggacaagag ttgtttgatc agattatgta ccacctggac ctgattgaaa 420
 gcgactattt tgggtctgaga tttatggatt cagcacaagt agcacattgg ttggatggta 480
 caaaaagcat caaaaagcaa gtaaaaattg gttcacccca ttgtctgcat cttcgagtta 540
 agttttatcc ctcaga 556

<210> 25
 <211> 422
 <212> DNA
 <213> Homo sapiens

<400> 25
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 tacacagtcc cgggctgccc ttggttctgg tgettctggc cctgggggcc ggggtggccc 180
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 catttgctgc ggtccgaagc caccaccatg agccagcagg ggaacccggc aatggcacca 360
 gtggggccat ctacttcgac caggtcctgg tgaacgaggg cgggtggcttt gaccgggcct 420
 ct 422

<210> 26
 <211> 506
 <212> DNA
 <213> Homo sapiens

<400> 26
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 atcaccagct tcattttctca atttcttggt taaagtgaga gaatctggct ccttgaaccc 180
 tgaccatgga cctgtggtga tccaccgtag tgcaggcact ggacgctcca gcaccttctc 240
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 tctcatatcat ggctataaca gaaggagcaa aatgtgtaaa gggagattct agtatacaga 420
 aacgatggaa agaactttct aaggaagact cctcctgct tttgatcatt caccaaacia 480
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<210> 27
 <211> 850
 <212> DNA
 <213> Homo sapiens

<400> 27
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<210> 28
 <211> 990
 <212> DNA
 <213> Homo sapiens

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<400> 28
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tcaagctgaa gtggtctgct catagtttgt gtgccaggtt gctcatcagt attgatactg      180
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<210> 29
<211> 622
<212> DNA
<213> Homo sapiens

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<400> 29
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ccatctgtta gccccggccc ggctctgtcc ccacctgca cactgccaga ccccgctctt      600
cgtgtctgtc cagctgtttt gg                                     622

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<210> 30
<211> 181
<212> DNA
<213> Homo sapiens

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<221> misc_feature
<222> (1)...(181)
<223> n = a,t,c or g

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 agtagctggg actacaggag cttcgcacc aattccagcc tggggtggac agagtgataa 180
 g 181

<210> 31
 <211> 1956
 <212> DNA
 <213> Homo sapiens

<400> 31
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 taataacatg atggccaaaa ctttggaaga gtgtagagtt accttggaag ggctaaaaat 1920
 ggagaatgga tctttgaagt ctcatctgca ggggtga 1956

<210> 32
 <211> 513
 <212> DNA

<213> Homo sapiens

<400> 32

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ctgcgcaaac	ttttgcagct	gtcgggacac	ttctgcaacc	ccgcagagcg	catccatcaa	300
agctttgcgc	aacgccaacc	tcaggcgaga	tgagagcaat	cacctcacag	acttgtaccg	360
aagagatgag	accatccagg	tgaaaggaaa	cggctacgtg	cagagtccta	gattcccgaa	420
cagctacccc	aggaacctgc	tcctgacatg	gcggcttcac	tctcaggaga	atacacggat	480
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<210> 33

<211> 712

<212> DNA

<213> Homo sapiens

<400> 33

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atacaccaag	caagatgggg	agtgtggcac	actgagcaag	ggtgaactaa	aggaacttct	180
ggagaaagag	cttcatccag	ttctgaagaa	cccagatgat	ccagacacag	tggatgtcat	240
catgcatatg	ctggatcgag	atcatgacag	aagattggac	tttactgagt	ttcttttgat	300
gatattcaag	ctgactatgg	cctgcaacaa	ggtcctcagc	aaagaatact	gcaaagcttc	360
aggggtcaaag	aagcataggc	gtgggtcaccg	acaccaagaa	gaagaaagtg	aaacagaaga	420
ggatgaagag	gatacaccag	gacataaatc	aggttacaga	cattcaagtt	ggagtgaagg	480
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caactccagg	aggctaggaa	gacaaggtaa	tttatccagc	tctgggaacc	aagagggatc	600
tcagaaaaga	taccacaggt	ccagctgtgg	tcattcatgg	agtgggtggca	aagacagaca	660
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<210> 34

<211> 600

<212> DNA

<213> Homo sapiens

<400> 34

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attctttttt	ctctcccatg	cttggtgttt	ctcattcaaa	caagactggc	atagctactt	180
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ctatttgatt	atcttgagt	gaaacatcat	catcatctca	gtcattcatt	tggatcacag	420
cctccacaca	cccatgtact	tctttctagg	tattctttct	atctctgaaa	tcttctacac	480
aactgttatt	ctgcccaaga	tgcttatcaa	cttattctct	gtattcagga	cactctcctt	540
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<210> 35
 <211> 985
 <212> DNA
 <213> Homo sapiens

<400> 35						
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gctcactccc	actccgtaga	cacaatgatc	agaggtcctg	ggtgtctggg	gaagctgggc	300
tgtgctgtga	tgcgtctacc	atgtgggggt	gcctgtgagt	gtgctggggc	gtctgcagtg	360
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<210> 36
 <211> 464
 <212> DNA
 <213> Homo sapiens

<400> 36						
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atgataaaaa	cagggggcaa	gggatgttgc	ttaatatgat	gtgtggctgt	cagctgtcgg	180
caatcagttt	gtgcctggcc	gtaacattcg	ctccactgtt	caatgcgcag	gccgatgagc	240
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aggcgcaagc	cacggcaata	atggcgggga	tccagccatt	gcctgaaggt	gcggcagaaa	360
aagcccgcac	gcaaatcgaa	tctcaattac	ccgcagggtta	caagccgggt	tatcttaacc	420
agcttcaact	gttgatgccc	gcacgcggta	tttctctgag	cgtg		464

<210> 37
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 37
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 ttcttcaacc gtgcggcgaa gtgcggtagg cgggatgtcg gcattagcgt tgtttgattt 120
 gctcaagcca aattatgcgc tggcgactca ggtagagttt accgaccggg aaattgttgc 180
 tgagtacatc acgtatcctt cgccaaatgg tcacggcgag gtgcgggggtt atctggtgaa 240
 gcccgcaaag atgagcggca aaacgccagc cgtagtggtg gtgcatgaga atcgtggact 300
 gaatccgtat atcgaagatg tggcacggcg agtggcggaag gcgggggtata tcgccctggc 360
 acctgacggc ttaagttccg ttggagggtta tccgggaaat gatataaagg tggatatccgc 420
 agcggcccc 429

<210> 38
 <211> 556
 <212> DNA
 <213> Homo sapiens

<400> 38
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 ggcaattcct tgctgacaac agaaacgaaa tgtatatcat gccgcttagg tgtgccgttg 180
 tcacctcaac ggcgattcca ggctataagg atagaagaag tgaaattgag atggtttgcc 240
 tttttgattg tgttattagc gggttgttca tcaaagcatg actatacgaa cccgccgtgg 300
 aacgcgaaaag ttccgggtgca acgtgcgatg cagtggatgc caataagcca gaaagccggg 360
 gcagcctggg gcgtcgatcc acaattgatc acggcgatta tcgctatcga atcgggtggg 420
 aatccgaacg cggtagtaaa atcgaatgcc attggtttga tgcagttaa agcttcaacc 480
 tccggacgtg atgtttatcg ccgtatgggc tggagtgggt agccgacgac cagcgagctg 540
 aagaattcct caagac 556

<210> 39
 <211> 890
 <212> DNA
 <213> Homo sapiens

<400> 39
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 tgagcaatct tcgtttttat aagaataaaa ttccattcaa gccagatggg gtttacattg 180
 aagaagttct aagtaaatgg aaaggagatt atgaaaaact ggagcacaac cacacttaca 240
 ttcaatggct tttccccctg agagaacaag gcttgaactt ctatgccaaa gaactaacta 300
 catatgaaat tgaggaattc aaaaaaaca aagaagcaat tagaagattc ctctggctt 360

ataaaatgat	gctagaattt	tttggaaataa	aactgactga	taaaactgga	aatgttgctc	420
gggctgttaa	ctggcaggaa	agatttcagc	atctgaatga	gtcccagcac	aactatttaa	480
gaatcactcg	tattctttaa	agccttgggtg	agcttggata	tgaaagtttt	aaatctcctc	540
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<210> 40
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 40						
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gagaacttca	ggttttccaa	cctattgggtg	gtatgtctga	cagtggatca	caacttggtt	180
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aggaaaataa	gaagaattgg	tttggacca	gtccttacgt	agaggtcaca	gtagatggac	300
agtcaaagaa	gacagaaaaa	tgcaacaaca	caaacagtcc	caagtggaag	caaccctta	360
cagttatcgt	taccctctgtg	agtaaattac	att			393

<210> 41
 <211> 437
 <212> DNA
 <213> Homo sapiens

<400> 41						
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ccaacaacaa	ttttacattt	tcgcgaccgc	tttggctgct	ttcagggtccg	tttcaatgat	120
atactgccag	tcgttaattc	aaaaatagtt	gataattaca	acaatctatt	gaattgaaac	180
gctttccttc	gtaattcgca	actggaacac	gcacgctatg	agtaaaccga	tttgtatgga	240
acgcggtggt	aaataccgcg	atgccgataa	gatggccctt	atcccgggta	aaaacgtggc	300
aacagagcgc	gaagccctgc	tgcgcaagcc	ggaatggatg	aaaatcaagc	ttccagcgga	360
ctctacacgt	atccagggca	tcaaagccgc	aatgcgcaaa	aatggcctgc	attctgtctg	420
cgaggaagcc	tcctgcc					437

<210> 42
 <211> 392
 <212> DNA
 <213> Homo sapiens

<400> 42
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 gtcaggatgc tacagtaata cattgatgta ctgcatgtat gcaaaggacg tcacattacc 180
 gtgcagtaca gttgatagcc ctttcccagg tagcgggaag catatttcgg caatccagag 240
 acagcggcgt tatctggctc tggagaaaag ttataacaga ggataaccgc gcatgggtgct 300
 tggcaaaccg caaacagacc cgactctcga atggttcttg tctcattgcc acattcataa 360
 gtacccatcc aagagcacgc ttattcccca gg 392

<210> 43
 <211> 555
 <212> DNA
 <213> Homo sapiens

<400> 43
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 ttcaccggga atgaggttga gtggattaag gatgccttta atggccactc ataattaagg 120
 ttttaaggatt agcgtgcaag aaagaattaa agcttgcttc actgaaagca ttcaaactca 180
 aattgcggcg gcagaggcgc ttccggatgc catctcccg gcagccatga cgctggttca 240
 gtctctgctc aatggcaaca aaatcctctg ttgtggtaat ggaacttccg ctgccaatgc 300
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 tacgaccatt gtggc 555

<210> 44
 <211> 553
 <212> DNA
 <213> Homo sapiens

<400> 44
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 cgcaagctgc ttgagcagga gatggtcaac ttctgttcg agggtaaaga ggtgcatatc 180
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 gattgcgcgg ttgctcatct cctgttcgac gacaaaaaaa ggcgatacct ataacgaagc 360
 ctgggtcaaa gataccaacg gttttgatat tctgatgggg caatttgccc acaatattga 420
 gaacatctgg ggcttcaaag aggtggtgat cgctgggtcct aaggactacg tgaaatacac 480
 cgatcaatat cagaccgca gccacatcaa cttcgatgac ggtacgatta ctatcgaaac 540
 catccccggg aca 553

<210> 45
 <211> 310
 <212> DNA
 <213> Homo sapiens

<400> 45
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 agaaaaaact ggatgaactg atcgaacagc actaaaccca ggacaggaat ccgcaatgaa 120
 caggcttttt tcaggtcgtt ccgatatgcc ctttgcgctg ctgcttctcg cgcccagctt 180
 attactgctg ggcggtcttg tggcgtggcc gatggtgtcg aatatcgaaa tcagtttttt 240
 acgtctgccg ctcaatccca acatcgagtc aacgtttgtt ggggtgagca actatgtgcg 300
 tatcctctcc 310

<210> 46
 <211> 627
 <212> DNA
 <213> Homo sapiens

<400> 46
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 agcgggtggg ctccccgagg cccctgccc tcgccgggct gctccaggtt gtcgctcctc 120
 tggctgctcc cgaaggggct tctggccctg aggacggttg tgccaagcga acttcatttt 180
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 cagaagctgg cattgatttg tgactcctcg tcttcagcag agttcttcgt cactgttget 540
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 aaccgggaaa acaaccgggg cccactg 627

<210> 47
 <211> 998
 <212> DNA
 <213> Homo sapiens

<400> 47
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 gaaaagccca atcttcagct cccaaagtta ggaaaagtgt cagtagtcga atccatgaag 180
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<210> 48
 <211> 864
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(864)
 <223> n = a,t,c or g

<400> 48	
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ctggcccgtg	gcatgccacc
cagaggattc	tggtaatcgc
ggctctgggt	gctgggcttc
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gaggaagtgg	tagagcacgc
gtagccgata	aggatctggg
aacaaacagc	cggtgggggc
gtctggctat	gtcaccagg
tcaagtgate	ctcccacctc
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	300
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	420
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	864

<210> 49
 <211> 1327
 <212> DNA
 <213> Homo sapiens

<400> 49	
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gaagcaggta	aggagtgtg	atctaattct	gggagccact	ggagggtgaa	agcagggatt	420
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<210> 50
 <211> 436
 <212> DNA
 <213> Homo sapiens

<400> 50

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<210> 51
 <211> 481
 <212> DNA
 <213> Homo sapiens

<400> 51

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cactaggaag	ggatcagcct	cagcctcaga	tcactggggc	tgccccctct	ggaggacctg	420
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<210> 52
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 52						
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<210> 53
 <211> 728
 <212> DNA
 <213> Homo sapiens

<400> 53						
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<210> 54
 <211> 2228
 <212> DNA

<213> Homo sapiens

<400> 54

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gggtcaaaactc	ttttaatgat	cagtgtgaaaac	ataaaacatc	catgatctgt	taacacacac	180
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<210> 55

<211> 405

<212> DNA

<213> Homo sapiens

<400> 55

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gagaatcact	tgaaccagga	ggcagagggt	gcagtgaagg	gagatcatgc	cactgcactc	180
cagcctgggc	cacagagcaa	gactccatct	gacaactagc	tgttccagcc	cccagccact	240

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ccctgggtcag	acatgatgac	ggtgggttca	cccggggggtc	tccgcacagc	agcggcctcg	360
ggtaagcaga	acctcgctcc	gggggtttaca	aatccttctc	cgtgc		405

<210> 56
 <211> 1652
 <212> DNA
 <213> Homo sapiens

<400> 56

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<210> 57
 <211> 1129
 <212> DNA
 <213> Homo sapiens

<400> 57

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taaatgttaa	gttccttata	attccatctc	tttcagcacc	caatacaggg	gtttacatag	360
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<210> 58
 <211> 475
 <212> DNA
 <213> Homo sapiens

<400> 58						
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catcggcaga	aacctggctg	ctaaaggcaa	ccaaacgggc	gccatcagat	accaccggga	420
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<210> 59
 <211> 711
 <212> DNA
 <213> Homo sapiens

<400> 59						
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gagccctggg cttttcaagc accagtcaat atccaggcgg agcaggcagg tactgctatg 660
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<210> 60
<211> 344
<212> DNA
<213> Homo sapiens

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<400> 60
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ttgccttcat tagctgctga ttttgttgaa agtaaggatg tttg 344

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<210> 61
<211> 594
<212> DNA
<213> Homo sapiens

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<400> 61
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acaccagacc ctacagcgac aaaggctgcc attgctcacc tgcagcagaa gatcctgaag 540
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<210> 62
<211> 1609
<212> DNA
<213> Homo sapiens

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<220>
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<222> (1) ... (1609)
<223> n = a,t,c or g

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<400> 62

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gttttncaaa	ggngnttttt	cattccanct	tgttttngct	taatttngcn	caacgnacc	1560
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<210> 63

<211> 615

<212> DNA

<213> Homo sapiens

<400> 63

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agaggacgtg	caaggtgtgc	ctggaccgcg	ccgtgtccat	cgtctttgtg	ccgtgcggcc	540
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ccgtccccga	gcggg					615

<210> 64

<211> 839

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(839)
<223> n = a,t,c or g

<400> 64

aagaatgtct	ggaagagatg	gaagaaaagg	ttttttgtat	tgggtgcaggt	cattcagtac	60
acgtttgcc	tgtgcagtta	tcgggagaag	aaagcggagc	ctcaggaact	tctacaattg	120
gatggctaca	ctgtggatta	caccgacccc	cagccagggt	tggaggggtg	ccgagccttc	180
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atcctgtggg	tccaggccat	gtatcgggcc	acggggcagt	cacacaagcc	tgtgcccccg	300
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tctcaatttt	acgcagatag	agctcaaaaa	catggcatgg	atgaatttat	ctcttccaac	420
ccctgtaact	ttgaccacgc	ttccctcttt	gagatggtag	aacgccttac	tttggatcac	480
agacttaatg	attcctattc	ttgcctgggc	tgggttcagtc	ctggccaggt	gtttgtacta	540
gacgagtatt	gcgcccgaag	tggagtccgg	gggtgtcacc	gacatctctg	ctacctcaga	600
gacttgcttg	aacgggcaga	aaatggcgcc	atgatcgacc	ccacccttnt	tcactacagc	660
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ctgttgaaga	aaaggaacgt	tttttgaagg	aatcaaaaag	aggaggnttc	cgnagtctctg	780
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<210> 65
<211> 1678
<212> DNA
<213> Homo sapiens

<400> 65

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ccctggccac	caagggccac	agcgccccgt	caaggacgag	ccacaggacg	gggagaatcc	180
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cggctatgga	gtggaagagt	tgatctctgc	ccttcagcgc	tcctggcgct	accgtgggga	300
cgtctactta	gtggcgccca	ccaacgcggg	caaatccact	ctctttaaca	cgtcctgga	360
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gccagggtact	acattaaacc	ttctgaagtt	tcctatttgc	aacccaactc	cttacagaat	480
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gcaagaacaa	aatcagctta	atgtcctcaa	aaagcatggg	tatgtcgtag	gaagagttag	600
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attaaacata	taacgcataa	ataaagctcc	cattcttacc	cttaaaaata	aaaggagaat	1500
gaaaaaaaaa	gatgccataa	ggcatatacg	tggttttggg	tattccgggg	tcttcccgtg	1560
gtctgttcac	tttgcggtgg	tggtgatata	ttaggcagtc	ggggcgccctg	atgtacgcct	1620
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<210> 66
 <211> 1888
 <212> DNA
 <213> Homo sapiens

<400> 66

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gctgccaaaa	gcctattgaa	caagaagtcg	gatggcggtg	tcaagccaca	gagcaacaac	180
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caaacactg	tggtacacaa	cgctacagat	gggatcaagg	gtccacaga	gagctgcaac	300
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gtgcctgaag	gacggagctc	ccgggacaga	acagccccct	ctgcaggcat	gcagccccag	420
ccttctctct	gtcctcagc	catgcgaaaa	caggagatca	ttaagattac	agaacagctg	480
attgaagcca	tcaacaatgg	ggactttgag	gcctacacga	agatttgtga	tccaggcctc	540
acttcttttg	agcctgaggc	ccttggtaac	ctcgtggagg	ggatggattt	ccataagttt	600
tactttgaga	atctcctgtc	caagaacagc	aagcctatcc	ataccaccat	cctaaaccca	660
cacgtccacg	tgattgggga	ggacgcagcg	tgcatcgcct	acatccgcct	caccagtac	720
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caccgtcgca	gtgagctcag	ccacaggggc	ttttaggaga	ttccagccgg	aggtccgaac	900
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<210> 67
 <211> 1712
 <212> DNA
 <213> Homo sapiens

<400> 67

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tcagtatcat	tggattttcc	aaccggatca	aagtatggaa	ggaccacttg	atatcagtca	180
ctccagacag	catcagggat	gggaaagtgt	acattcacca	tatgtcaccc	actggaggca	240
cagacatcaa	cggggccctg	cagagggcca	tcaggctcct	caacaagtac	gtggcccaca	300
gtggcattgg	agaccggaga	gtgtccctca	tcgtcttcct	gacggatggg	aagcccacgg	360
tcggggagac	gcacaccctc	aagatcctca	acaacacccg	agaggccgcc	cgaggccaag	420
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cgctggagaa	ctgtggcctc	acacggcgcg	tgcacgagga	ggaggacgca	ggctcgagc	540
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ccccagctc	agtgggtgcag	gccaccaaga	cctgtttccc	caactacttc	aacggctcgg	660
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gcgtgcgagg	agctggcacg	cagccaggac	ctttgtctaa	gaagccatac	cagccaagaa	1140
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caaattggcca	caagaaacag	cgcacttact	tgcgcactat	caccatcctc	atcaacaagc	1380
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gcgagggcct	ttccagcaac	tgcagggtct	tctgtgagtc	tggcatcctg	attcaggaac	1680
tgaccacagca	gtccgtggca	gttgctggtc	ga			1712

<210> 68

<211> 839

<212> DNA

<213> Homo sapiens

<400> 68

gtttttttctc	gagcagggtta	gccaatatac	ctttgtctatg	tgcagttata	gagaaaagaa	60
gtctgaacca	caagaattaa	tgcagcttga	aggctatact	gtggattata	ccgatcccca	120
cccaggcctt	cagggtgggt	gtatgttctt	taatgtctgt	aaagaaggag	atactgtaat	180
ctttgccaagt	gatgatgaac	aggacagaat	attatgggtt	caagccatgt	atagggccac	240
aggtcaatca	tataaaccag	ttcctgcaat	tcaaaccacg	aaactgaatc	ctaaaggagg	300
aactctccat	gcagatgctc	agcttttatgc	agatcgtttt	cagaaacatg	gtatggatga	360
gtttattttct	gcaaaccctt	gcaagcttga	tcatgccttc	cttttttagaa	tactccagag	420
gcagactttg	gatcacagac	tgaatgatcc	ctattcttgc	ttgggatggg	ttagccctgg	480
ccaagtcttt	gtgttagatg	agtactgtgc	ccgttatggg	gtgagaggct	gtcacagaca	540
tctgtgtaac	tctgcagaac	tgatggaaca	ttcagaaaat	ggtgctgtca	ttgaccctac	600
cctgtctccat	tacagctttg	cattctgtgc	ctctcgatgt	gcacggcaac	aggcctgatg	660
gaattggggac	tgtttcagtg	gaagaaaaag	aaagatttga	ggagataaaa	gagagactct	720
cttccctttt	agaaaatcag	ataagccatt	tcagatactg	ttttcccttt	ggacgacctg	780
aagggtgctct	aaaagctaca	ctttcattac	ttgaaagggt	tttaatgaaa	gatattgcc	839

<210> 69
 <211> 801
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(801)
 <223> n = a,t,c or g

<400> 69
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 tgtgaagatg cctgtgggca tcctcccctg cggctcgggc aacgcgctgg ccggagcagt 120
 gaaccagcac gggggatttg agccagccct gggcctcgac ctgttgctca actgctcact 180
 gttgctgtgc cggggtgggt gccaccact ggacctgtc tccgtgacgc tggcctcggg 240
 ctcccgtgt ttctccttcc tgtctgtggc ctggggcttc gtgtcagatg tggatatcca 300
 gagcgagcgc ttcagggcct tgggcagtgc ccgcttcaca ctggggcacgg tgctgggcct 360
 cgccacactg cacacctacc gcggacgcct ctctacctc cccgccactg tggaacctgc 420
 ctgcccacc cctgcccata gcctgectcg tgccaagtcg gagctgacct taaccccaga 480
 cccagccccg cccatggccc actcaccct gcacgttct gtgtctgacc tgctcttcc 540
 cctgccccag cctgcccctg cctctcctgg ctgcccagaa cccctgccc tctgtccct 600
 caacggtggg ggcccagagc tggctgggga ctgggggtgg gctggggatg ctccactgtc 660
 cccggaccca cagctgtctt cacctcctgg ctctcccaag gcagctctac actcaccctg 720
 ctaaaaaaag gccccgtaa ttccccccga catgnnnccc cgctctagag gatcaagcaa 780
 ctacgcggcg gctcacgacg c 801

<210> 70
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 70
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 tcagaggagt tttggagggt gtaattgggt tggcaactgg atctgttctt ggatttttca 180
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 gactgtgcac gttggtcatg gctttccttg caggcatggg atggaccagc gaaaaggcag 360
 aggttgaaaa gataattgca gttgcctggg acatttttca gcccttctt tttggactaa 420
 ttgggagcag aggtatctat ttgcatctct cagaccagaa actgtaggcc tttgtgttgc 480
 caccgtaggc atttgcaagta ttgatacgaa tttttgacta cattttctga a 531

<210> 71
 <211> 540
 <212> DNA

<213> Homo sapiens

<400> 71

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gaaaacctga	gtgattctgt	ccttccctca	tcctctatcc	ctgaaccagg	gcagacatag	120
atggaatcag	agcaggagtt	gggtttgatg	tggtttcagg	tcacacctatc	agagtttgag	180
agatttaggc	catgaacctat	tatgaatata	gatgagaacc	tttgtaattg	ctgaaggagg	240
tagtagtgca	ggcaagtcct	gtgtgcaaga	cctgctgctc	ccagttagta	cggaccctctg	300
tgacattcac	agaagttcag	aatgtctgag	atgctctgca	ggctacctta	tctccgtctg	360
cagctacacc	tccagtgatc	acaatcagtg	ctacgctggc	acagccagcc	tggccctgct	420
ctggattgga	ggcatcctca	agggctgctt	gctgtggaag	cagtttcgct	ggaccgagag	480
gagccactgg	aattttgggt	actgggcctt	atggtcaccc	gggaatggga	atggctgctg	540

<210> 72

<211> 428

<212> DNA

<213> Homo sapiens

<400> 72

cgagcgcgtc	cgcccacgcg	tccgcccacg	cgctccgctag	aaatttctgt	ggaactccat	60
ttgactttct	atctgtgaaa	tccaaactgt	ctctgaagaa	ataagaaaaa	tagtgttttg	120
acttttagga	gacaactatg	tttattattt	tgccttgcaa	attaatgtct	aaatttgtac	180
aagcacctat	ctacagatgt	ttccaggtaa	accatcatgt	tttatgtgta	aaggtagatt	240
gatgtgcatt	tactttatac	tttggtaact	aggccattac	acatctttgc	actggaattg	300
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agcatgacac	acacagtcct	tgcctgatg	gagctcatag	actagtgaag	gaatagggtc	420
ctatgacc						428

<210> 73

<211> 584

<212> DNA

<213> Homo sapiens

<400> 73

gctggagtc	ttgcctgggt	tcaaagagat	tgtgagcagg	ggagtaaaag	tggattactt	60
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ttgtgaagtc	catcagatga	tccgggaacta	catgtgggac	cccaccacca	acaagtcctt	180
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tccgcagagg	aaagatgccc	tcaaggctgg	tagacactgt	cctgaagtac	atgaccaagt	540
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<210> 74
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 74
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 gaaaatcaca gaagaggtga aaaggagtat agcacaacag tatctagatt tgacagtagc 120
 ccggaacaag tggaccctga tgccgaagtc gatgcagccc catctaccac atcttcatgt 180
 ggacattgag attcacacgc tggctcctga aggggtgctca gtctccttgg tgattaaggt 240
 cctgcttgaa ctggtgccaa ctccatggca ggggaagttgc ttttggttgc ctggctgggt 300
 ttcccagatc cttctgggg caaggagcta tcagaccctg ctttcaag 348

<210> 75
 <211> 365
 <212> DNA
 <213> Homo sapiens

<400> 75
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 tgaatgccag agcccccccc acatgacagg gccccggtgt gaggagcacg tcttcagcca 180
 gcatcagcca ggacatataa cctccatcct aatccctatg ctgtagctgc tgctgctggg 240
 tctggtggcc ggagtगतत tctgccataa acggcgagtc caaggggcta agggcttcca 300
 gcaccaacgg atgaccaacg gggccatgaa cgcgagatt gcaaacccca cctacaagat 360
 gtacc 365

<210> 76
 <211> 700
 <212> DNA
 <213> Homo sapiens

<400> 76
 caagaaccat cagcaccaac acaaatttat ctttgcagac cgaaggaatc agctaaacaa 60
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 atttctttct ctctctctct tttgtcctt gcgatgaggc attcatctct ccttgagcct 180
 ccgttctgaa gagataacag tatagcaaca actctgccac tgaatcctg ttctctgacc 240
 gatattggca cctgcaaaga gaaacaacca gtaacaggca gcagcagcat cagtattaat 300
 ctccatgat gaaatcttta caggtaaga acaagtacac agctcttttc tcaactcttc 360

acagtggacc	atgcaactag	ttgaggtgga	agacaatgga	ttgtctacaa	gccttttgaa	420
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gtttggaaa	agtcagaaat	cttcacatac	gtgagctgaa	aagaataaac	aatgaagata	540
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gtagaggtgg	ctttagttaa	gtgtataagg	taatgtatgg	tttattctgg	tttttttaca	660
ctaattgtac	aaggatatag	gagtatgtgg	ttaagaagtg			700

<210> 77
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 77

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aatgattcca	atcctgaaac	cgacaaccgt	caagaaagtc	cttcccagga	aaacattgac	180
cgagtgagt	acaggccttt	gtgccctcag	cttgacagc	ctcggtggg	gttgcttggg	240
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ggctccaggt	gtaacctgcc	cacctcagag	gccaccacg	cagtaacaga	gggcagggga	360
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cctttg						426

<210> 78
 <211> 358
 <212> DNA
 <213> Homo sapiens

<400> 78

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aagaccctgt	tgagctactt	cttacaaaat	tcctctactc	ctgggaagcc	caaaaccggc	180
aaaaaaagca	aacagcaagc	tttcatcaag	taagttgaga	atcctgagct	tgcaaatac	240
aatagtttagc	tgctgaactg	aaaaggggaa	ctctgatgag	cgtaagctaa	catacagaac	300
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<210> 79
 <211> 322
 <212> DNA
 <213> Homo sapiens

<400> 79

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aagagcagtt	ttccaagcaa	agacgccaga	cactccagtg	tgccaccgta	gttcacccaa	180
ctgcattggg	gaccgccctc	tcatactcca	gccaggccgt	gacgtgaccg	acctccgact	240
tctgcgcaaa	ggcagcgcaa	gccgttggga	tccctgtctc	ccctctgctc	aacagtcggg	300
ccattacacc	tttcatactg	cg				322

<210> 80

<211> 310

<212> DNA

<213> Homo sapiens

<400> 80

cgaaagcacg	ccagaaaaca	aaataaaagc	aatacataac	cacaaaaata	atagcgtata	60
gatgatcaac	aagaattaaa	acgcgtaaca	tagtatagtc	aaaaagaata	cacgaaaaag	120
aaactccata	aaaaatgcaa	tatcatacag	gcagatatca	agccagacaa	tatcctggat	180
aatgaatcca	taactattct	aaagcttagc	gattttgggt	cggtttcaca	tggtgcggat	240
aatgacataa	caccttcata	ttctcagacc	acatccgctg	catcatcgcc	cccgcggacg	300
ctacgcccg						310

<210> 81

<211> 134

<212> DNA

<213> Homo sapiens

<400> 81

tcgagtaaac	catgggacta	aagcttggct	ccaaagcatt	caggctgaac	gaaaaacatg	60
gactgctatt	gcataatacc	aacgtgcatt	ggacgagaac	gatgctatgg	aacctgcata	120
ggcgacacgg	tcgg					134

<210> 82

<211> 358

<212> DNA

<213> Homo sapiens

<400> 82

ctctggggaga	gaaagactaa	tgggcaggat	cccattactt	cattggtaaa	gatagtcgga	60
tactctcacc	acttttaata	ccttttagtat	tacagttgat	cagattacct	ttacttgata	120
tgaattattt	ctaagttcat	tcccctgtgt	tgtagcttat	ttcaacaatt	ccaactagcc	180

gtttaaaatt	cctcaaagaa	actgggtcatg	gaacaccaat	ggaagaaata	cctgaggagg	240
aattatcaga	ggatgttgaa	cagattgatc	acgctgatag	ggagttgcgg	cgtggccaaa	300
acttgaggtg	caaaggaatt	catagattgc	ctactcatat	acaagtaggg	caaaatcg	358

<210> 83
 <211> 723
 <212> DNA
 <213> Homo sapiens

<400> 83

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atcgtgtatt	ttacacaggt	atccaaacat	aaaaatactt	tagaattgct	tactgtatgg	120
acaggttata	tggaatggag	tttgtagtat	ccacattaac	aaagcaagtt	tatatggact	180
ggttatgata	ttagggatat	gaattagaaa	tggatgttgt	tgcactcatt	taaaatattt	240
tgcctctcac	tttatcccca	gttatagtgt	ccttttgaat	ttttctcaca	cagtgtctact	300
atatttcatg	aactgggtata	taaacaaacc	aaaattattt	cttcaaataca	agaacttata	360
tacgaagggc	gacgcttagt	cttagaacct	ggaaggctgg	cacaacattt	ccctaaaact	420
actgaggaaa	accctatat	tgtagtaagc	cgggaacctc	tgaataccat	aggattaata	480
tatgaaaaaa	tttccctccc	taaagtacat	ccacgttatg	atttagacgg	ggatgctagc	540
atggctaagg	caataacagg	ggttgtgtgt	tatgcctgca	gaattgccag	taccttactg	600
ctttatcagg	aattaatgcg	aaaggggata	cgatggctga	ttgaattaat	taaagatgat	660
tacaatgaaa	ctgttcacaa	aaagacagaa	gttgtgatca	cattgggatt	tctgggtatcc	720
aga						723

<210> 84
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 84

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gacgtgctg	atcgccctca	ggcggggagg	tcaccgcgag	ctgggttaaag	aaaatgggaa	180
cccgaggagag	gggaccttac	gtgggaagaa	tcagaggaag	atgtacataa	gagtaagtgg	240
acaagatgtg	tggatgagaa	gggcgcgtag	tgctaaacag	acaataagag	accgctcagg	300
tgtggggtga	cctaattggg	agacgtggaa	tatgtttggt	ggcacggagg	aaagtctaata	360
ggatatcgtg	tttaggagga	cgatggagtc	ttacgtgctc	gttgatg		407

<210> 85
 <211> 342
 <212> DNA
 <213> Homo sapiens

<400> 85

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atagacaagc	tggagctgct	ggctcccggg	tgaatttcag	acctgggggt	ctcagctcca	180
ggcaacttgg	actcccagga	cctcctgacg	gtcctgacta	tactgtttac	taccggttcc	240
atcgacttgc	catggtgact	gctgcctcac	gattggagcg	tgaacacctt	acgcatttat	300
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<210> 86

<211> 420

<212> DNA

<213> Homo sapiens

<400> 86

cgctccgcag	gttttagcacc	gactgtagct	ctgatcagca	ggaccgatta	aacggaactg	60
cccctagcgg	ttttaaccgc	tcctgaccag	tcccgttgcc	gcaccccatc	ttggaagtat	120
gccctggcca	gtaggagcca	caaagcgcga	ttagcctcac	tgcatttcag	gtacaggccg	180
gcgccagccg	tgcctcacca	ggccaccggg	ctccgagcag	cagcaagccc	ggtcggaaag	240
cgaaagtggc	ctcgccatgt	ccagaccggc	cagctccccc	gcctacctga	ccccgccccg	300
cagccgcacc	tgggtccgag	tcctgcgcgc	ggccgcaccg	gccccgcaca	ggaaggcggc	360
agcaaagagc	gcacgctcga	cgcgctgcag	ccaggacagc	gccatggcgc	ccctcgtgcc	420

<210> 87

<211> 392

<212> DNA

<213> Homo sapiens

<400> 87

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cttttctgac	accctcaaag	gtcagaaggt	taaaggggca	gaaggcattc	ggaaagctcc	120
cctcccacag	tgacacctct	ctgacttctg	acctagggtt	ccaccaccgc	ttcaatccca	180
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gggtagatgg	aatcctgagt	gaggacaagc	tgactgtgag	tggcctttga	ctccaggaag	300
cctcgagcct	gggagaaccc	tgttgtctaa	gatcatctgg	cttagggagg	ggcttgaggt	360
gcaggggctt	cctgagccga	tggatggggc	tt			392

<210> 88

<211> 332

<212> DNA

<213> Homo sapiens

<400> 88
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 ggccagtatt gatgctatgt tttcccttac ctatcagact ctttcaaaga gaaaagaggg 180
 agcagttgga attttatgtt tgttggtcta ttttgtctat tatgaattgt gacaaaacca 240
 ttataaaaga tgacaagtgt gtgtgtttct ttttttcttt ttaaactgta ggggaacatag 300
 tcattagtga tctcaaatac cgaaagacat tt 332

<210> 89
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 89
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 gatttcagga gacaagtatt atctttaaat ctaaatgggt gcaattcatt aatgaaaaaa 120
 ttacagcatc tttttgcctt tctggcccat acacagaggg aagcatacgc acctcggata 180
 ttctttgagg cttccagacc tccatgggtt actoccagat cacagcaaga ctgttctgaa 240
 tacctcagat ttctccttga caggctccat gaagaagaaa agatcttgaa agttcaggcc 300
 tcacacaagc cttctgaaat tctggaatgc agtgaaactt ctttacagga agtagctagt 360
 aaagcagcag tactaacaga gaccctcgt acaagtgcag gtgagaagac tttaatagaa 420
 aaaatgtttg gaggaaaact acgaactcac atacgttggt tgaactgcac gagtacctca 480
 caaaaagtgg aagcctttac agatctttcg cttgcctttt ggccttcctc ttctg 535

<210> 90
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 90
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 agcagcgtaa tgggctgcat tactagttag ttccttatgt gagtgtgcga gcatatgctg 120
 gatgacttat ctagaataat gtagaagaga attaaacatt gaatgggagc tttaaattagt 180
 taattttctga gggtcccttc cattcttaga attctttgat ttttatattg aattgagaga 240
 actagtatag tttttatttc agcaaattat aacaccattg ttctcaaggc atggaaaatg 300
 tgcttttcat ctttaagata ctaaaccttt tcaactcatgg caattttttt tagctagcct 360
 ctaagcttgg aaagcagtggt accccattaa taatcctggc caactctctt agtggaaacta 420
 atatgggaga ag 432

<210> 91

<211> 780
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(780)
 <223> n = a,t,c, or g

<400> 91

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cagaaaaatga	aggtagttgt	cacagtgatc	agatgagcaa	cgatttctcc	aatgatgatg	180
gtgttgatga	aggaatctgt	cttgaaacca	atagtggaaac	tgaaaagatc	tcaaaatctg	240
gacttgaaaa	gaattccttg	atctatgaac	ttttctctgt	tatggttcat	tctgggagcg	300
ctgctgggtg	tcattattat	gcatgtataa	agtcattcag	tgatgagcag	tggtacagct	360
tcaatgatca	acatgtcagc	aggataacac	aagaggacat	taagaaaaca	catgggtggat	420
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aacgagaaat	tgagcgcaat	acatgcaaga	taaaattatt	ctgtttgcat	cctacaaaac	660
aagtaatgat	ggaaaantaa	attgaggttc	ataaggataa	gacattaaag	gaagcagtag	720
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<210> 92
 <211> 867
 <212> DNA
 <213> Homo sapiens

<400> 92

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cttccatggg	accctgcagc	tgggccaggc	cctcaacggg	gtgtacagga	ccacggaggg	180
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ctgaatctgc	ctggatggaa	ctgaggacca	atcatgctgc	aaggaacact	tccacgcccc	660
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ccacttttga	gcacagagca	gagacagacg	caggcgggga	caaaggcaga	ggatgtagcc	780
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agcagagtca	aggcattctca	aaaaaaaa				867

<210> 93
 <211> 690

<212> DNA
 <213> Homo sapiens

<400> 93
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 gagcctcatt tcacagaaag aacattacac atcttaattg ccaattctgg ctgcgctgga 420
 ggggaagcct ctctctggga ttgtatacga tgggagtgga aacagactgc gtgtcattta 480
 aatatggaag caagtttgat ctgctcagcc cacaggcagc ccaggctggt tggagctgat 540
 atgccctgct ctggacgtgt tgaagtgaag catgcacaca catggcgctc tgtctgtgat 600
 tctgatttct ctcttcatgc tgccaatgtg ctgtgcagag aattaaactg tggagatgcc 660
 atatctcttt ctgtgggaga tcactttggg 690

<210> 94
 <211> 948
 <212> DNA
 <213> Homo sapiens

<400> 94
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 cctcacgctt ccgagtagct ggaattacag gtgtcaagct agggatgcgg tccattccca 180
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 cccctaaggc cctggcccag gcctgcccac agagaagcca catctgcgtt tgtcctttga 780
 gaggactttg actacaatac aggcattgaca tcaatgaaag gaaagtcag aaatcgatga 840
 gactgaatcc ctacggattt cttaaaagcc agattttag ggagaatgaa tgtgcaacgt 900
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<210> 95
 <211> 541
 <212> DNA
 <213> Homo sapiens

<400> 95

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gggagcacga	gctcagggtt	agggagggtt	taaccacggg	tgaagagggt	tctgttgaca	480
gacgtgagg	cgcgaaacgc	tcctcctctc	tcttcacact	cgccaacacc	gcgggtggcgc	540
t						541

<210> 96

<211> 603

<212> DNA

<213> Homo sapiens

<400> 96

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gggagggcca	agaatgatga	tagacggtga	gggactgagg	gatcagctga	tgagttaagc	180
ctcaaacacct	gtcctagggc	tttgcatg	gccctcaaac	gtgtttacac	cctcctgagc	240
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cccaccaaag	agaacgttcg	ccagtgcctg	caggatgatg	agttgttcag	cttcctcgt	600
gcc						603

<210> 97

<211> 1385

<212> DNA

<213> Homo sapiens

<400> 97

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ctcgggaaac	aaacaggatc	ttctctgccc	tgctccagtc	gagttggcct	gaccgcttg	180
gatcagtgc	catttgctgg	cagacagggg	agagcagctt	ccagcctggg	tcagaagggg	240
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gccccaaactc	aggttcagt	cagaaccagg	tcagcaggta	tgcccgcccc	tacgttaagg	360
gggcctctc	aaccccttgc	ctggcctcac	ctggccagct	cacccctttt	gggtgtaggg	420
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gagcagcagg	ccccgagccc	cttcaggccc	agcactgccc	cagactcgct	ggcactcagt	660

tccctcatct	gtaaaggtga	aggggtgatgc	aggatatgcc	tgacaggaac	agtctgtgga	720
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gcactttcat	ggctgccctc	tggcagggca	gggcagggca	gtgacactgt	aggagcatag	960
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tcattcccac	atcttgccaa	gacagccttt	gtccagctgt	ccacattgag	tcagactgct	1260
cccggggaga	gagccccggc	ccccagcaca	taaagaactg	cagccttggt	actgcagagt	1320
ctgggttgta	gagaactctt	tgtaagcaat	aaagtttggg	gtgatgacaa	atgttaaaaa	1380
aaaaa						1385

<210> 98
 <211> 2191
 <212> DNA
 <213> Homo sapiens

<400> 98						
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tatcacagga	caaggaggtg	gctgtaaaga	agctcctcaa	aatagagaaa	gaggcagaaa	300
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tcattttcaat	cctggagtc	atgtcaaatg	acacgagcct	tcttgacaag	tgtaactcat	960
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cctgagcaac	ctagtaagac	ctcgtctcta	ctaataatta	aaaaactagc	tggcatggta	2040
gcacacacct	gtagtcccag	atacttggga	ggccaaggca	ggaggattgc	ttgagacctc	2100
gcaatcagtc	agggctgcag	tgagccatga	tggcaccact	gcactctagc	ctgggcaaga	2160

gaacaagatc ctgtctcaaa aaacagggaa a

2191

<210> 99
 <211> 335
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1) ... (335)
 <223> n = a,t,c or g

<400> 99
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 ctatatactc cttgttgcca ctgctgagtg actagactgg cccagagatc cgcgggtgcac 120
 atgctggcgg ctccctccctc agaaaaaggc aatggcctaa atactgttta aatgacctga 180
 ctcgatgctg tgggaaaactg gctgctctgc tgcagccgt gtgactgtca gtccaaccgt 240
 tacatttgcc acgttctcca cacgggggat agacgcaatg cgcccaggtc ccagttttct 300
 ttggaggcag cagctctcgc agggctgaat gttgn 335

<210> 100
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 100
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 tgtactagaa aaaattgtaa tcctcttact ataaactgtcc atgaccctaa ttcaactcag 120
 tagtattatg gcatgtcatg ggaattaaga ttttatatcc caggatttga tgttgggact 180
 atgttcacca tccaaaaaat cctggtctca tggagcccac ccaagccaat cgggccttta 240
 actgatctag gtgaccctat gttccagaaa cccctaaca aagttgattt aactgttcct 300
 ccaccattct tagtcataaa agatacactc caaaagtctg agaaaatc 348

<210> 101
 <211> 416
 <212> DNA
 <213> Homo sapiens

<400> 101
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ggagcaaata	tgattggtta	taaaatgtct	gccatttctg	ttcacgggtg	gagtacctct	180
ggaggacaga	tgtaccacta	tgacatgaat	acagcatccc	tttctcaaca	gtaggatcag	240
aagcctat	ttaatgtcat	cccaccaatt	cccgttgggt	ctgaaaattg	gaatagggtg	300
caaggatctg	gagatgacaa	cttgacttcc	ttggggactc	tgaatttccc	tggtcgaacg	360
gtttcttttt	cttttgagat	ggagtctcgc	tctgtcgcgc	aggctggagt	gcagtg	416

<210> 102
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 102						
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actaattctg	aaatcaccaa	tatgtatctg	tgcttgggaa	atagaggcat	acacaggaat	120
gcagatgccc	acacactcac	attcacactc	acactcactc	tcacactcac	tctcacactc	180
actctcactc	gcactctcac	actacaccga	gatgctcaca	cactcagcct	ccccatgccc	240
aggccccctgc	tctttgttaa	tcataagaag	accgtggaca	acccacctgg	aaactatgtg	300
cccacagacc	cagactgaag	gtgataaaaag	agggtggctg	gcttgggggc	tg	352

<210> 103
 <211> 702
 <212> DNA
 <213> Homo sapiens

<400> 103						
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tggtggtatg	agaagcagag	gctaattgtc	tacccctgc	ctccaagtag	aattactcct	180
tgtctgtgta	cctggtgagg	cagttgactg	caggaaccct	tctacaaaaa	ctcagagcaa	240
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cccacctgat	ctggattcaa	gtcttctctg	ccctccagcc	ttcataatta	aaccataacc	360
tcttttttga	caacttactc	cccttctcac	atgaacccca	accctcccc	tctacctctg	420
accagtcttc	cagtctttat	agttgaagtt	ggaccactcc	caggcaccct	tgaatttcca	480
atcatgtatc	tgctttgcac	ctcacagtcc	ctaactccag	ccctgctaga	atatgggctc	540
tcgggactgg	aaagaatctt	aggggtcctc	taatctaacc	ctcacatgat	gcttcaactc	600
ctccagatca	tctctaacat	agccagagtg	tcacgctatg	tttaagcatc	ttcagggatg	660
ggaaaatccc	ccacacccat	gtattgcggc	cgtctagag	ga		702

<210> 104
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 104

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gtgacccgcc	aggacatac	aaagcctcag	tgtcatactg	tatttcagga	atacagtagg	180
tagaagggcc	aggactttgc	ccttttactc	agggaagcct	ccaaacttca	agaaaaaatt	240
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tactaatgct	gaacgccagg	aagtgtcctt	cactgtaact	gatgaaaaat	ccatgggtga	360
aaagtagcca	gaagatgcca	ctgataccat	acgaagagcc	actcctggac	caccccaaac	420
aatccagctc	atggtggcca	tgggatttca	ggccaagaac	atctctgtgg	caatcataga	480
aagaaaattc	aactatcca	tggccaccta	cctcatttta	gagcacacaa	aacaagagag	540
gaagtgtcc	accatcagag	aactgtccct	tccctccggg	gttcccacct	ctccttcccc	600
atccactgaa	ctttccacct	tccctctctc	actgatgcgg	gctcataggg	agccagcttt	660
taacgttcag	cctcccgaag	aaagccagg				689

<210> 105

<211> 776

<212> DNA

<213> Homo sapiens

<400> 105

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agtcttctg	caccacgcc	aagctggcac	catcattgcc	cgccagggag	accaggacgt	120
gagcctgcac	ttcgtgctct	ggggctgcct	gcacgtgtac	cagcgcatga	tcgacaaggc	180
ggaggacgtg	tgcctgttcg	tagcgcagcc	cggggaactg	gtggggcagc	tggcgggtgt	240
cactggcgaa	cctctcatct	tcacactgcg	agcccaacgc	gactgcacct	tcctgcggat	300
ctccaagtcc	gacttctatg	agatcatgcg	cgcacagccc	agtgtggtgc	tgagtgcggc	360
gcacacgggtg	gcagccagga	tgtcgccctt	cgtgcgccag	atggacttcg	ccatcgactg	420
gactgcagtg	gaggcgggac	gcgcgctgta	caggtgcagc	tcccaccgcg	ctgctcaggc	480
ccggcctagg	ggtggggacc	tgggggtggt	cagaccttgc	tgacctccac	gcccactcag	540
gcagggcgac	cgctccgact	gcacttacat	cgtgctcaat	gggcgggtgc	gtagcgtgat	600
ccagcgaggc	agtggcaaga	aggagctggt	gggcgagtag	ggccgcggcg	acctcatcgg	660
cgtggtgagc	gcgaccccc	cccactgacc	tctggccttt	tccaggccag	tccttcggca	720
actcacacgc	atcatcccgg	gtaatccagg	gagtggtgaa	gtttttcccg	gggctc	776

<210> 106

<211> 707

<212> DNA

<213> Homo sapiens

<400> 106

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acacagttgc	ttccactcca	ggaaccagcg	agactacagc	ttcagctgag	ggaagacgaa	120
ccccaggagc	aaccaggcca	gcagctccag	ggacaggcag	ctgggcagag	ggttctgtca	180
aagcacctgc	tccgattcca	gagagtccac	cttcaaagag	cagaagcatg	tccaatacaa	240

cagaaggtgt	ttgggagggc	accagaagct	cggtgacaaa	cagggctaga	gccagcaagg	300
acaggagggg	gatgacaact	accaaggctg	ataggccaag	ggaggacata	gaggggggtca	360
ggatagctct	tgatgcagcc	aaaaagggtcc	taggaaccat	tgggccacca	gctctgggtct	420
cagaaacttt	ggcctgggaa	atcctcccac	aagcaacgcc	agtttctaag	caacaatctc	480
agggttccat	tggagaaaca	actccagctg	caggcatgtg	gaccttggga	actccagctg	540
cagatgtgtg	gatcttggga	actccagctg	cagatgtgtg	gaccagcatg	gaggcagcat	600
ctggggaagg	aagcgctgca	ggggacctag	atgctgccac	tggagacaga	ggtccccaag	660
caacactgag	ccagaccccg	gcagtatgac	cctggggacc	ccctggg		707

<210> 107
 <211> 485
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(485)
 <223> n = a,t,c or g

<400> 107						
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ctgtgggtatc	acctggagca	actcctggag	ctccaggtag	cagcaccct	ggggaagcag	120
acattggaaa	caccagtttt	ggaaaatcag	ggaccccaac	agtatctgct	gcctcaacta	180
ccagtagccc	tgtgagtaaa	cacaccgatg	cagcctcagc	cacagcagtg	acaatctctg	240
gaagcaaacc	aggtacacct	ggaacaccag	gtggtgcaac	tagtggaggc	aaaattacac	300
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atttcctgt	aaatcctcac	cagaacccat	gtgctgattc	cctgtaatct	tcccacaata	420
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actcg						485

<210> 108
 <211> 565
 <212> DNA
 <213> Homo sapiens

<400> 108						
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tcttgatctt	ccatctttcc	agggcagtga	gcttgctctt	gttctgctg	cagaagttgt	120
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gccgcctccc	caccgaggag	ccagcgtcgc	tctctcctc	tttctcctc	tcccttcccc	480
acctccggtg	cccttctgct	aaaaacctct	ogtttcggct	ctgccactcg	tgaatgatcc	540
tctccacgtc	ctcgtcctcg	accgc				565

<210> 109
 <211> 986
 <212> DNA
 <213> Homo sapiens

<400> 109
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 tgggtggcgtg gtcgacagtg gtgtgtatgc ggtgcctccc ccagctgaac gtgaagcccc 180
 ggcagagggc aagcgctgt cggcctccag caccggcagc acacgcagca gccagtctgc 240
 gtcctccttg gaggtggcag ggcggggccg ggaacccctg gagctggaag ttgctgtgga 300
 ggcctggca cggctgcagc aggggtgtgag cgccaccgtt gccaccttc tggacctggc 360
 aggcagcgcc ggtgcgactg ggagctggcg tagccctct gagccacagg agccgctggg 420
 gcaggacctg caggctgctg tggccgcccgt ccagagtgc gtccacgagc tgttgagatt 480
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 cctcgacgtg ggcgggggag gctctggagc cacccttgag gacctggacc ggctgggtggc 660
 ctgctcgagg gctgtgcccg aggacgcca gcagctggcc tccttcctgc acggcaatgc 720
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 taagttcacc tcccaggact cgccagatgg gcagtacgag aacagcgagg ggggctggat 900
 ggaggactat gactacgtcc accttacagg ggaaggagg agtttttaga agaccagaa 960
 ggagcttctg ggaaaaaggg cagcat 986

<210> 110
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 110
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 aggtaaagcat gggaggaagg aagatggcga cagatgaaga aaatgtctat ggtttagaag 120
 agaacgctca gtcccgagc gagtccacgc ggaggtcat ccttggtggg agaacagggg 180
 ccgggaagag cgccactggg aacagcatcc tgggacagag acggttcttc tccaggctgg 240
 gggccacgtc tgtgaccagg gcctgcacca cgggcagccg cagggtgggac aagtgccacg 300
 tggaagtcgt ggacactccg gacattttca gtcaccaagt gtccaagaca gatcctggct 360
 gtgaggagag aggtcactgc tacctgctct cgcccccg accccacgag ctgg 414

<210> 111
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1)...(419)

<223> n = a,t,c or g

<400> 111

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gctcatcgtc	atcttcattg	gcagcctgtg	cgggctgtgc	accaagtgcg	ctgtgtccaa	180
cgacctcacc	cagcaggaga	tacagacccc	ggagatacaa	cagagaaatg	cataatgtcc	240
agtcaattta	ttaaagttcc	aaagtnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	300
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnatttcaa	tatgattaaa	gcaggagtga	360
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<210> 112

<211> 1191

<212> DNA

<213> Homo sapiens

<400> 112

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gcgcctctcc	ctggggccga	ggcctcctca	ccagcctacc	tggtgctctg	gaaaaaaatc	120
cgtcccccg	actccgtccc	tacccccagt	cttcggcccg	ctctggcccc	tggggagggg	180
gctgcacggg	ggaaggaggc	tggctatggg	cccggctgcc	cgctgcatgt	acctcctcct	240
ccacctatcg	cctcttgcc	gggggtaact	ttgcctgggg	ctcattcttt	ggttaagctg	300
aagctgccgt	gggtggccaa	accgcagatt	ctttgcaa	at	tctgagctgg	360
agccgggagc	cggccgggga	agaggagact	tgcgcgcgcg	aagccgcctg	cctccaccct	420
gctctccatc	tcccgtctca	gaagggtctg	gaagctcgcg	gccgggggtc	cacctggaag	480
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tgagtgttga	tgaaaagcaa	tgcaattatg	ccaaacagta	ttgagcagaa	taattttattt	1020
cttttttttc	ttttgcttta	aatcatgaat	cccgccaggt	acggtggctc	acgcctgtca	1080
tcccagcact	ttgggaggcc	aaggcgggcg	gattacttaa	tacttaaggt	caggagtctg	1140
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<210> 113

<211> 1240

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(1240)

<223> n = a,t,c or g

<400> 113

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gtggtaggat	gcttttcctt	ttaggtcttt	actgaacttt	caagggatta	aaaccaatgt	120
atgtcaactt	tatagcaaaa	gattcagatt	ctaatacctga	ataccaatgc	atttttagagg	180
gggaaaaaat	gagggatgta	aaatatatat	agtagggtaa	gagttttgcc	tttgaacaat	240
gtgcatattc	tattttaatt	tggaaatgttt	tataacttgca	tttcatgtta	tgtagttttt	300
ggactggact	gtgtttttcc	acaaaatgaa	aaatcaacta	ttttgccacc	ttattattca	360
acctacctgc	ccatagtgtg	ctatgccagt	tactaatcta	tttaaattta	ataaatcaaa	420
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<210> 114

<211> 810

<212> DNA

<213> Homo sapiens

<400> 114

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cacgcctcaa	agcggcaaca	gagccgaacc	cctttctcag	gcttcggacg	gcccagaccc	420
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tcagttcccc	tcaggccct	aggaacccta	ctctccagca	gtacagtctg	tagacccccg	540
aatcagttcc	ccactcaacc	tcagaactcc	tctggcgccg	actggcccca	ctcggggcaa	600
ggatggcggt	ggataggatg	acccgaacca	ccagagccag	caaacttacc	ccagccgcca	660
tggtgattcc	gcaaagaaag	ggggtggggg	tctcggcgct	gccgcaaagt	aagcccgccc	720
gggagagaag	ggagggggaa	agaggagagc	cgtggagaaa	cagcagccga	aaaacgagga	780
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<210> 115

<211> 320

<212> DNA

<213> Homo sapiens

<400> 115

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caagaggagg	tgatgatgcg	gccctgtcct	gagtgcaccc	aaccctccc	cagtactaca	120
cctgcagctg	tgctctgggc	ttcattgcct	gctccatctt	cttgagatg	agcctgaagc	180
caaagggtcat	gctgctgaca	gtggccctgg	tgccctgtct	cgtgctcttc	aacctctccc	240
agtgtggca	gcgggactgc	tgagccaag	gcctgggcaa	cctcactgag	cccagtggca	300
ccaacaggta	gggccccgcc					320

<210> 116

<211> 456

<212> DNA

<213> Homo sapiens

<400> 116

ggcaaggcag	gcggcgcggc	cggcctcttc	gccaaagcagg	tgacagaaga	gtttagcagg	60
gcccaggaga	agtagacaag	gcggtttggg	aagacatgtc	agccagaaga	aagagcgagg	120
gaagaaagac	aagaaggacc	tgagatagag	tttgggtttt	cctttttttc	tctctctctt	180
tattaagccc	aacctgcctt	ctacaacgga	gaagttttgg	ttttctaaga	gctgatggac	240
ttagaagcat	ttggatgaac	agctctgctt	accaactgaa	atatccctat	tatcttctaa	300
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tttatcagca	gaaaactgat	ggaatgtaga	tgtagctcct	gactttaaga	gaccacaatg	420
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<210> 117

<211> 2398

<212> DNA

<213> Homo sapiens

<400> 117

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gtccgtccag	ccctctcttc	agccggccca	tccagcggtta	ccacagatga	cctcacaggc	180
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tctcgattcc	cactcagctg	tatctggaaa	tgcccaatcc	tttcagccct	atgcagggtat	300
gcaagcctac	gcttatcccc	aggcatctgc	cgtcacctcc	cagctgcagc	ccgttcggcc	360
tttgtaccca	gcaccgctct	ctcagcctcc	ccatttccaa	ggatcagggtg	atatggcttc	420
atttctcatg	actgaagccc	ggcaacataa	cactgaaatt	cgaatggcag	tcagcaaagt	480
ggctgataaa	atggatcatc	tcatgactaa	gggtgaagag	ttacagaaac	atagtgtctg	540
caattccatg	cttattccta	gcatgtcagt	tacaatggaa	acaagcatga	ttatgagcaa	600
catccagcga	atcattcagg	aaaatgaaa	attgaagcaa	gagatccttg	aaaagagcaa	660
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cacacaggca	agagtattgc	atgctgaaca	agagaaggcc	aaggtgacag	aggagttagc	840
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<210> 118
 <211> 800
 <212> DNA
 <213> Homo sapiens

<400> 118						
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agctaccagt	acacgttggt	atccgacgac	ctggcgccac	tgcgagaatg	ggagccgaaa	180
atccgcaaaa	aactggcgac	gttgcccggaa	ctggcgagc	tgaactccga	tcagcaggat	240
aacggcgcg	agatgaatct	ggtttacgac	cgcgacacca	tggcacggct	gggaatcgac	300
gtacaagccg	ccaacagtct	gttaaataac	gccttcggtc	agcggcaaat	ctcgaccatt	360
taccagccga	tgaaccagta	taaagtgggt	atggaagtgg	atccgcgcta	taccaggagc	420
atcagtgcgc	tggaaaaaat	gttcgttatc	aataacgaag	gcaaagcgat	cccgtgtca	480
tatttcgcta	aatggcaacc	ggcgaatgcc	ccactatcgg	tgaatcatca	gggattatcg	540
gcggccttga	ccatttcgtt	taacctgccg	accggaaaaat	cgctctcgga	cgccagtgcg	600
gcgatcgatc	gcgcaatgag	ccagcttggt	gtgccttcga	cggtgcgcgg	cagttttgcc	660
ggcccggcgc	aggtgttcca	ggagaccatg	aactcgcagg	tgatcctgat	tattgccgcc	720
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<210> 119
 <211> 427
 <212> DNA

<213> Homo sapiens

<400> 119

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aggaaaaatt	tccgctgaaa	gaattaaata	atccagagca	tgacagttac	gcaatcagtg	180
aaaagagtca	cggcagagaa	gaaatccgtc	ttcatattgt	ttgcgatgtc	cctgatgaac	240
ttattgattt	cacgtttgaa	tggaaagggc	tgaagaaatt	atgcgtggca	gtctcctttc	300
ggtccataat	agcagaacaa	aagaaagagc	cagaaatgac	ggtcagatac	aatatcagtt	360
agttgggtat	cgccggggat	atatcagtc	cagcgatctc	cgggacggac	gattgaatct	420
cgtaatc						427

<210> 120

<211> 378

<212> DNA

<213> Homo sapiens

<400> 120

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cttccccggc	tatcgatttt	tacacgcctt	gcgtaaagcg	gcacggcgcg	gggtgcggat	120
caaactgac	attcaggggc	aaccggatat	gccgattgtc	agagtcgggtg	cgcgcttgct	180
gtataactat	ctggttaaag	gcggcggtca	ggttttttgag	taccgcccgc	gcccgcctcca	240
cggcaaaagt	gcattgatgg	acgatcactg	ggcgacagta	gggtccagta	atctccatcc	300
ggtcagttag	tcgggggaatc	tccaagcaaa	tgtcatcctc	cacgttctac	gggtaccgac	360
attgaatccg	taatcatg					378

<210> 121

<211> 508

<212> DNA

<213> Homo sapiens

<400> 121

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aataacatac	tcgttaattg	ctcaatccag	ccacaacgcg	agaactgacc	agtctgggac	120
gaaacctgaa	ccgattgtta	aaaagtgaac	gcgaacgtta	cgacaaatac	cgtacgacgc	180
tcaccgacct	gacctatagt	ctgaaaacgc	cactggcggt	gctgcaaagt	acgctgcgtt	240
ctctgcgtag	tgaaaagatg	agcgtcagtg	atgctgagcc	ggtaatgctg	gagcaaatca	300
gccgcatttc	acagcaaat	ggctactacc	tgcctcgtgc	cagtatgcgc	ggcgggacat	360
tgctcagccg	cgagctgcat	ccggctcgccc	cactgctgga	caatctcacc	tcagcgctga	420
tcaaaggcaa	gccgcgtaaa	gggggcaacg	tactgtttt	tccattcaca	gcgatgtaca	480
gggacggaca	ttgaatccgt	gatcagtg				508

<210> 122
 <211> 724
 <212> DNA
 <213> Homo sapiens

<400> 122
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 tggaccactg acctcgactc tctatgacct cacagagatc gactcctcag gggatgagca 120
 gtccctgctg gaacttatca tcaccaccaa gaagcggggag gctcgccaga tcctggacca 180
 gacgccggtg aaggagctgg tgagcctcaa gtggaagcgg tacggggcggc cgtacttctg 240
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 cccctcaag ccaggacca ataaccgcac gagcccccg gacaacaccc tcttacagca 360
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 ggtgactgtc attggggcta tcatcatcct gctggtagag gttccagaca tcttcagaat 480
 gggggtcact cgcttctttg gacagaccat ccttgggggc ccattccatg tcctcatcat 540
 cacctatgcc ttcattggtgc tggtagccat ggtgatgcgg ctcatcagtg ccagcgggga 600
 ggtggtaccc atgtcctttg cactcgtgct gggctgggtgc aacgtcatgt acttcgccccg 660
 aggattccag atgctaggcc ccttcaccat catgattcag aagatgattt ttggcgacct 720
 gatg 724

<210> 123
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 123
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 tttagtctg tatttttaaaa tcttggtgat cttcacatta ttacatttaa tttcagggtga 180
 atataattta aggagaatcc aactagtag tagtactatg gacctcttga gcttgcctgat 240
 atgcctgtgt gtctctatgt atgttttgcc tcctgctgcc agtatatgtg tgtttgaaat 300
 taacatagaa ttaaattaac tagattagag tagacattgg caagttgtaa ttgccagttg 360
 agcatttatt tgaaaaactg tattcacaag tcctactaaa ttctgtgttg atttttagctt 420
 gaaatgttct caaaa 435

<210> 124
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 124
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cctcctcaga	acatgctgct	tgaggaatt	caacatcatg	gaaaagaata	aaggatgggc	120
tctcctggga	ggaaaagatg	gccatcttca	gggactatth	ctccttgcca	acgcattgct	180
ggaaagaaat	cagctccttg	cacagaagg	catgtactta	ttagtccctc	ttcttaaccg	240
agggaatgat	aaacataaac	tcacatctgc	aggctthttt	gtggagcttc	tccggagtcc	300
agtggccaag	agactgcccc	gcataactc	tgthgcccc	tttaaagact	ggctacaaga	360
tgg						363

<210> 125
 <211> 373
 <212> DNA
 <213> Homo sapiens

<400> 125						
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tcgggggatg	gcgaagcgaa	gagtgcggcg	tcgggtgtgg	gggggagcag	gaggaggac	120
gaagtccgcc	cgccgcgccc	ccgcccgcgc	tgacaccgag	cggagcgagg	aaggaggacg	180
agcgggtgaag	gaagcctacc	cttccagccg	tcagccgcgc	ccgcccgcgc	cgtgaccct	240
gcgttgccgc	cgccgctgcc	acccgaactt	agccccctcg	atgccaatth	caaataggga	300
aggaaaaggg	aaaagaaggg	aagagaaaa	ccggccgctg	agtcccgcgt	ccactcacac	360
ctccgctcgt	gcc					373

<210> 126
 <211> 362
 <212> DNA
 <213> Homo sapiens

<400> 126						
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acccctaga	gtactgcagc	cctaaagggg	atccccagcg	agtggacatg	cagcctagtg	120
tgacctctcg	gcctcgttcc	ttggactcgg	agggtgccac	aggggaaacc	caggthttcca	180
gccatgtcca	ctaccaccgc	caccggcacc	accactacaa	aaagcggthc	cagaggcatg	240
gcaggaagcc	tggcccagaa	accggagtcc	cccagtcacg	gcctcctatt	cctcggacac	300
agccccagcc	agagccacct	tctcctgatc	agcaagtcac	cagatccaac	tcagcagccc	360
ct						362

<210> 127
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 127

catggctgac	cccgaccccc	ggtaccctcg	ctcctcgatc	gaggacgact	tcaactatgg	60
cagcagcgag	gcctccgaca	ccgtgcacat	tcgaatggcc	tttctgagaa	gagtctacag	120
cattctatct	ctgcaggatc	tcttagctac	tgtgacttcg	acagataatt	tagcctttga	180
ggatggacgg	actgactggc	tgcaaaggcc	tgactgtgtc	tccttcaaaa	ttcatgtgct	240
gccaatgtga	cgggtattaag	aggagggggc	ttagaggggg	attagatcct	gaaagggtcct	300
tacttttttg	agtgacgagg	atgcatacga	tgaaagcatc	tcgtagatac	g	351

<210> 128

<211> 374

<212> DNA

<213> Homo sapiens

<400> 128

gaactcccca	aaggcaccat	ccagggttttt	accccgcttg	tcaaattccc	ctctggccca	60
gggctggctg	ctcagcagga	gtgtttaata	agcacttaat	tgcccgggtga	gtacagacca	120
ttccagctca	ccttaactgt	ttcctggctg	actcgcctct	cggcctgatt	gccctgctca	180
tctggctgag	tgagctggaa	tgagtgtagt	ggtagtgcc	cctatagggt	cctcttacct	240
tggtcttatt	tcacaggagc	acttcccga	cgagtttacc	tcgggagatg	gaaagaaagc	300
tcaccaggac	tttggctact	tttatggctc	gagctatgtg	gcagcctctg	acagcagccg	360
gactcctggg	ctgt					374

<210> 129

<211> 392

<212> DNA

<213> Homo sapiens

<400> 129

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ggtcagaggt	cagacaggtc	atcaggaatt	ttgcttcaag	tgagttgctg	ctgccctgac	120
tcttttcccc	cagcaattaa	gtccccccgg	ggcttggggg	ttgggtttgt	cagcttgctt	180
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tctctctagg	accaactgcc	cctgtaagta	cagttttttg	gataacctca	agaagttgac	300
tcctcgacgc	gatgttccca	cttaccctaa	ggtaagatga	gattccggcc	cagaagaagc	360
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<210> 130

<211> 359

<212> DNA

<213> Homo sapiens

<400> 130

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caccaatgcc	caggaccagc	cggtgacct	ggggactttg	gggaccaact	ttggccgctg	120
tgtggacctc	tttgccccag	gggaggacat	cattggagcc	tccagcgact	gcagcacctg	180
ctttgtgtca	cagagtggga	catcacaggc	tgctgcccac	gtggctggca	ttgcagccat	240
gatgctgtct	gccgagccgg	agctcacccct	ggccgagttg	aggcagagac	tgatccactt	300
ctctgccaaa	gatgtcatca	atgaggcctg	gttccctgag	gaccagcggg	tactgacct	359

<210> 131

<211> 389

<212> DNA

<213> Homo sapiens

<400> 131

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aattcggcat	ctgttgcccc	aatggattga	aatcaagac	tggtaggatc	aaacatattt	120
tccctagaag	ttgatgcaca	aatgtctgat	gctctatcca	tgtgaattta	ttttatggtc	180
cactttttac	tcagtagatg	cattcttttc	aggtaaagaa	ctttctcaag	gatttgaaa	240
ccttcccaaa	gaaggggaat	aattgtcctt	tctggttcca	ttcattgtaa	atgaaaagtt	300
aatggttcca	gtgcttcttt	tctctgtaaa	caaaaaccca	aataattttt	catgtattaa	360
aaaaagaagc	aaatcaattg	attgtcagt				389

<210> 132

<211> 465

<212> DNA

<213> Homo sapiens

<400> 132

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ggggcccgtg	gaagcggaag	agcctcctca	ggaggatagt	agcagtcagt	cagactctgt	120
ggaggaccgg	agtgaggatg	aggaagatga	acattcagag	gaggaagaaa	caagtggaag	180
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gcagagttag	gcagatgcag	gcagtggggc	tctactcca	gggcccacta	ctctaggtcc	360
aaagaaagaa	attactgaca	ttgctgcagc	agctgaaagt	ctccagccca	agggttacac	420
gctggccacg	accaggttaa	agacgcccat	tcccctgctt	ctgcg		465

<210> 133

<211> 354

<212> DNA

<213> Homo sapiens

<400> 133

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ttgccagagt	ctttgacaga	acttagtcta	attcaaacca	atatatacaa	cataactaaa	120
gagggcattt	caagacttat	aaacttgaaa	aatctctatt	tggcctggaa	ctgctatttt	180
aacaaagttt	gcgagaaaac	taacatagaa	gatggagtat	ttgaaacgct	gacaaatttg	240
gagttgctat	cactatcttt	caattctctt	tcacacgtgc	cacccaaact	gccaagctcc	300
ctacgcaaac	tttttctgag	caacacccag	atcaaataca	ttagtgaaga	agat	354

<210> 134

<211> 326

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(326)

<223> n = a,t,c or g

<400> 134

cccacgcgtc	cggngacagg	cctggccggc	ctctgcagag	acgtccaacc	tcgtgcgcat	60
gcgcagccag	gccctgggcc	agtccggccc	ctcgtccacc	gccagcctga	aggagctgag	120
tctccccaga	agaggaagtt	tccctgtgtg	tccaaatgct	gggagaacat	cacccttgg	180
atgaattgcc	accacattaa	ataaaatata	tccaaagctc	nnnnnnnnnn	nnnnngggggg	240
gccgttttaa	aggacccttg	ggggggccaa	ggtttacgcg	ggctggcaag	gtaatagttt	300
tttccttata	gggagccgaa	ttaaaa				326

<210> 135

<211> 210

<212> DNA

<213> Homo sapiens

<400> 135

cttctgtgtg	tctgtcttcc	tgtgggtgcc	tgcccgctct	tttctcttct	aacagccctt	60
ttgaaccagc	tgatgcgctg	tcttcggaaa	taccaatccc	ggactcccag	tccctctcta	120
cattctgtcc	ccagtgaat	agtgtttgat	tttgagcctg	gccagtggt	cagaggtagt	180
tgggctcttc	tttcttggtc	gacgcggccg				210

<210> 136

<211> 310

<212> DNA

<213> Homo sapiens

<400> 136

tttttccaat	acacatatataa	accatcattc	actaaaatgt	actatatatt	caatattttg	60
tgtataactca	ctgcttttcc	taacgtgaaa	aattttaccaa	aatgctaatt	gtgacttata	120
aggtatttta	cagactcccg	acaaaaagca	gaatgatcag	cgaaatcgga	aaagaaaagc	180
tgaaccatat	gaaactagcc	aaggtagtaa	taatttcgta	tcaacaaaag	tactcaattc	240
taatgtactt	agatagaatt	ttctaactca	tactaaataa	ttagtttgta	cacagggatt	300
cctgataaag						310

<210> 137

<211> 502

<212> DNA

<213> Homo sapiens

<400> 137

cttaaagtga	aattttaaaaa	gtaataataa	tttttaaaaa	tgtttaaaagg	cttacttttg	60
agagacagtt	ttacatagct	taatatTTTta	tcatttaaagg	catgggtggag	ctggttcctg	120
cttccgatac	cctcaggaaa	atccaagtgg	aatatgggtg	gacaggatcc	tttaaagata	180
aaccacttgc	agagtggcta	aggaaataca	atccctctga	agaagaatat	gaaaaggctt	240
cagagaactt	tatctattcc	tgtgctggat	gctgtgtagc	cacctatgtt	ttaggcatct	300
gtgatcgaca	caatgacaat	ataatgcttc	gaagcacggg	acacatgttt	cacattgact	360
ttggaaagtt	tttgggacat	gcacagatgt	ttggcagctt	caaaagggat	cgggctcctt	420
ttgtgctgac	ctctgatatg	gcatatgtca	ttaatggggg	tgaaaagccc	accattcgtt	480
ttcagttggt	tgtggacctc	tg				502

<210> 138

<211> 963

<212> DNA

<213> Homo sapiens

<400> 138

ctcctagtcc	cctccctagc	ctgtcccttc	ctcctcccgt	tgctcctggg	ggccaggaga	60
gcccttcacc	ccacacagct	gaggtggaga	gtgaggcctc	accacctcct	gtcgggcccc	120
tcccagggga	agccaggctg	gcgcccattc	ctgaagaggg	aaagccgcag	cttggtgggc	180
gtttcccaag	tgacttcatc	caaggaaacc	gctgagcctc	ttcccttgca	gccaacatcc	240
cccactctct	ctggttctcc	aaaaccttca	acccctcagc	tcacttcaga	gagctcagat	300
acagaggaca	gtgctggagg	cgggccagag	accaggggaag	ctctggctga	gagcgaccgt	360
gcagctgagg	gtctgggggc	tggagttgag	gaggaaggag	atgatgggaa	ggaaccccaa	420
gttgggggca	gcccccaacc	cctgagccat	cccagcccag	tgtggatgaa	ctactcctac	480
agcagcctgt	gtttgagcag	cgaggagtca	gaaagcagtg	gggaagatga	ggagttcttg	540
ctgagctgc	agagtcttcg	gcagaagcac	ttgtcagagg	tggaaacact	acagacacta	600
cagaaaaaag	aaattgaaga	tttgtacagc	cggctgggga	agcagccccc	accgggtatt	660
gtggccccag	ctgctatgct	gtccagccgc	cagcgccgcc	tctccaaggg	cagcttcccc	720
acctcccgcc	gcaacagcct	acagcgctct	gagccccag	gccctggtga	gactgcagtc	780

accagcttc	catcttttcc	ctgagacccc	tttctgtcga	ctgtttttct	ccagggccctg	840
ggggtctgcc	ccgggggaat	agaccccctc	tccccacctc	ccctttcctc	acttagtgct	900
ctccttcccc	catcctggct	ccaggcatca	tgcgaaggaa	ctctctgagt	ggcagcagca	960
ccg						963

<210> 139

<211> 376

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(376)

<223> n = a,t,c or g

<400> 139

cgcgcgtttg	tttctcaaga	gactgggaat	ctgtatatgt	ccaaagtaga	aaaatcagat	60
gttgggaatt	atacctgtgt	ggttaccaat	accgtgacaa	accacaaggt	cctggggcca	120
cctacaccac	taatattgag	aatgatgga	gtgatgggtg	aatatgagcc	caaaatagaa	180
gtgcagttcc	cagaaacagt	tccgactgca	aaaggagcaa	cggatgaagct	ggaatgcttt	240
gctttaggaa	atccagtacc	aactattatc	tggcgaagag	ctgatggaaa	gccaatagca	300
aggaaagcca	gaagacacaa	gtcaagagtg	gggaaanntc	ttgagaaatc	ccttaatttt	360
tcagcagggg	ggatgc					376

<210> 140

<211> 968

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(968)

<223> n = a,t,c or g

<400> 140

gcaaggggca	gttgggtgaac	ttgctgcctc	cagagaatth	tccctgggtg	ggaggcagcc	60
agggacccag	gatgctccgg	acctgttacg	tgctctgttc	ccaagctggg	ccccgcctca	120
ggggctggca	gtccctgagc	tttgatggcg	gggccttcca	ccttaagggc	acaggagagc	180
tgacacgggc	cttgcctggt	ctccggctgt	gtgcctggcc	cccactcgtc	actcacgggc	240
tggtgtctca	ggcctgggtc	cggcgactcc	tgggctcccc	gctctcaggc	gcattttctcc	300
gagcatccgt	ctatgggcag	tttgtggctg	gtgagacagc	agaggaggtg	aagggtgcg	360
tgcagcagct	gcggaccctc	agcctccgac	caactgctggc	agtgcctcct	gaggaggagc	420
cggactctgc	tgccaagagt	ggtgaggcgt	ggtatgaggg	gaacctcggt	gctatgctgc	480
ggtgtgtgga	cctgtcacgg	ggcctcctgg	agccccccag	cctggctgag	gccagcctca	540
tgcagctgaa	ggtgacggcg	ctgaccagta	ctcggctctg	taaggagcta	gcctcgtggg	600
tcagaaggcc	aggagcctcc	ttggagctga	gccccgagag	gctggctgaa	gctatggact	660
ctgggcagaa	cctccaggtc	tcctgcctca	atgctgagca	gaaccagcac	ctccgggcct	720
ccctcagccg	cctgcacctg	gtggcacagt	atgcccgggc	ccagcacgtg	cggctcctgg	780

tgatgcgga	gtacacctca	ctgaaccctg	cgctctcgct	gctgggtggct	gccctggctg	840
tgcgctggaa	cagcccgggt	gaaggcgggc	cctgggtgtg	gaacacctac	caggcctgtc	900
taaaggacac	attctagcgg	ctggggaggg	atgcanaggc	tgcgcacagg	gccggcctgg	960
ccttcggg						968

<210> 141
 <211> 306
 <212> DNA
 <213> Homo sapiens

<400> 141						
agacggctga	aaagggaggg	gtattgaggg	cggttcagag	ggcgaggaga	ggggcgtaga	60
gaacctgtgg	agaagaagtt	cactggaggg	gcattaggcc	tcgcactatg	tatccagatc	120
atcagtaggg	gaagagaaaa	gatgggcaat	atgtatagtc	agacgagaag	tgggatcaaa	180
cagagggctc	atggagaagt	aggctaccca	ccacataacc	ccatcatagg	attgcaggag	240
atacagctat	agataagaat	atccaccagt	cggtgagtga	gcagatcaag	aagaactttg	300
ccaaga						306

<210> 142
 <211> 316
 <212> DNA
 <213> Homo sapiens

<400> 142						
ccacactcac	atttaatat	ctgttaggtt	gtttactttg	aggcaatgtc	atcctcatta	60
gtatagggca	ttatatctct	gaatagcaga	atactcctcc	attcatgaag	ttcagtatta	120
tacattctta	ttattgcaca	acaaatagaa	gactttggat	ttccttatat	aagtaccttg	180
acagatgact	aaccattttt	tcctatgctt	tacaactatg	atcagtaact	gtaatttttt	240
taaaggtoct	cctggacccc	cggtgaaaa	aggagatcga	ggtccactg	gagaaagtgg	300
tccacgagga	tttcca					316

<210> 143
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 143						
gacaatacca	aatgaatgaa	cgtgactgtg	ttccaacaaa	actttattta	caaaaacagg	60
gatgggcccg	atgtagccag	aggccataat	ttgccaaccc	ctgatttaga	cgaaggaaag	120
gagcagtgtc	tcactgcttt	taaattaatt	ctgtattctc	acaaggccta	cattgaaatg	180

gaattatagc	ctcatttttt	cttagaacct	ttatatatttg	ttttatttcat	atacagggtt	240
gtcaagctgg	acagactatt	aaagttcaag	tctcctttga	tttgcttagt	ctgatgttta	300
catttgtaag	tccatgtacc	aacgatttaa	tcatacacg			339

<210> 144
 <211> 2018
 <212> DNA
 <213> Homo sapiens

<400> 144

acaagttatc	tgtgaatcat	aggagaacac	atcttacaaa	actcatgcac	actgttgaac	60
aagctacttt	aaggatatcc	cagagcttcc	aaaagaccac	agagtttgat	acaaattcaa	120
cggatatagc	tctcaaagtt	ttcttttttg	attcatataa	catgaaacat	attcatcctc	180
atatgaatat	ggatggagac	tacataaata	tatttccaaa	gagaaaagct	gcataatgatt	240
caaatggcaa	tgttgcagtt	gcatttttat	attataagag	tattggctct	ttgctttcat	300
catctgacaa	cttcttattg	aaacctcaaa	attatgataa	ttctgaagag	gaggaaagag	360
tcatatcttc	agtaatttca	gtctcaatga	gctcaaacc	accacatta	tatgaacttg	420
aaaaaataac	atttacatta	agtcacgaa	aggtcacaga	taggtatagg	agtctatgtg	480
cattttggaa	ttactcacct	gataccatga	atggcagctg	gtcttcagag	ggctgtgagc	540
tgacatactc	aaatgagacc	cacacctcat	gccgctgtaa	tcacctgaca	cattttgcaa	600
ttttgatgtc	ctctggctct	tccattggta	ttaaagatta	taatattctt	acaaggatca	660
ctcaactagg	aataattatt	tcactgattt	gtcttgccat	atgcattttt	accttctggg	720
tcttcagtga	aattcaaagc	accaggacaa	caattcacaa	aaatctttgc	tgtagcctat	780
ttcttgctga	acttggtttt	cttggtggga	tcaatacaaa	tactaataag	ctcttctgtt	840
caatcattgc	cggactgcta	cactacttct	ttttagctgc	ttttgcatgg	atgtgcattg	900
aaggcataca	tctctatctc	attgttggtg	gtgtcatcta	caacaaggga	tttttgaca	960
agaattttta	tatctttggc	tatctaagcc	cagccgtggg	agttggattt	tcggcagcac	1020
taggatacag	atattatggc	acaaccaaa	tatgttggct	tagcaccgaa	aacaacttta	1080
tttggaagtt	tataggacca	gcatacctaa	tcattcttgt	taatctcttg	gcttttggag	1140
tcacatata	caaagttttt	cgtcacactg	cagggttgaa	accagaagtt	agttgctttg	1200
agaacataag	gtcttggtga	agaggagccc	tcgctcttct	gttccttctc	ggcaccacct	1260
ggatcttttg	ggttctccat	gttggtgcag	catcagtggt	tacagcttac	ctcttcacag	1320
tcagcaatgc	tttccagggg	atgttcattt	ttttattcct	gtgtgtttta	tctagaaaga	1380
ttcaagaaga	atattacaga	ttgttcaaaa	atgtccctctg	ttgttttggg	tgtttaaggt	1440
aaacatagag	aatgggtgat	aattacaact	gcacaaaaat	aaaaattcca	agctgtggat	1500
gaccaatgta	taaaaatgac	tcacaaatt	atccaattat	taactactag	acaaaaagta	1560
ttttaaatca	gtttttctgt	ttatgctata	ggaactgtag	ataataaggt	aaaattatgt	1620
atcatataga	tatactatgt	ttttctatgt	gaaataggtc	ctgtccaaaa	atagtattgg	1680
ccagatattt	gggaaaagta	aattgggttt	cctcagggag	tgatatcccc	ttgcacccaa	1740
gggaaaagat	tttcttttcta	acacgagaag	tatatgaatg	tcctgaaggg	aaacctggg	1800
ccttgatatt	tctgtgactc	gtgtgcctt	tgaaactagt	cccctaccac	ctcggtaatg	1860
agctccatta	cagaaagtgg	aacataagag	aatgaagggg	cagaatatca	aacagtgaaa	1920
agggaatgat	aagatgtatt	ttgaatgaac	tgttttttct	gtagactagc	tgagaaattg	1980
ttgacataaa	ataaagaatt	gaagaaacaa	aaaaaaaa			2018

<210> 145
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 145
 ggacgaggg aagctgcccc gtccagggtc atgttcctct tattttctct cactgtgtgag 60
 ctggctgcag aagttgctgc agaagttgag aaatcctcag atggctctgg tgctgcccag 120
 gaacccacgt ggctcacaga tgtcccagct gccatggaat tcattgctgc cactgagggtg 180
 gctgtcatag gcttcttcca ggatttagaa ataccagcag tgcccatact ccatagcatg 240
 gtgcaaaaat tcccaggcgt gtcatttggg atcagcactg attctgaggt tctgacacac 300
 tacaacatca ctgggaacac catctgcctc tttcgctgg tagacaatga acaactgaat 360
 ttagaggacg aagacattga aagcattgat gccaccaa at tgagccgttt cattgagatc 420
 aacagcctc 429

<210> 146
 <211> 717
 <212> DNA
 <213> Homo sapiens

<400> 146
 gatgaaactt ccggtctcat tgtccgggaa gtgagcattg agatttcgcg ccagcaagtg 60
 gaagaactct ttggacctga agattactgg tgccagtgtg tggcctggag ctccagcgggt 120
 accacaaaga gccggaaggc gtatgtgcgc attgcatagg aactcatgac ctgacatcca 180
 ttagcagagt catcagagtc atctggctgc tgtgttgaga atggaccatg ctgggcaagg 240
 ggagaagcag gaagaccagt gatgagactg cagctatgag agatgttaag ctactgtaga 300
 ttggaagcag tggaggtggg gaggccagga tttcagatat atttaaaagt agagataaca 360
 gcttttgttg agaccttggg tgtgtgatgt gagagaaaga agagaaagga tgattttgaa 420
 agggcctaag cctttatcca aggatttctt tcaaatgtct ttagtgaagc cattcctgcc 480
 tcacagaggg aggaggctgg gcattccttt ctcaatactt tcagagcagt ttgtccatac 540
 ccctaataata gtgcttgtct catttcgaat tatattcact cgtaaaattt gtgtttcatg 600
 ccagtgaagt ccatgagatc aagaattcta ttgtacttaa ttttataatc ctctgtctta 660
 gcacaatacc tagagtatca cagatgttta acaattttct tgaattaaaa ctgttat 717

<210> 147
 <211> 367
 <212> DNA
 <213> Homo sapiens

<400> 147
 ggacgagat cgattcatgt aaagctggac gtgggcaagc tgcacaccca gcctaagtta 60
 gcggcccagc tcaggatggg ggacgacggc tctgggaagg tggagggcct acctgggatt 120
 tgaccagagt ccgcctggct ccaggctctg ccacccacag gaagaagaaa ctacactgac 180
 agatgtgaga cagtgtttcc ccttcagtct ttgaacaggc tttgtgtttt ctaaatgaca 240
 ctggataaaa ggggaattcat tcaagagctc caaggcttcc ctttcgccc ggcttctgtt 300
 gccctggcct gagcagcgag cagctgggag gggactgaac tgcccctaac cagggttgtg 360
 gctggcg 367

<210> 148
 <211> 791
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1) ... (791)
 <223> n = a,t,c or g

<400> 148
 cgagaccga ccctgggctg ggtgcatcga ggtagatgca aagatgctgg ccagagcaag 60
 tgtcgcttgg agcgggctca agccctggag caagccaaga agcctcagga agctgtgttt 120
 gtcccagagt gtggcgagga tggctccttt acccagggtgc agtgccatac ttacactggg 180
 tactgtctgt gtgtcacccc ggatgggaag cccatcagtg gctcttctgt gcagaataaa 240
 actcctgtat gttcaggttc agtcaccgac aagcccttga gccagggtaa ctcaggaagg 300
 aaagatgacg ggtctaagcc gacacccacg atggagaccc agcgggtgtt cgatggagat 360
 gaaatcacag cccaactct atggattaaa cacttggtga tcaaggactc caaactgaac 420
 aacaccaaca taagaaattc agagaaagtc tattcgtgtg accaggagag gcagagtgcc 480
 ctggaagagg cccagcagaa tccccgtgag ggtattgtca tccctgaatg tgcccctggg 540
 ggactctata agccagtgc atgccaccag tccactggct actgctgggtg tgtgctgggtg 600
 gacacagggc gcccgctgcc tgggacctcc acacgctacg tgatgcccag ttgtgagagc 660
 gacgccaggc ccaagactac agaggcggat gaccccttca aggacagga gctaccaggc 720
 tgtccagaag ggaagaaaat ggagtttatc accagcctac tggatgctct caccactgac 780
 atggntcagg g 791

<210> 149
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 149
 ggacagagca aactcggggc tcagcttggg gacgggagtt gatagtcagg tgcctggaac 60
 ataattggaga ccgtccatat tggttgaatg agtggatgaa tgaattaatg aatttctttt 120
 ctcttaagtc ctgcagctga ttaagtcaca gaaatttctg aataagttgg tgatcttggg 180
 ggaaacggag aaggagaaga tcctgcgga ggaatatgtt tttgctgact ccaaagtaag 240
 tgacagcaaa cttctaaagt gggctgtgag gtagggaggg gacacaagcg ttttgaggct 300
 cgctgtgtgc caggagtggt atcattagct cactc 335

<210> 150
 <211> 1293
 <212> DNA
 <213> Homo sapiens

<400> 150

cgacgcctgt	ccctcttaga	cttgacgctc	ggtcctcttg	gcagagaccc	cccgcaggag	60
tgcagcacct	tctccccaac	agacagcggg	gaggagccgg	ggcagctctc	ccctggcggtg	120
cagttccagc	ggcggcagaa	ccagcgcgcg	ttctccatgg	aggacgtcag	caagaggctc	180
tctctgcca	tggatatccg	cctgccccag	gaattcctac	agaagctaca	gatggagagc	240
ccagatctgc	ccaagccgct	cagccgcatg	tcccgcgggg	cctccctgtc	agacattggc	300
tttgggaaac	tggaaacata	cgtgaaactg	gacaaactgg	gagagggcac	ctatgccaca	360
gtcttcaaag	ggcgcagcaa	actgacggag	aaccttgtgg	ccctgaaaga	gatccggctg	420
gagcacgagg	agggagcgcc	ctgcactgcc	atccgagagg	tgtctctgct	gaagaacctg	480
aagcacgcca	atattgtgac	cctgcatgac	ctcatccaca	cagatcggtc	cctcaccttg	540
gtgtttgagt	acctggacag	tgacctgaag	cagtatctgg	accactgtgg	gaacctcatg	600
agcatgcaca	acgtcaaggt	gaggcctcgg	gggcagggtc	ccccatctt	ggcagccacc	660
tgtccagaag	cccagtgtgg	ggacccactc	tcaccaccag	ggatccggct	gctgaggtgg	720
ctcaaacctt	cccacgtagg	aaagagggag	agggcaatgc	catcaacgag	tccaggaact	780
gggttgagcg	ctttacccca	agaacagaca	cacactgtct	gccactgtct	agctgttggg	840
ataaaaccca	ctctcaactc	tgaacatcag	tttcccagtc	tgtcaaattg	gagtgtgagc	900
tacctgccaa	aatgcaggga	ggcttctggg	gaagctcggg	gttatgaatg	acctctcctg	960
gtgtttgtta	agaatcaag	actgggcatg	gtggcccacg	cctgtaatcc	cagcactggg	1020
aggccaaggc	aggaagatgg	cttgagccca	ggagtgttgg	accagcctgg	gcaacatggc	1080
aagacctcat	ctctactaaa	aattgaaaaa	ttagccgggc	acagtagcgt	gcacccatag	1140
tcccagctgc	ttgagaggct	gaggcaggag	ggccacttga	gcccgggagg	ttgaggctgc	1200
agtgaagcat	gatcacacca	ctgcactcca	gcatgggtga	cagagtaaaa	ccttgacatg	1260
tattgcgggc	gctctagagg	ataacaagca	tac			1293

<210> 151
 <211> 349
 <212> DNA
 <213> Homo sapiens

<400> 151

ggcacgagcg	gcacgagcct	tctcctactg	cattagcatt	tggggaccac	cctattgtac	60
aaccaaagca	attatccttt	aaaattattc	aggtaaata	taattaaaat	gtttttttct	120
atggcttcta	agaaaccatt	gactaactta	ctaacaacta	agatgtctgt	ttgttttata	180
tgtagtcata	aagcagaatt	acacatcaag	aaagataact	tactaaacaa	aaacaacaga	240
atttgtagga	aggagtgaga	aactgaaaca	cacaatttac	tatcagcttt	ttaaacaacc	300
gttaacatgt	cagttctgtt	tactgattct	ttctgaactt	aatttccag		349

<210> 152
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 152

ggcacgagga	ccttccttgc	tttcagaatt	tcacccaggg	tctgacaggc	ctcaagaaag	60
gagaactagt	tatgaaccga	ttcatccagg	cccatcccca	gtggatcatg	attcactgga	120
atcgaagcga	ccacgtctgg	aacaggcttc	tgattctcat	tatcagggtc	acatcactgg	180
cgaatcccta	ccaggacgtg	tacactagca	gctcctcact	gtggaatctg	atgggcaatg	240

ccatggtgat	tacccactat	atccgtctta	ccccatatgt	tcaaagtaaa	ctcggttccc	300
tagggaacct	gatgccatgt	tacc				324

<210> 153
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 153						
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atcacagtta	atattttattg	agagttttaa	tatgtgcccc	cagattagat	tacctatttt	180
acatacggtg	ttttaatttt	caaaacattc	ctgtgagatc	agctctattt	tcactattac	240
tttgccaagt	attttcacat	gtactttattt	cactgctatt	ctctacaata	gtcttgtgac	300
attgagaaag	gcaggtctgt	tctttgtaaa	atgaaaatca	tttaatatct	gattttaaagt	360
aactgtcgaa	ctactat					377

<210> 154
 <211> 1224
 <212> DNA
 <213> Homo sapiens

<400> 154						
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acaatggccc	cgtgatgcag	gcaggcaggc	gagtgggggt	ctccccctct	tatccacagg	180
gccaccgaaa	ggcccacgag	acggccttgc	ccgaggtcac	ccagcggagt	ggcttgctgg	240
gagccctggg	aataacagtc	ccacacaagg	ctctctccct	ccgcagctgg	acctgtacgc	300
gggggctctg	tttgtgcaca	tctgcctggg	ctggaacttc	tacctctcca	ccatcctcac	360
gctcggcatc	acagccctgt	acaccatcgc	aggatatggtg	cctgcagcag	ggaggtccac	420
ccaggggacg	tgtaaagggg	tcagaaggcc	acctccccct	acaggcccga	gggagcagcc	480
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taagcagagc	caggagctcg	tgcc				1224

<210> 155
 <211> 345
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(345)
 <223> n = a,t,c or g

<400> 155
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 aatcacagtc ttcaagagac ttctgagcaa aacgttattc tacagcatac tcttcagcaa 120
 cagcagcaaa tgttacaaca agagacaatt agaaatggag agctagaaga tactcaaact 180
 aaacttgaaa aacaggtgtc aaaactggaa caagaacttc aaaaacaaag ggaaagttca 240
 gctgaaaagt tgagaaaaat ggaggagaaa tgtgaatcag ctgcacatga agcagatttg 300
 aaaaggcaaa aagtgattga gcttactggc actgccaggc aagtn 345

<210> 156
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 156
 ggcacgagct tctacttgta caggaaaggt tacttgagtt tgtccaaagt ggtgccgttt 60
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 gtcgctggg cctacccccca cttcccgcag tttctcgcca tctcctctcc gatccatctc 180
 tacctgacgt cataactcta tatgcatgtt atgcgggtcca tcttagtctt ctaaaaaggc 240
 catttttagct tacctgccat caagctatac atgtggaaat atacactgta ttattttccc 300
 tttccaggtg attacttacc tcactctgttc ttatatctgc 340

<210> 157
 <211> 478
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(478)
 <223> n = a,t,c or g

<400> 157
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gagcctgcac	ctgaccccc	ggggcctcat	ttcctccggc	aggagcgag	cttcgagtgc	180
cgcattgtgcg	gcaaggcctt	caagcgctcg	tccacgctgt	ccaccacct	gctcatccac	240
tcagacacgc	ggcctaccc	ctgccagttc	tggggcaagc	gtttccacca	gaagtccgac	300
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aaggccttca	gccagagctc	caacctcatc	acccacagac	tcagagagaa	cccaccatgg	420
tgctgtctcc	tgccgacaag	accaacgtca	aggccgcctg	gngtaagggt	cgcgcgca	478

<210> 158
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 158						
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aagtggcagc	cagcaccgca	ccaagtctgt	ttgggcagca	gactgggtatc	acagccagca	120
cagcagttgc	cactccacag	gtaatcagct	caaggttcat	taatctagat	ttttagtata	180
tagtattatt	gaatatatat	aatgttttat	atattagact	ttatacttga	gacataggaa	240
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tttattaatg	aattatatct	aattatgtga	ca			332

<210> 159
 <211> 868
 <212> DNA
 <213> Homo sapiens

<400> 159						
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aactgcatac	aagttataaa	gtttaataat	ctttatcatc	ttggaaaata	aatctcttct	180
tgctaagtat	cagtttttaa	aaattgcccc	atgtattaga	tatgtatttt	tttaacaaaa	240
atgttctgtg	tattaattat	tttgaaataa	attttaagtt	cacaaaaagc	cattacaaga	300
agtggaaata	gcagcaatta	cacatgggtc	tcttcaggga	ttagcctact	tacattctca	360
tactatgatt	catagagata	tcaaagcagg	aaatatcctt	ctgacagaac	caggccaggt	420
gaaacttgct	gactttggct	ctgcttccat	ggcatcacct	gccaattcct	ttgtgggaac	480
gccgtattgg	atggccccag	aagtaatttt	agccatggat	gaaggacaat	atgatggcaa	540
agtagatgtg	tgggtctctg	gaataacatg	tattgaacta	gcggaaagga	agcctccttt	600
atttaatatg	aatgcaatga	gtgccttata	tcacatagcc	caaaatgaat	cccctacact	660
acagtcta	gaatgggtgag	tattgtta	atatatattg	ctcagtgttg	aataaatgaa	720
atgctttttc	ataatctgtt	atcaaagtga	tttaatttca	gttaggtaaa	atgtatcacc	780
ttataagata	ttaaaataga	tgtattttac	ccttttaaat	atattttattc	tttatcatgt	840
ttccatttca	tggcatacgt	ataactgg				868

<210> 160

<211> 1404
 <212> DNA
 <213> Homo sapiens

<400> 160

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ggaggaggaa	acgcaacctg	ggcggctcct	aggacgcaga	gacgccgtcc	ccgccttcac	120
tgagcccaac	gtgcgcttct	ggatcaccga	gcgccaatcc	tttattcgac	gatttcttca	180
atggacagaa	ttattagatc	ctacaaatgt	gttcatttca	gttgaaagta	tagaaaactc	240
gaggcaacta	ttgtgcacaa	atgaagatgt	ttccagccct	gcctcggcgg	accaaaggat	300
acaggaagct	tggaagcgga	gtcttgcaac	agtgcattcc	gacagcagca	acctgatccc	360
caagcttttt	cgacctgcag	cgttcctgcc	tttcatggcg	cccacggtat	ttttgtcaat	420
gacgccactg	aaagggatca	agtccgtgat	tttacctcag	gttttcctct	gtgcctacat	480
ggcagcggtc	aacagcatca	atggaaacag	aagttacact	tgtaagccac	tagaaaatc	540
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ccagatgaag	tatggcctga	ctggcccttg	gattaaaaga	ctcttacctg	tgatcttctc	660
cgtgcaagcc	agtggaatga	atgtctacat	gtcccgaagt	cttgaatcca	ttaaggggat	720
tgcggtcatg	gacaaggaag	gcaatgtcct	gggtcattcc	agaattgctg	ggacaaaaggc	780
tgtagagaa	acgctagcat	ccagaatagt	gctgtttggg	acctcagctc	tgattcctga	840
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gattttgaaa	ctgtcttgta	ctgtcctggc	aatgggactg	atggtgccat	tttcttttag	960
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ttatgtggtt	ccctgcttga	aaaccttccc	cctctcccag	gttcggttta	gagaactttg	1140
cccacaggtc	ttctggggac	cccagagggtg	tctgtgctga	caaggcgact	tcagattcca	1200
tactgagatc	gttcccaggc	tggcgtctct	ggggttttta	aggctggctg	gagaagacag	1260
tgggaagggt	gccccgtctg	acacccctgg	ggttgctgag	ggaacggttg	gagtggggat	1320
cggcctgcga	aaggatactg	tgaatcact	aattaactaa	taaacctgtc	tcaagttgag	1380
gatttgaaga	aaaaaaaaaa	aaag				1404

<210> 161
 <211> 562
 <212> DNA
 <213> Homo sapiens

<400> 161

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ggaacatcac	cacagccata	gcaggcattg	tgtgcaggca	gctgggctgt	ggggagaatg	120
gagttgtcag	cctcgccctt	ttatctaaga	caggctctgg	tttcatgtgg	gtggatgaca	180
ttcagtgctc	taaaacgcat	atctccatat	ggcagtgcc	gtctgcccc	tgggagcgaa	240
gaatctccag	cccagcagaa	gagacctgga	tcacatgtga	agatagaata	agagtgcgtg	300
gaggagacac	cgagtgtctt	gggagagtgg	agatctggca	cgcaggctcc	tggggcacag	360
tgtgtgatga	ctcctgggac	ctggccgagg	cggaagtgg	gtgtcagcag	ctgggctgtg	420
gctctgctct	ggctgccctg	agggacgctt	cgtttggcca	gggaactgga	accatctggt	480
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ggggacagag	tgactgtgga	ca				562

<210> 162

<211> 1812
 <212> DNA
 <213> Homo sapiens

<400> 162

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gatttctttt	tgcgggactt	gcgccctttg	ggtgccaacg	gtccaggatc	cccctggaac	120
cagatgggtac	ggccatgccg	gtcctgcagg	gagctcatgc	ctggcatgcc	atagcagcgc	180
agccaggctc	gaaaggcagc	aaagtcctcc	tcccgcctct	ctgaccogta	gcccctgccc	240
cccaactgga	ccacttcctt	gggcaactgag	tgacatagct	ccagcaggct	tggattctgc	300
agcttggtcc	ttatcttctg	gctcagggtc	agctccgggc	tcggcctgtg	ctgctgcagg	360
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tcctgcaaga	cacaggggcc	gcgcccgccg	tgccactttc	ccccaaaggc	ccagcggccg	600
aaccggcgga	tgtccacgaa	acatagggcg	agccgggggc	caggcggggc	cgtgtaaaag	660
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gccctgcagg	cctcattcac	aaactggctg	gccaggtgca	gctcggggcc	ctcaggcatc	960
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gcgtaataaa	attatgtggc	tttgtaagaa	attggttttt	agagatgcat	gttaaagtat	1740
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aatagaatta	ac					1812

<210> 163
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 163

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ctgatattct	tttgcgaaatg	cttgaaaaag	cacttcttta	tagtgaacac	cagaacatca	120
gcaacactgg	actgtcatcc	caaggcttat	tgatatttgc	ggagttgatt	cctgccatta	180
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ctcatttagg	aacaggcatg	caccgtgtga	tcggactgat	gcttctatac	ttaatctttg	300
caaatgctga	aagcgtgatt	agagtcattg	ggg			333

<210> 164
 <211> 134
 <212> DNA
 <213> Homo sapiens

<400> 164
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 tggctcactg caagctctgc ctcccagggt caccgccattc tcctgcctca gcctcccagag 120
 tagctgggac taca 134

<210> 165
 <211> 839
 <212> DNA
 <213> Homo sapiens

<400> 165
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 ttgcagaact taatatgaat gtgaagaact tgcaaagaaa cttgaaaaca gccaaaggga 120
 tggcatatca agaaataaat tggccttggc agaattgtat gaagatgaag tgaagtgcaa 180
 atcttccaag tctaataagac ctaaagccac agtcttcaag agcccacgga caccacctca 240
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 agccacaaga gcttcagggtg atgataaatc taagtcattt acagggtggag gatacagatt 420
 gggtagttct ttttgtaagc ggtctgaata tatctatgga gaaaatcagc tgcaagatgt 480
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 tgcattgtatg cctgaaattc agcaacttat gttagaaatc ttttaattgtg gcattactgc 660
 tggcagaaga tttcaaaagg ttagtttgaa gttataattt gtgaaagtaa actcagatat 720
 tcagtgtctc caccatcca aagaacattg taacttacca gctcttcttg ctaaaggatg 780
 aggaatcaag tgattttgct atgataataa aagcttttct gtgttatgat taacaaaaa 839

<210> 166
 <211> 1256
 <212> DNA
 <213> Homo sapiens

<400> 166
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 actgaagatg ttttcatcag aagagatgag aggacatctt catcatcatc ataaatgtct 180
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cccttttgac	ctgggcaacc	agctgctggg	actgaaaggt	gtgatggaga	tgatggtggc	480
actatgtggc	tcagagcgcg	agacggacca	gctggtggcc	gtggaggccc	tcatccatgc	540
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gatctacaag	accaccaaaa	atgagaagat	caagatccgc	acactggtgg	gactctgtaa	660
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catctctgcc	ctggcttgca	tgggtgaaagc	agatagtgcc	atcctcactg	accagaccaa	1140
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<210> 167
 <211> 892
 <212> DNA
 <213> Homo sapiens

<400> 167						
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acttttagga	gcgagaccct	gacctgggag	acgggctgga	gaatgggctg	ggcagcccct	180
tcgggaagtg	gacactgtcc	agcgcggtc	agaccacca	gctgcggcga	ctgcggggcc	240
cagccaagtg	ccgcgagtgc	gaagccttca	tggtcagcgg	gacggagtgt	gaggagtgt	300
ttctgacctg	ccacaagcgc	tgcctggaga	ctctcctgat	cctctgtgga	cacaggcggc	360
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<210> 168
 <211> 394
 <212> DNA
 <213> Homo sapiens

<400> 168						
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gagcttgaca	gtgaacgtgt	gtctgcattt	cttgtcactg	agaccctggt	gttctatttg	120
ttctgtctcc	ttgcagatga	aaccgtcgtg	ccaccagatg	ttccaagcta	cctctcttct	180

caggggaccc	tttctgaccg	acaagaaacc	gtggtcagga	ccgaggggtgg	ccctcaggcc	240
aatgggcaca	ttgagagcaa	tggttaaggcc	tcagtaaccg	tgaagcagag	ctctgctgtg	300
actgtgtctc	tgggtgctgg	aggtggcctc	caggtcttta	cagggcaggt	acctggcatt	360
agatggggca	aacttggtga	agcccacgcg	tccg			394

<210> 169
 <211> 550
 <212> DNA
 <213> Homo sapiens

<400> 169						
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acccggcttt	ccccgtggcc	ccccgcctcc	tcccggcttc	gctccttttc	atgtgagcat	120
ctgggacact	gatctctcag	accccgctgc	tcgggctgga	gaatagatgg	ttttgtgaaa	180
aattaaacac	cgccctgaag	aggagccccg	ctgggcagcg	gcaggagcgc	agagtgtctg	240
cccagggtgt	gcagaggtgg	cgcctccccg	gcccgggacg	gtagccccgg	gcgccaacgg	300
catgacagac	tcggcgacag	ctaacgggga	cgacagggac	cccagatcg	agctctttgt	360
gaaggctgga	atcgatggag	aaagcatcgg	caactgtcct	ttctctcagc	gcctcttcat	420
gatcctcttg	ctgaaaggag	tcgtgttcaa	tgtaaccact	gtggatctga	aaagaaagcc	480
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cgtgaagaca						550

<210> 170
 <211> 422
 <212> DNA
 <213> Homo sapiens

<400> 170						
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aaaaaaaaatct	cgctctccac	accaaagccc	cggccacctc	ggcctcttcc	tgttgcacca	180
ggttcttcga	aaactgaagc	agatgttgaa	caacaagtgc	tctacaagta	tagaaagaag	240
ccttctctct	cccaccgtcc	ccagacacca	cataatggaa	aaagcaagaa	ttttctgcat	300
aagcaaggcc	ttaaaaaaaaa	aaaagccagc	ctctgatggg	acttttttcc	tgccaaaaat	360
cccactggtc	cactgtcgca	attttttacaa	aaggccacga	taaaagagta	aggcccatth	420
tg						422

<210> 171
 <211> 1042
 <212> DNA
 <213> Homo sapiens

<400> 171
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 ctgctgccgc tgctgctggg cctgaacgca ggagctgtca ttgactggcc cacagaggag 120
 ggcaagggaag tatgggatta tgtgacggtc cgcaaggatg cctacatgtt ctggtggctc 180
 tattatgcca ccaactcctg caagaacttc tcagaactgc ccctggatcat gtggccttcag 240
 ggcggtccag gcgggttctag cactggattt ggaaactttg aggaaattgg gcccttgac 300
 agtgccttca aaccacggaa aaccacctgg ctccaggctg ccagtctcct atttgtggat 360
 aatcccgtgg gcactgggtt cagttatgtg aatggtagtg gtgcctatgc caaggacctg 420
 gctatgggtg cttcagacat gatgggtctc ctgaagacct tcttcagttg ccacaaagaa 480
 ttccagacag ttccattcta cttttctca gagtcctatg gaggaaaaat ggcagctggc 540
 attggtctag agctttataa ggccattcag cgagggacca tcaagtgcaa ctttgcgggg 600
 gttgccttgg gtgattcctg gatctcccct gttgattcgg tgcctcctg gggaccttac 660
 ctgtacagca tgcctcttct cgaagacaaa ggtctggcag aggtgtctaa ggttgacagag 720
 caagtactga atgccgtaaa taaggggctc tacagagagg ccacagagct gtgggggaaa 780
 gcagaaatga tcattgaaca ggtaaaaagg ggaaacactc agaggcgagc ctgcttggct 840
 ttttctgggt ggtacagggc ccatgggttg tgttgtcaaa cttggagtct acactgagge 900
 tccccacata tctgcaaagt attgcatgct ggataataaa tctcttgggt ctaagcagtg 960
 atgtagtggc tccttacaga gtcagaaagc caccaggcc tgcaagactt gcttgtcctt 1020
 cactaaatgt aaaaattcta tt 1042

<210> 172
 <211> 890
 <212> DNA
 <213> Homo sapiens

<400> 172
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 ttttttcttt ttaaatTTTtTt gttgccacta attcttataa aaatcctcac acaaggctgg 180
 gctcagtggtc tcacacctgt aatcccagca ctttgggagg ctgaggcagg cggatcacga 240
 ggtcaggaga tcgagaccat cctggctaac acggtgaaac ccccgctctc actaaaaata 300
 caaaaaaatt agccggggcgt ggtggcgggc gcctgtagtc ccagctactc gggaggctga 360
 ggcaggagaa tggcggtgaac ccgggaggca gagcttgtag tgagccgaga tagcgccact 420
 gcactccagc ctggggcgaca gagcaagact ccatctcaaa aaaaaaaaaa agtgataata 480
 ctgtaatccc agcacttttg gaggccgagg caggcggatc acgaggctcag gagatcgaga 540
 ccactcctgg taacacgggtg aaaccccgctc tctactaaaa atacaaaaaa ttagctgggc 600
 gtggtggcgg gcacctgtag tcccagctac ctgggagggt gaggcaggag aatggcgtga 660
 acccaggagg cggagcttgc agtgagcgga gatcatgcca ctgcacttca gcctgggcga 720
 cagagcaaga ctccatctca aaaaacacac acacacacac acacacacaa 780
 atagaaaaat aataatagtt ttaagcacct ctaaagtaca gatattgtgc caagcaattt 840
 atgtgaattg attagattga taactctaaa aatagtttcc ctaatcaact 890

<210> 173
 <211> 1922
 <212> DNA
 <213> Homo sapiens

<400> 173

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tcataatttg	cttcatcaaa	ctcatcaaat	ctgtagctta	tacatttctt	tgttcttgtt	180
gacctccttt	caaagcaagt	ttgctttgga	tttttttgaa	tctttttctt	tttcttcttg	240
atcttcagaa	aagtctggct	ctttgtggag	gaatgatgtt	ttcaatactg	gataccaaca	300
tacaccaagc	gttcttttcc	ttcgttccgg	caacgctctt	tcttcttta	aggcaacatc	360
ccaaatcctg	gaaactggtc	ctctaatttt	tccaacaaga	gcaagtttaa	tgttgggcaa	420
aagggtggggc	aagaacccat	cctcccatct	ggggatggat	catcagagga	ggggcgaaag	480
gcagggcagt	atggtatcca	ctatcgcaag	agtcacacag	aagaattagc	tcaggatggg	540
ttggaaggcc	acattttttg	catggttcat	catcatctgc	taggatggct	tcttcacttt	600
ccttttcttc	ctcctcttct	gaagctgcag	atgatttttc	actgccagac	ccttcacttt	660
catcattgct	ggaatatctt	catctgccac	gtgtccgaga	accagtccat	cgaactttgc	720
ctttgggttt	taccttgctt	actttagaat	ttgtatcttt	ctctgatttt	ttcaaaattt	780
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ttcttgagaa	tcttcttaaa	gtacgacca	catttgtttt	ctcctcttcc	ttttctgtct	960
tctcttgctt	gttttctggg	tctagaactt	tggggggaga	atcgggcttc	ttttccgac	1020
ttgatatcct	gattgttaat	ttgatgccct	ctttctgcct	ttcagagggt	atctctgtat	1080
tttctgaggc	agtgttttct	tcttcaggaa	ccaacttata	tttgaatttg	cttttttgca	1140
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ccatttctac	ctttgtgaac	tcagaatcct	cttttagggg	ttctaggtct	acttttttca	1260
cagactggcc	accaacagta	cttgactctt	ggcattctac	cacttctttt	tctgaggcta	1320
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gtgcgtcctt	atcaagaaaa	gtcttttttg	acttctctaa	cttttcaaga	cattctagga	1500
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gagaagtttc	catttctgga	ggatcgggtt	cctctatttg	tgctttttga	ctatggatct	1680
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cacctgtttt	catacttggt	tatgacagaa	tttaaggact	ctgttccatt	tccctccgtg	1800
atgatatttc	tgtccttagg	ggggctatag	ctctcttctt	ttgtctcata	aaactttgtc	1860
tctacttggt	tctgtcttaa	aatttgagc	taccctttca	tcactaactt	ctccatttac	1920
ca						1922

<210> 174

<211> 537

<212> DNA

<213> Homo sapiens

<400> 174

aaaagcggcg	cggctcgttc	aagatggcgg	agctcgacca	gttgccctgac	gagagctctt	60
cagcaaaagc	ccttgtcagt	ttaaaagaag	gaagcttatc	taacacgtgg	aatgaaaagt	120
acagttcttt	acagaaaaca	cctgtttgga	aaggcaggaa	tacaagctct	gctgtggaaa	180
tgcttttcag	aaattcaaaa	cgaagtcgac	ttttttctga	tgaagatgat	aggcaataaa	240
atacaaggtc	acctaataaa	aaccagaggg	ttgcaatggg	tccacagaaa	tttacagcaa	300
caatgtcaac	accagataag	aaagcttcac	agaagattgg	ttttcgatta	cgtaatctgc	360
tcaagcttcc	taaagcacat	aatgggtgta	tatacgagtg	gttctattca	aatatagata	420
aaccactttt	tgaaggatgat	aatgactttt	gtgtatgtct	aaaggaatct	tttctaatt	480
tgaaaacaag	aaagttaaca	agagtagaat	ggggaaaaat	tcggcggctt	atgggaa	537

<210> 175
 <211> 659
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(659)
 <223> n = a,t,c or g

<400> 175
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 gctacgggca tttctgtatc agcttatgaa cttaatggct tgttttctgt gctgatgttg 120
 gcctgggtct tcctacccat ctacattgct ggtcaggcca ccacgatgcc agaataccta 180
 cggaagcgct tcggtggcat cagaatcccc atcatcctgg ctgtactcta cctatttata 240
 tacatcttca ccaagatctc ggtagacatg tatgcgggtg ccattcttcat ccagcagctc 300
 ttgcacctgg atctgtacct ggccatagtt gggctactgg ccactactgc tgtatacacg 360
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 ataggagcgc tcaccttgat gggctacagt ttgcgcggg ttggtgggat ggaaggactg 480
 aaggagaagt acttcttggc cctggctagc aaccggagtg agaacagcag ctgctgggctg 540
 ccccggaag atgcctttca tatttttcga gatccgctga catctgatct cccgtggccg 600
 ggggtcctat ttggaatgtc catcccatcc ctctggtact ggngcacgga tcagggtgaa 659

<210> 176
 <211> 1033
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(1033)
 <223> n = a,t,c or g

<400> 176
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 ggctgtccg caggggtctc tccatccttc ttgatttgcc tgtcattgag gctgcccgtc 120
 ctgggcgcca ttccccagcc taacacctct tctcagtcct tccttgcagg tccctggagt 180
 ccaggccttg gggcagtga gaaaccgtgg ggaggggcat gagatgccag tccccaaagt 240
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 ggtcacccag tgagcctagg ctccccctc ctcccatccc cagcctgggg gaaccttcag 360
 cgtctctcct ccctgtaggc cccggctcag ctccccagga acttttgttg gtgggtacta 420
 gtagggtaag gcagttcttc ccactcatgag ggagaccttg ggagactttc attaccaaatt 480
 ccattgctgc cccgaccttc ctgggactga tctgggtcac cctgggtctc tgatcttggg 540
 gaagtcaagt tcttatccca gacttgagag gttacaagcc tccaggctctc tggcaaagtg 600
 tggagatgat ggacagccat ttgtacacac accagccagt cccttagcat atctctcttg 660
 gttttgtctc aggtctgcct cagccacctc cctgacgctg tcccactgtg tggatgtggg 720
 gaaggggctt ctggatttta agaagaggag aggtcactca attggggggag cccctgagca 780
 gcgataccag atcatccctg tgtgtgtggc tgcccgaact cctaccgggg ctcaggatgt 840
 gctgcagcct cctggccact ggaggggctg accgctgat ccacctctgg aatgttgtgg 900
 gaagtgcctt ggagggccaac cagaccctgg agggagctgg tggcagcatc accagtgtgg 960
 actttgacct ctggggctac caggttttag cagcaactta caaccagggt gccaggtttt 1020
 ggaaggtngg gga 1033

<210> 177
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 177
 gtcaaaaacg atttcctagc aactgtggcc gtgatggaaa actgtttcct tggggacaag 60
 cacttcatat catcgcaaaa ctcttgggta agtggagaag attgggaatg gtattttttt 120
 ccttggttatt aagctattag aaataaatat gcctttgctg gcacataata gtactttggt 180
 acaacaggat atcctatgga gtttaaaaat aagtatttaa aatataacaa atctgtatta 240
 gtccattctc atgctactaa taaagatata cccaagactg ggtaatttat aaaggaagga 300
 gttttaatgg cctcacagtt ccgtcgacgc gggcg 335

<210> 178
 <211> 556
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(556)
 <223> n = a,t,c or g

<400> 178
 gttcacgtct gcagcagtaa gatgggagct ttgtccacgg agcggctaca gtactacact 60
 caggaactgg gggctcggga gcgcagtggc cacagcgtgt ccctcatcga cctctggggc 120
 ctccctgttg agtatctcct gtaccaggag gagaaccctg ccaagctgtc tgaccaacag 180
 gaggcgggtcc gccagggtca gaacccttac cccatttaca ccagtgtcaa cgtccgcacc 240
 aacttgagtg gggaagattt tgcagagtgg tgcgagttca cgccctatga ggttggtctc 300
 cccaagtaag gggcttatgt tcccaccgag ctcttcggct cagaactctt catgggacga 360
 ttgctgcagc tccagcctga accccggatc tgttacctgc aaggtatgtg gggcagcgcc 420
 tttgccacca gcctggatga gatcttccta aagaccgccg gctcgggcct cagcttcctg 480
 gagtgggtaca gaggcagtgt gaatatcaca gacgactgcc agaagcctca gctgcacaac 540
 ncctcgacgc gggaat 556

<210> 179
 <211> 631
 <212> DNA
 <213> Homo sapiens

<400> 179

gaatttctgg	gtcgtccac	gcgtcccgca	aaggatgagg	gaaacgatga	gggaaaggat	60
gagggaaaagg	atgagggaaa	ggatgaggga	aaggatgagg	gaaaggatga	gggaaaggat	120
gagagaaaagg	atgagggaaa	ggatgaggga	aaggatgaga	gaaaggatga	gggaaaggat	180
gagggaaaagg	atgagggaaa	ggatgaggga	aaggatgagg	gaaaggatga	gggaaaggat	240
gagggaaaagg	atgagggaaa	cgatgaggga	aaggatgagg	gaaaggatga	gggaaaggat	300
gagggaaaagg	atgagggaaa	ggatgaggga	aaggatgagg	gaaacgatga	gggaaacgat	360
gagggaaaacg	atgagggaaa	ggatgaggga	aaggatgaga	gaaacgatga	gggaaaggat	420
gagggaaaagg	atgagggaaa	ggatgaggga	aaggatgaga	gaaacgatga	gggaaaggat	480
gagagaaaagg	atgagggaaa	ggatgaggga	aaggatgagg	gaaaggatga	gggaaaggat	540
gagggaaaagg	atgagggaaa	cgatgaggga	aaggatgaga	gaaaggatga	gggaaaggat	600
gagggaaaagg	atgagggaaa	ggataagtaa	g			631

<210> 180

<211> 469

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(469)

<223> n = a,t,c or g

<400> 180

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acttcagcta	cggcctgcag	ccctactgcg	ggtactcctt	ccaggttggtg	ggggagatga	120
tccggaaccg	ggaggtgctg	ccttgccccg	atgactgtcc	cgcctgggcg	tatgcctca	180
tgatcgaggg	ctggaacgag	ttccccagcc	ggagggccccg	ctttaaggac	atccacagcc	240
ggctccgagc	ctggggcaac	ctttccaact	acaacagctc	ggagcagacc	tcgggggggca	300
gaaacaccac	cgagaccagc	tccctgagca	ccagcccact	gtgcaatgtg	agcaacgccc	360
cctacgtggg	gccaagcag	aaggtccccg	cctttccaca	gaccaggtc	atccccatga	420
agggccagat	cagacccatg	gtgccccgc	cgcagctata	cgtccccgg		469

<210> 181

<211> 453

<212> DNA

<213> Homo sapiens

<400> 181

caggaattcc	ggcgccacc	cacgcgttcg	atggatcctg	gaagagcgca	agcgggtgat	60
gcaggaggcc	tgcgccaagt	accgggcgag	cagcagccgc	cgggccgtca	cgccccgccca	120
cgtgtcccgt	atcttcgtgg	aggaccgccca	ccgcgtgctc	tactgcgagg	tgcccaaggc	180
cggtgctcc	aattggaagc	gggtgctcat	ggtgctggcc	ggcctggcct	cgtccactgc	240
cgacatccag	cacaacaccg	tccactatgg	cagcgctctc	aagcgcttgg	acaccttcga	300
ccgccagggt	atcttgcacc	gtctcagcac	ctacaccaag	atgctctttg	tccgcgagcc	360
cttcgagagg	ctgggtgtccg	ccttccgcga	caagtttgag	cacccaaca	gctactatca	420
cccggctcttc	tgcatggcca	tactggccccg	gta			453

<210> 182
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 182
 cataatgtat agtattttctc ctgccaaactc tgaggaaggc caggaacttt atgtctgcac 60
 agtcaaggat gatgtgaact tggatacagt acttctccta ccctttttga aagaaatagc 120
 agtaagccaa ctggatcaac tgagcccaga ggaacagttg ctgggtcaagt gtgctgcaat 180
 cattggtcac tccttccata tagatttgct gcagcacctc ctgcctggct gggataaaaa 240
 taagctactt caggtcttga gagctcttgt ggatatacat gtgctctgct ggtctgacaa 300
 gagccaagag cttctgctg agcccatatt aatgccttcc tctatcgaca tcattgatgg 360
 aaccaaagag aagaaga 377

<210> 183
 <211> 621
 <212> DNA
 <213> Homo sapiens

<400> 183
 ctcatcctta aagtgcaga gttaaattaac tctaaggccc catccaggac tcaagctgtg 60
 tgattttaca aaaatgaaaa ttatattaat aatcccattg taaaatccca aaagaaagtc 120
 aagagactag cagaaagaca ggtgggtgat gggatgtcct ggacagagcc tggatcatga 180
 ggtcccatg tagtgcttgt actacgcaga tgtttcctct tgagctattt taaagggtgtg 240
 gaaaaagcca aagcaatgcc ctctccacgg atactaaaga ctcaccttcc cactcagctg 300
 ctgccaccgt ctttctggga aaacaactgc aaggtaagat accaacagct ccctgtgaca 360
 gaaggggaaag taagccaacc aaagcgagtc ctgcagaccc caacgcagag cattcgtgat 420
 cacctttgcc tctccactgt ctctgatgct taccagcaaa gagaaaacat aaagttctac 480
 attcagcagg acattcacct gaacagtttc aaataggaca tgaaggcagg atccagattg 540
 aatgtttgga gggaactaga gacatgggga ggcagtgagt gcagtaagcg tagctgtgaa 600
 atgaagggga gaagatggtg g 621

<210> 184
 <211> 415
 <212> DNA
 <213> Homo sapiens

<400> 184
 accgggacga cccacgcgtc cggaattta attctattat atatgcagac tttctaaaga 60

agataaagct	tttttatggg	agaaacgtta	ttattgcttc	aaacacccaa	attgtcttcc	120
taaaatatta	gcaagcgccc	caaactggaa	atgggttaat	cttgccaaaa	cttactcatt	180
gcttcaccag	tggcctgcat	tgtaccctact	aattgcattg	gaacttcttg	attcaaagta	240
agtcaaatac	atattattgc	tcttgtttta	ttgtcagttt	ttccagtaag	gtatgttgcc	300
agaagtattt	cctttccttt	taacatgaaa	gcaattcaat	ataatccaaa	tgtgtaaagt	360
tatatttata	caaacatatc	ttctgcattg	aagttgtcaa	taaagcattg	catgt	415

<210> 185
 <211> 359
 <212> DNA
 <213> Homo sapiens

<400> 185

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actttcttca	ggtgttgaga	aatccaatag	agacctctgc	ttgtctcctc	ctttggcaag	120
agctccaagg	ggagagagag	gatggggccac	cacgatgaat	actacaggct	gcggggaagg	180
ataaccctag	tccagaccat	tcctacaaaa	gaaatgggga	atccgaaagg	aaaaggaaga	240
aatctcacta	gcacatgtca	aagagccagg	agaggcacia	ttcaccaagc	agaggaagaa	300
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<210> 186
 <211> 1616
 <212> DNA
 <213> Homo sapiens

<400> 186

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<210> 187
 <211> 916
 <212> DNA
 <213> Homo sapiens

<400> 187

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 <211> 1080
 <212> DNA
 <213> Homo sapiens

<400> 188

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 <211> 1344
 <212> DNA
 <213> Homo sapiens

<400> 189

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<210> 190
 <211> 550
 <212> DNA
 <213> Homo sapiens

<400> 190

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<210> 191
 <211> 562
 <212> DNA
 <213> Homo sapiens

<400> 191						
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<210> 192
 <211> 2171
 <212> DNA
 <213> Homo sapiens

<400> 192						
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 <211> 2095
 <212> DNA
 <213> Homo sapiens

<400> 193						
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 <211> 1051
 <212> DNA
 <213> Homo sapiens

<400> 194

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 <212> DNA
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<400> 195

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acctagacac	ctggacttgg	tctggaagga	ttactattaa	tgagaaagc	ccaaaacatc	300
ggtcatggca	tactttaaca	cctatagctg	atgataaact	tttcctatgt	ggtggactaa	360
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aac						423

<210> 196
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 196
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 cccaagtag ttgtgcctcc taggcacaca acactatgcc ccggcaaatt tttttgtatt 180
 ttgtattttt tgtagaaaca ggatttcgcc atgttgGCCa ggctggcttc gaacaccctg 240
 ggctcaactg atccgcctgc ctccggcctcc caaagtgcctg ggattacagg tgtgagccac 300
 cctgctcaac cagggttttat tatttaagtt agttaaactt tggatagatt gtataatata 360
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<210> 197
 <211> 751
 <212> DNA
 <213> Homo sapiens

<400> 197
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 ctgggcccag caggagtacc ggggctcctt cacctgtcgc atttggcagt ttggacgctg 180
 ggtggagggtg accacagatg accgcctgcc gtgccttgca gggagactct gtttctcccg 240
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 tgggtcctac gagcacctgt gggccgggca ggtggcgat gccctgggtg acctgaccgg 360
 cggcctggca gaaagatgga acctgaaggc cgtagcagga agcggaggcc agcaggacag 420
 gccaggccgc tgggagcaca ggacttgtcg gcagctgctc cacctgaagg accagtgtct 480
 gatcagctgc tgcgtgctca gcccagagc aggtgaggca cgtggccagc atgggagggc 540
 tgcagccagc gtgcccccca ctgccaggcc tcaggcacac tgtagctttt tatgtgactg 600
 gctacacagc cctgtcagga ctaagtggga agaagtaagc ttgttctcaa ggggtggtgc 660
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 gaccagtcct ttccactagt gcgaggcagg g 751

<210> 198
 <211> 636
 <212> DNA
 <213> Homo sapiens

<400> 198
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 gcgggcccga aggttcgac aaacgtcgct ggcagattgt gaaccagaac gatcgtcagg 180
 tgctgtttgc cctgagttca gatgatggtg atcagggctt cccgggtaac ctccggcgca 240

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ataaaccttg	cccgggtgaat	atgactaatc	acgtctatct	caatcttgac	ggcgagcagt	360
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ccaaaatcat	cgccagtgaag	tttcttgccg	acgacgatca	gcgcaaagtg	aaagggttacg	540
atcacgcatt	cttggttacag	gccaaaggcg	atggcaagaa	agtggcgggcg	catgtctggt	600
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<210> 199
 <211> 690
 <212> DNA
 <213> Homo sapiens

<400> 199						
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gacagtcaag	ggttatgtca	gaaaaggatg	agtatcagtt	tcaacatcag	ggagcgggtg	180
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atcatcgatt	ccgcttcttg	catgaaaactg	gaggagcaat	ggtgtatgac	aagccgccga	300
aatttgccat	gtcacgagag	caaatgtcac	agtcatgttc	tcacacggca	cataatgcaa	360
gtctgttgac	agatgcgggt	ccattgtcat	gtggggagtc	gagggcgagc	tgtttgtttt	420
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tgcaccgatg	aacattacga	agttctagaa	caaacatcac	ttcaaaatgc	ctggagtaat	540
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cacaacgtca	taactaaacg	agcacaacac				690

<210> 200
 <211> 433
 <212> DNA
 <213> Homo sapiens

<400> 200						
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ccctgggtgct	gcaactcctc	tccttcacgc	tcttggtctg	gctccttgct	caagtgtcca	180
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cccagcttaa	agctgcagtg	ggtgagctct	cagagaaatc	caagctgcag	gagatctacc	300
aggagctgac	ccagctgaag	gctgcagtg	gtgagcttcc	agagaaatct	aagctgcagg	360
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<210> 201
 <211> 782

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(782)
<223> n = a,t,c or g

<400> 201
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gcagtttctt tttgggagag ctagtccagtc ccacagagtg gtatccctag aaggggagaag 180
taaggattgc cctcttcttt aaaatgaaaag ccagctatct ttcacgccct ttaactgcag 240
gtctgtctta ttttcttttc tctctctgga gctgagagtc agagggccct tctcctcctc 300
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aaccacctg gcaagtcttc ttaggatctg atcccagttt tctggaagca atcctacccc 420
agccattct tcccagagtc gagccttaat ccttctcact tctcagtgtc agagcagaaa 480
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agtgtgagct gccttgggag cctcagttag ggcactggga ctggcctcac tctcttgccc 600
ccagcctagt gggctttctc ctctgtctct ccggtggccc caggcaatcg actgcatcac 660
gcanggacgt gagttggagc ggccacgtgc ctgcccacca gaggtctacg ccacatgccc 720
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ca 782

<210> 202
<211> 714
<212> DNA
<213> Homo sapiens

<400> 202
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tgggcgccat atgctgcggc tgaggtgctc caggtgtacc ggctcttga cattcgtgag 180
cataagggca agacccctct cctggtggcg gctgctgcca accagcccct gattgtggag 240
gatctgttga acctgggagc agagcccaat gccgctgacc atcagggacg ttcggtcttg 300
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gcccttaacg ttgctatgcg cccttccgac ctctgtccc' ggggtgctgag cacacaggcc 480
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gtgagcgggg atgtggggcg tcagaccctg ggagatttgt tggaatgggg ccacttggat 600
gtccgggagc tccaggcaaa tgctgacttt gcctcttctt tgctgcgtgc ccttgaacat 660
gttacttcac ttctctgtgc cttaaggggtt ttttgcttgt ttctttgtca gtta 714

<210> 203
<211> 477
<212> DNA
<213> Homo sapiens

<400> 203

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ccgctgagct	cattcgctcc	ctgacagagc	tgcaggagct	ggaggctgta	tacgaacggc	180
tctgcggcga	ggagaaaagt	gtggagagag	agctggatgc	tcttttgga	cagcaaaaca	240
ccattgaaag	taagatggtc	actctccacc	gaatgggtcc	taatctgcag	ctgattgagg	300
gagatgcaaa	gcagctggct	ggaatgatca	cctttacctg	caacctggct	gagaatgtgt	360
ccagcaaagt	tcgtcagctt	gacctggcca	agaaccgcct	ctatcaggcc	attcagagag	420
ctgatgacat	cttggacctg	aagttctgca	tggatggagt	tcagactgct	ttgagga	477

<210> 204

<211> 706

<212> DNA

<213> Homo sapiens

<400> 204

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gccagtgtgg	cccgggcctg	gagctctgct	tttgacaacc	tgattgggaa	ccacatctct	180
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tcggccctgg	ttaccaaagt	gttcacaggc	gtgaaccttt	tggttcttgg	gttcgtcatg	360
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ttggccatgg	ctgaactcaa	tgacacctat	agcttgggtc	ctctgggctc	tggaggattt	480
gtgcctttcg	gcttcgaggg	aattctccgt	ggagcagcga	cctgtttcta	tgcatttggt	540
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atgggcattg	ggatctcact	gtctgtctgc	tttttgccgg	attttgctgt	ctcttctgca	660
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<210> 205

<211> 852

<212> DNA

<213> Homo sapiens

<400> 205

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tattcttttg	aaatggtgca	gccagatttt	gagttgcatg	ccatcagtgg	ggaaattaca	180
aatactcatc	agtttgacag	ggagtctctt	atgaggcgga	gaggggactgc	tgtgttttagc	240
tttacagtca	tagcaacaga	tcaggggatc	cctcagcctc	tcaaggatca	ggccactgta	300
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gttgatgaag	gtaataatgg	acttattcac	tattctataa	taaaaggaaa	tgaagaaaga	480
cagtttgcta	tagacagtac	ctctggtcag	gtaacactaa	ttggcaaatt	agactatgaa	540

gcaacacctg	cctattccct	tgtaattcaa	gcagtggatt	cagggacaat	ccccctcaat	600
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taaatcaaca	cttctttgtt	gatgttttgg	aaaacatgag	aattgggtgaa	ctcggggcct	720
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<210> 206
 <211> 361
 <212> DNA
 <213> Homo sapiens

<400> 206						
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agtattacat	ggaacatcat	gggcaattaa	aagagaagaa	tggagatggt	attgagctta	120
aaaatcctct	gaactgtgca	gacccactct	ctcaaagggtg	gtttcatgga	cacctctctg	180
gaaaagaagc	agagaaattg	ttaactgaaa	aaggaaagca	tagtagcttt	cttgtagcag	240
agagccagag	ccaccctgga	gattttgttc	tctccgtgtg	caccgggtgat	gacaaaggag	300
agagcaatga	cggcaagtct	aaagtgactc	atgtcatgat	tactgtcag	gaactgaaat	360
c						361

<210> 207
 <211> 2483
 <212> DNA
 <213> Homo sapiens

<400> 207						
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gaattaaatg	acatcatcca	tgtaaagcat	atagcagaat	gcctggcaca	tagatgcctt	120
tagtgaattt	ttgctgttgt	tgtgattctt	ttgggagcag	tcatagtaac	atattctcat	180
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ggatgaccat	gtgaaatcgg	gaaacatcac	tgctcgtgat	cctgccatta	tgggactccg	420
aaatatactc	aaagtttgct	gtacccatga	catcacaaca	ataagcatte	ctctcttgct	480
ggtacatgat	atgtcagagg	aaatgactat	accctgggtg	ttaaggagag	cgggaactgt	540
gttcaagtgt	gtcaaagggt	tcatgatgga	aatggcttca	tgggatggag	gaatttctag	600
gacagtgcaa	tttctagtac	cacagagtat	ttctgaagaa	atgttttatc	aacttagtaa	660
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gaatcatgtt	tatggtgtta	cca				2483

<210> 208
 <211> 366
 <212> DNA
 <213> Homo sapiens

<400> 208						
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tgttctgggt	gggcatcctc	atggctttgt	gtccttttat	ggggctcccc	tggtacgtgg	180
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cccctgggga	gcagccccag	tttctgggag	tcagggaaca	gagagtaacc	ggcatcatcg	300
tcttcattcct	gacgggaatc	tctgtcttcc	tggctcccat	cctaaagtgt	atccccctgc	360
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<210> 209
 <211> 574
 <212> DNA
 <213> Homo sapiens

<400> 209						
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aaaaaatacg	catatctatt	ctggtggcac	gcaaattggt	gataacacca	gcacctcgga	360

tgttattgaa	gtttattctg	gtggcgtgct	tgatgttagg	ggtgggtacgg	caacaaatgt	420
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gaatagttaa	ggtgcattct	ccatccacaa	tcacgtggca	gacaatgtgt	tgctggaaaa	540
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<210> 210
 <211> 383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = a,t,c or g

<400> 210						
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gctgtttttc	ttattttacct	cct				383

<210> 211
 <211> 592
 <212> DNA
 <213> Homo sapiens

<400> 211						
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cagcagctct	ggcggccatc	ctgacacgcc	tccgggagaa	caagaagggtg	gaacggctcc	540
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<210> 212
 <211> 2166
 <212> DNA

<213> Homo sapiens

<400> 212

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<210> 213

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(392)

<223> n = a,t,c or g

<400> 213

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attattatctc	cccaannnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	300
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<210> 214
 <211> 425
 <212> DNA
 <213> Homo sapiens

<400> 214	
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agcgggtccag	ttggacagac
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ctgct	

<210> 215
 <211> 608
 <212> DNA
 <213> Homo sapiens

<400> 215	
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ggctctcctc	ggcaccatct
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tgccatgaact	gtgtgcacgc
catccacca	ctgcgcacatca
gggcaccctc	actgaggacg
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<210> 216
 <211> 858
 <212> DNA

<213> Homo sapiens

<400> 216

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ctatcatttc	ttgagcttcc	ttattgtctt	gttctgccat	tttcaaagta	ttgcttaaat	180
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agtgggcgct	atatggaatt	agagcaacgt	tacatggacc	tcgctgagaa	tgcccgtttt	420
gaacgggagc	agcttcttgg	tgtccagcag	catttaagca	atactttgaa	aatggcagaa	480
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tacaaagcca	cagtggccag	tgaccagata	gagatgaatc	gcctgaaggc	tcagctggag	660
aatgaaaagc	agaaagtggc	agagctgtat	tctatccata	actctggaga	caaactctgat	720
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<210> 217

<211> 399

<212> DNA

<213> Homo sapiens

<400> 217

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cccgaactacc	gtgggtgcga	cgggcgctgt	gagcagtacc	gatgctactg	ccattgctgc	180
caccaccgaa	gccacaacag	tccccatcat	cccaactgtc	gcacctacca	ccatggccac	240
caccaccacc	gtgcgcacaa	ctactacaac	cactgctgcc	gccaccacca	ccacggagag	300
tcctcccacc	accacctccg	ggactaagat	acacgaatcc	gccccctgatg	agcagtcctat	360
atggaacgtc	acggtgctcc	ccaacagtaa	atggggccaa			399

<210> 218

<211> 662

<212> DNA

<213> Homo sapiens

<400> 218

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ggtgccagcc	tgaccgacct	ggccaacctg	agcgaaggcg	tctccctggc	agagaggggc	180
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caagagtgtc	atccggatcc	tttcagaca	gaagaccctt	tcaaactctga	cccatttaaa	300

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gccactgacg	acttcttcaa	gaaacagaca	aagaatgacc	catttacctc	ggatccattc	480
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tcctccagtg	tctcctcaaa	aggatcagat	ccctttggaa	ccttagatcc	cttcggaagt	600
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cg						662

<210> 219
 <211> 752
 <212> DNA
 <213> Homo sapiens

<400> 219						
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cggctctgtca	gtggccctgg	gagatccata	agtggctcaa	ttccagctgg	acggactgtc	660
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<210> 220
 <211> 582.
 <212> DNA
 <213> Homo sapiens

<400> 220						
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gccaccacgc	ttggccctgc	ccaggagtca	tttttgtatc	tacaggatc	ttcctatgct	180
gtagacagat	gccctttttc	aaggcaaaaa	ccctagccat	ttttctcttc	tccttcagag	240
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gatccacaca	acttaaagat	ctgctgtcga	gtgaatgggg	aagtgggtcca	gagcagcaac	540
accaaccaga	tggatttcaa	gacagaggac	ctgatagcct	gg		582

<210> 221
 <211> 440
 <212> DNA
 <213> Homo sapiens

<400> 221
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 tccaaaacaa tctaattaag tgctagaagt ttgccatgga cagacaaagt gctacttggg 180
 aaggaagttc cagaaacacc acagctgggt acattcttca ccactctgag tgggtggcagt 240
 gacgcgttgg ctttgtgaga atggtgtgtc ttacttgaga aagtgtgtgt gttctgcctg 300
 caggcatggg actcgtctgt ctggagaagt ggcagccgct gcaaacaatt cgactgcac 360
 agtcggaatt gctttcaacg ccaagatcgg aggtatggga aaccaactca cgtggatgta 420
 gaaatgcgcc agttagctct 440

<210> 222
 <211> 489
 <212> DNA
 <213> Homo sapiens

<400> 222
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 ccgggagcat gcagcctgca ctgcggggga tgtgatgtc ggctctaact cgcctggctg 120
 gccgcccacg gacgcctcag cttgcaacca tggtaacgtt tctggcgggg gacacccccg 180
 ggagcccacc gcgatgggca gcctcctggt gactgatgga cgagtgtcca cctcccagac 240
 cgagagcgct tagtaggtcg gaggaagtgg agaggatgta acacgcccc agccggggagt 300
 gaagccctga ggagctcctc cccccttcgt tcccaccctc aagtctgacg atgacacctc 360
 caattttgat gaaccaaga agaattcgtg ggtttcatcc tctccgtgcc agctgagccc 420
 ctcaggcttc tcgggtgaag aactgccgtt tgtgggggtt tcgtacagca aggcactggg 480
 gattcttgg 489

<210> 223
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 223
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 cctggggggc gacgccttc tgccggcgct gaccgaggaa ctcatctgga gcccgacat 180
 tggggacacg cagctggacg tagagtttct tatggagctc ttagatccag atgagctgcg 240
 gggagaggct ggggtactacc tgaccacgtg gtttggggcg ctgcaccaca ttgccacta 300
 ccagcccga acagaccgcg ctccccgggg gctcagctcc gagggccgcg cctccctgca 360

ccagtggcac	cgcaggcgga	cgctgcacag	aaaggatcat	cccagagccc	aacagctgga	420
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cctcgtctgc	tgg					493

<210> 224
 <211> 883
 <212> DNA
 <213> Homo sapiens

<400> 224						
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gatggttttg	atagtgatag	ctcactgtca	gactcagacc	ttgaacaaga	ccctgaaggg	120
cttcaccttt	ggaactcttt	ctgcagtgtg	gacccctata	atccccagaa	ctttacagca	180
acaattcaga	ctgctgccag	aattgttcct	gaagagcctt	ctgattcaga	gaaggatttg	240
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gtcctctttc	aaacatcagg	ggaaaatgag	aaaggctgtc	gtgactcaaa	gaccccatct	480
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agtgggtgatg	aggatcgcaa	aggaccatgg	gaagaatttg	caagggatgg	atgcaggttc	720
cagaaacgaa	ttcaagaaac	agaagatgct	attggatatt	gcttgacatt	tgaacacaga	780
gaaagaatgt	ttaatagact	ccaggggaaca	tgcttcaaag	gacttaatgt	tctcaagcaa	840
tggtgagttg	gcagcctgta	gtcctagcta	gcatacacta	cct		883

<210> 225
 <211> 389
 <212> DNA
 <213> Homo sapiens

<400> 225						
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ttaatcgctc	aggtcatact	cagagtgtcg	actgggggtc	ttttgggggg	ttaatgggaa	120
ggtttgaatt	tgggattttt	ttaaagggga	aggagattgt	taagtgagga	tcaacagggg	180
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aaaaacatta	ttgcgtgcag	tataaaagga	ctatgaaatc	tgtagctgc	gtctatctca	300
tcctaatttg	aaagggcaaa	aaaaaatatt	accatagatt	tctgctaata	agtaacaatc	360
taaagcatta	atgggtgttg	gtctttttgg				389

<210> 226
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 226
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 gtcctatggg gacatcagga agatggagg gggcaggaag gagtcaggcc tttagggaga 180
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 tttggtgata gaaaattttt tgagaaagga caagaggagc ctttgcttat ctctcacctg 300
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 tctgttttgc tgcaggggtg gggagccata tgcctctac aatttggatg tg 412

<210> 227
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 227
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 cccagcaaag cagacaacct ccatctgctc accatccagc cggacctcag caccaccacc 300
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<210> 228
 <211> 777
 <212> DNA
 <213> Homo sapiens

<400> 228
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 caatccttcc acaatgtgca acaaatggcg attgactggc tactcgaat tctctatttt 180
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 agccgattta atgggactga tattcactca ttaattaaaa ttgagaatgc ttgggggaatc 660
 cgaatttatc aaaaaagaac tcaaccaaca gtcagaagcc atgcatgtga agtcgatcca 720
 tatggaatgc cagggggctg ttcacacatc tgtctactca gcagcagtta caggaatc 777

<210> 229
 <211> 486
 <212> DNA
 <213> Homo sapiens

<400> 229
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 tgatcg 486

<210> 230
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 230
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 gtatgttctg atcctccctc ttgaagtgtc cttctgtggt ctaaggaggg cctgaaggtt 360
 caggtaaaaa cttcagggtg accttcactg ggggtg 396

<210> 231
 <211> 713
 <212> DNA
 <213> Homo sapiens

<400> 231
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 caaagcattg gcagaaggct atctgaagag caccatcact cagatagaga gaagggttga 120
 tatcccttct tcactggtgg gagttattga tggtagtttt gaaattggga atctcttagt 180
 tataacattt gttagctact ttggagccaa acttcacagg ccaaaaataa ttggagcagg 240

gtgtgtaatc	atgggagttg	gaacactgct	cattgcaatg	cctcagttct	tcatggagca	300
gtacaaatat	gagagatatt	ctccttcctc	caattccact	ctcagcatct	ctccgtgtct	360
cctagagtca	agcagtcaat	taccagtttc	agttatggaa	aaatcaaaat	ccaaaataag	420
taacgaatgt	gaagtggaca	ctagctcttc	catgtggatt	tatgttttcc	tgggcaatct	480
tcttcgtgga	ataggagaaa	ctcccattca	gcctttgggc	attgcctacc	tggatgattt	540
tgccagtga	gacaatgcag	ctttctatat	tgggtgtgtg	cagacgggtg	caattatagg	600
accaatcttt	ggtttcctgt	taggtcatt	atgtgccaaa	ctatatgttg	acattggctt	660
tgtaaacct	gtcattttta	ggtggaagca	tgttacagca	cattatcgag	gaa	713

<210> 232
 <211> 1067
 <212> DNA
 <213> Homo sapiens

<400> 232						
cagccttcca	aggtagggca	caccaaggcc	taagggaatca	gaaagggccc	gaggggtgggc	60
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ccagggcgcc	aagcctcagg	accgtgggtg	gggcccgaagg	acactctgga	cccccgttcc	180
attcatgaga	ggccctcagc	acgccacgtg	tctgctgtga	cagcccgcag	ggaggggtgga	240
agccttctgt	aaattccaca	tgtggggccga	gggcatgaag	tccttgatga	aggccgcgct	300
ggacctcacc	taccccatca	cgtecatgtt	ctccggagcc	ggcttcaaca	gcagcatctt	360
cagcgtcttc	aaggaccagc	agatcgagga	cctgtggatt	ccttatttctg	ccatcaccac	420
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cacgggtgtt	gacatctggg	gccgcagcgg	cgtgctggag	aagatgctcc	gcgaccagca	960
ggggccgagc	aagaagcccg	cgagtgcggt	cctcacctgt	cccaacgcct	ccttcacgga	1020
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<210> 233
 <211> 704
 <212> DNA
 <213> Homo sapiens

<400> 233						
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gggtagtctt	aactttgggt	aataatgttt	gtcagctacc	tgatattaac	attgtccac	180
gttcaaacag	cagtgttagc	aagacctggg	ggagagagca	ttggctgtga	tgactactta	240
ggctccgaca	aagtcgtgga	caaagtgtgg	gtgtgtggag	gagacaacac	gggctgtcag	300
gttgtgtcgg	gcgtgtttta	gcatgccctc	accagcctgg	gctaccaccg	cgctgtggag	360
attcccagag	gagccacgaa	aatcaacatc	acggagatgt	acaagagcaa	caactatttg	420
gccctgagaa	gtcgttctgg	acgtccatc	atcaatggga	actgggcaat	tgatcgacca	480

<210> 236
 <211> 467
 <212> DNA
 <213> Homo sapiens

<400> 236
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 tttaaatgc ctgtcaaaac ttccaaggca tatctcaccg ttctgggtgt tcctgaaaag 120
 cctcagatta gtggattctc atcaccagtt atggagggtg acttgatgca gctgacttgc 180
 aaaacatctg gtagtaaaacc tgcagctgat ataagatggg tcaaaaatga caaagagatt 240
 aaagatgtaa aatattttaa agaagaggat gcaaatacga agacattcac tgtcagcagc 300
 acactggact tccgagtggg ccggagtgat gatggagtgg cggtcatctg cagagtagat 360
 cacgaatccc tcaatgccac ccctcaggta gccatgcagg tgctagaaat gcactataca 420
 ccatcagtta agattatacc atcgactcct tttccacaag aaggacg 467

<210> 237
 <211> 416
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(416)
 <223> n = a,t,c or g

<400> 237
 ggtacaacca gaaagtggat ctcttcagcc tgggaattat cttctttgag atgtcctatc 60
 accccatggg cacggcttca gaaaggatct ttgttctcaa ccaactcaga gatcccaactt 120
 cgcctaagtt tccagaagac tttgacgatg gagagcatgc aaagcagaaa tcagtcatct 180
 cctggctggt gaaccacgat ccagcaaaac ggcccacagc cacagaactg ctcaagagtg 240
 agctgctgcc cccaccccag atggaggagt cagagctgca tgaagtgtctg caccacacgc 300
 tgaccaacgt ggatggaaag gcctaccgca ccattgatgg gccagatct tttcggcagc 360
 gcatctcccc tgccatcgnr ttacacctat gaccagcgac atattgaagg gcaact 416

<210> 238
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 238
 ggaccaggac tacaagtacg acagtacctc agacgacagc aacttcctca accccccag 60
 ggggtgggac catacagccc caggccaccg gacttttgaa accaaagatc agccagaata 120
 tgattccaca gatggcgagg gtgactggag tctctggtct gtctgcagcg tcacctgcgg 180
 gaacggcaac cagaaacgga cccggtcttg tggctacgag tgactgcaa cagaatcgag 240

gacctgtgac	cgtccaaact	gcccaggaat	tgaagacact	tttaggacag	ctgccaccga	300
agtgaagtctg	cttgcgggaa	gcgaggagtt	taatgccacc	aaactgtttg	aagttgacac	360
agacagctgt	gagcgctgga	tgagctgcaa	aagcgagttc	ttaaagaagt	acatgcacaa	420
ggatgatgaat	gacctgcca	gctgccccctg	ctcctacccc	actgaggtgg	cctacagcac	480
ggccgacatc	ttcgaccgca	tcaagcgcaa	ggacttccgc	tggaaaggacg	ccagcggggcc	540
caaggagaag	ctggagatct	acaagcccac	tgcccggtac	tgcattccgt	ccatgctgtc	600
cctggagagc	accacgctgg	cggcacagca	ctgctgctac	ggcgacaaca	tgcagctcat	660
caccaggggc	aagggggcgg	gcacgccccaa	cctcatcagc	accgagttct	ccgaggagct	720
ccactacaag	gtggacgtc					739

<210> 239
 <211> 611
 <212> DNA
 <213> Homo sapiens

<400> 239

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tgtaccatta	gttgcctgtg	gtccttgtga	tgatgaaggc	attgtgacta	gcacaggcgc	120
aaaagaggaa	gacgaggaag	gggaggatgt	tgtgactagt	actggaagag	gaaatgaaat	180
tgggcatgct	tcaacttgta	cagggttagg	agaagaaagt	gaaggggtct	tgatttgtga	240
aagtgcagaa	ggggacagtc	agattggtac	tgtggtagag	catgtggaag	ctgaggctgg	300
agctgccatc	atgaatgcaa	atgaaaataa	tggtgacagc	atgagtggca	cagagaaagg	360
aagtaaagac	acagatatct	gctccagtgc	aaaagggatt	gtagaaagca	gtgtgaccag	420
tgagctctca	ggaaaggatg	aagtgcacac	agttccagga	ggttggtgagg	gtcctatgac	480
tagtgctgca	tctgatcaaa	gtgacagtca	gctcgaaaaa	ggtgaagata	ccactatttc	540
actggcctg	gtcgggggta	gttacgatgt	tcttgatctc	ggtgaagtec	cagaatgtga	600
agttgctcac	a					611

<210> 240
 <211> 1090
 <212> DNA
 <213> Homo sapiens

<400> 240

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ttattcacag	tgcagtaagt	gtgtatcatc	tgtttgatat	tttcatatta	cagttttgat	120
agtgtctctc	agtctgcgaa	atcttctttg	ggtggaaaatg	atgaactgtc	agctactttc	180
ttagaaatga	aaggacattt	ctatatgtat	gctggttctc	tgctcttgaa	gatgggtcag	240
catggtaata	atgttcaatg	gcgagctctt	tctgagctgg	ctgcgttggt	ctatctcata	300
gcatttcagg	taagtcttcc	acttggagca	attgacattt	cacggagtct	tgatgtgttt	360
taaatgaagg	tgtgctctgg	tatgtaatga	caatatgtga	acaaacctgt	ggaattaaag	420
ttaaaatgaa	atagtcaatt	tgatacagtg	gaaaataact	aagcatacac	aatactggtg	480
aggctggtga	aacagggatg	ttgaatgcac	tcttgctgaa	agcctgcatt	gcatgattt	540
gtttgtagac	aaatttgaag	agtttgatct	ttttactctg	ccatttttgg	gaacatgata	600
aagatgtaat	ctcgtattat	gggtaaagct	tgattcaaaa	agatgtgtta	cttggacaaa	660
atcctaataa	gtagacgtag	ggcaatggct	ttatagccta	tgatagaaga	atatgattgc	720
aatttaacat	gttaattgaa	acacatgtat	ataacattta	tgactgtatt	gtgtatatgt	780
aacagtatat	ctattaatct	ttgaaaacat	aaaacctttt	cttatttttt	atttttttat	840

ttttttttga	gaccaagtct	ctctctgtcg	ccaggctgga	gtgcagtggg	gtgatctcgg	900
ctcactgcag	cctccacctc	ctgggttcga	gtgattctcc	tgccctcagcc	tcccagagtag	960
ctgggactac	aggcccatgc	taccaagccc	agctaatttt	ttgtattttt	aatagagatg	1020
gggtttcacc	atgttggcc	ggatggctgc	aatctcttga	cctcttgatc	tacctgcctt	1080
ggtctcccaa						1090

<210> 241
 <211> 680
 <212> DNA
 <213> Homo sapiens

<400> 241						
gcaacaccca	ttccaggaaa	agccacaagt	cctgaccccc	agccccagga	agcagaagct	60
gaacagaaag	tacaggtccc	accatgacca	gatgatctgc	aagtgcctct	ccctgagcat	120
atcctactcc	getaccattg	gcggcctgac	caccatcatc	ggcacctcca	ccagcctcat	180
cttcttgga	cacttcaaca	accagtatcc	agcctcagag	gtggtgaact	ttggcacctg	240
gttctcttc	agcttcccca	tatccctcat	catgctggtg	gtcagctggg	tctggatgca	300
ctggctgttc	ctgggctgca	attttaaaga	gacctgctct	ctgagcaaga	agaagaagac	360
caaaaggga	cagttgtcag	agaagaggat	ccaagaagaa	tatgaaaaac	tgggagacat	420
tagctaccca	gaaatgggtga	ctggattttt	cttcatcctg	atgaccgtac	tgtgggtttac	480
ccgggagcct	ggctttgtcc	ctggctggga	ttctttcttt	gaaaagaaaag	gctaccgtac	540
tgatgccaca	gtctctgtct	tccttggctt	cctcctcttc	ctcattccag	cgaagaagcc	600
ctgctttggg	aaaaagaatg	atggagagaa	ccaggagcac	tcactgggga	ccgagcccat	660
catcacgtgg	aaggacttcc					680

<210> 242
 <211> 491
 <212> DNA
 <213> Homo sapiens

<400> 242						
cttgaaagag	aaggggacaa	aggaacacca	gtattaagag	gattttccag	tgtttctggc	60
agttgggtcca	gaaggatgcc	tccattcctg	cttctcacct	gcctcttcat	cacaggcacc	120
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aggaacactg	accaccagtt	ggatgagtct	caaggctctc	ctctatgtga	caaccatgtg	240
aatggggagt	ggtaccactt	cacgggcatg	gcgggagatg	ccatgcctac	cttctgcata	300
ccagaaaacc	actgtggaac	ccacgcacct	gtctggctca	atggcagcca	ccccctagaa	360
ggcgacggca	ttgtgcaacg	ccaggcttgt	gccagcttca	atgggaactg	ctgtctctgg	420
aacaccacgg	tggaagtcaa	ggcttgccct	ggaggctact	atgtgtatcg	tctgaccaag	480
cccagcgttt	g					491

<210> 243
 <211> 983
 <212> DNA

<213> Homo sapiens

<400> 243

tgcggccgca	ccatgagcga	catccgccac	tcgctgctgc	gccgcgatgc	gctgagcgcc	60
gccaaaggagg	tggtgtacca	cctggacatc	tacttcagca	gccagctgca	gagcgcgccg	120
ctgcccacgc	tggacaaggg	ccccgtggag	ctgctggagg	agttcgtgtt	ccaggtgccc	180
aaggagcgca	gcgcgcagcc	caagagactg	aattcccttc	aggagcttca	acttcttgaa	240
atcatgtgca	attattttcca	ggagcaaacc	aaggactctg	ttcggcagat	tattttttca	300
tcccttttca	gccctcaagg	gaacaaagcc	gatgacagcc	ggatgagctt	gttgggaaaa	360
ctggtctcca	tggcgggtggc	tgtgtgtcga	atcccgggtgt	tggagtgtgc	tgctctctgg	420
cttcagcgga	cgcccgtggt	ttactgtgtg	aggtagcca	aggcccttgt	agatgactac	480
tgctgtttgg	tgcggggatc	cattcagacg	ctgaagcaga	tattcagtgc	cagcccagaga	540
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attctcatca	cttttttaaa	tactccgatt	gcggccaatc	tgccaatagg	attcttagag	720
ctcaccgccg	tcgttggtg	gatccgctgg	tgcgtgaagg	caccctggc	ttataaaagg	780
aaaaagaagc	cccccttacc	caatggccat	gtcagcaaca	aggtcacaaa	ggaccggggc	840
gtggggatgg	acagagactc	ccacctcttg	tactcaaaac	tccacctcag	cgctctgcaa	900
gtgctcatga	cgctgcagct	gcacctgacc	gagaagaatc	tgtatggggc	gcctggggct	960
gacctcttc	gaccacatgg	tcc				983

<210> 244

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(526)

<223> n = a,t,c or g

<400> 244

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cggctcagcc	acgcgttcgc	tcacgcgtcc	ggccaaccag	aagggttgcg	acggggaccg	120
cctgtactac	gacggctgtg	ccatgatcgc	catgaacgga	agcgtctttg	ctcaaggatc	180
ccagttttct	ctggatgacg	tggaaagtcct	gacggccacg	ctggatctgg	aggacgtccg	240
gagctacagg	gcggagattt	catctcgaaa	cctggcggtg	agtgtctccag	tagacacctg	300
tgtgggatgc	tcatcaaaga	cgtggaaagt	ggccccattc	gtgcgggcct	ggtggaggcc	360
gtgagggtgc	agtgcctgaa	aagtctgaca	gggaagttcc	ggacttcccc	agcgtggaaa	420
ggggctggtg	ccgcagacag	aacctgtctc	catctgttcc	ccgtcatcct	ctgcttgggc	480
caggccctga	gctgggggtga	gctgggggaca	ggcaggcagg	tgtatt		526

<210> 245

<211> 418

<212> DNA

<213> Homo sapiens

<400> 245

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cactcctatt	cactcctact	tgccactcct	tctattcatt	actcactgcc	cctgccccta	120
gtcccatg	taccctgag	ccatgggcat	ttcctgagcc	ccactcagca	ggctctgctt	180
cccccaggtc	ctgggtgaacg	agggcggtgg	ctttgaccgg	gcctctggct	ccttcgtagc	240
ccctgtccgg	ggtgtctaca	gcttccggtt	ccatgtgggtg	aaggtgtaca	accgccaaac	300
tgtccaggtg	acctcagcac	tggcccccac	ccccggctca	ggaggggtggg	gagggggaag	360
aaggggagcc	cagctgacct	cgggtggac	tctccattga	cctgtgtcct	ggacgaaa	418

<210> 246

<211> 706

<212> DNA

<213> Homo sapiens

<400> 246

acctcatatt	attggagcag	aagatgatga	ttttggtact	gaacatgaac	agatcaatgg	60
acagtgcagc	tgtttccaga	gcattgaatt	gctaaaatct	cgcccggtc	atttggctgt	120
tttcttacgc	catgtagttt	cacaatttga	ccctgcgact	ttgctttgtt	atctctattc	180
agacctgtat	aaacatacca	attccaaaga	aatcgtcgc	atcttccttg	agtttcatca	240
gttctttcta	gatcgatcag	cacacctgaa	agtttctgtt	cctgatgaaa	tgtctgcaga	300
tctagaaaag	agaagacctg	agctcattcc	tgaggatctg	catcgccact	atatccaaac	360
tatgcaagaa	agagtcctac	cagaagttca	aaggcactta	gaagattttc	ggcagaaacg	420
tagtatggga	ctgaccttgg	ctgaaagcga	gctgactaaa	cttgatgcag	agcgagacaa	480
ggaccgattg	actttggaga	aggagcggac	atgtgcagaa	cagattgttg	ccaaaattga	540
agaagtattg	atgactgctc	aggctgtaga	ggaagataag	agctccacca	tgcagtatgt	600
tattctcatg	tatatgaagc	atttgggagt	aaaagtgaag	gagcctcgaa	atttggagca	660
caaacggggt	cggattggat	ttcttcccaa	aatcaagcaa	agtatg		706

<210> 247

<211> 439

<212> DNA

<213> Homo sapiens

<400> 247

caagggaggg	gggttgatcc	cctggcacag	gtcgaggccc	tggaccacaca	tcctttgtct	60
gcctccccac	cccacagtgc	ccgttcacgc	acgatttcat	cctggccctc	cataggaaga	120
tcaagaatga	gcccgtggtg	tttctgagg	ggccagaaat	cagcgaggag	ctcaaggacc	180
tgatcctgaa	gatgttagac	aagaatcccg	agacgagaat	tggggtgccca	gacatcaagt	240
tgcacccttg	ggtgaccaag	aacggggagg	agcccccttc	ttcggaggag	gagcactgca	300
gcgtggtgga	ggtgacagag	gaggagggtta	agaactcagt	caggctcatc	cccagctgga	360
ccacggtgat	cctggtgaag	tccatgctga	ggaagcgttc	ctttgggaac	ccgtttgagc	420
cccaagcacg	aatggcgaa					439

<210> 248
 <211> 730
 <212> DNA
 <213> Homo sapiens

<400> 248
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 aagaagatca aaagaaactt catgattttg aagagcagtg tggtgaaatg tatttcaatg 120
 aaaaagatga caaatttcat tctgggagtg aagagagaat tcgtgtcact ttgaaagag 180
 tggaacagat gtgcattcag attaaagaag ttggagatcg tgtcaactac ataaaaagat 240
 cattacaatc attagattct caaattggcc atttgcaaga tctttcagcc ctgacggtag 300
 atacattaaa aacactcact gccagaaaag cgtcggaagc tagcaaagtt cataatgaaa 360
 tcacacgaga actgagcatt tccaaacact tggctcaaaa ccttattgat gatggctctg 420
 taagaccttc tgtatggaaa aagcatgggtg ttgtaaatac acttagctcc tctcttcttc 480
 aaggggatct tgaaagtaat aatccttttc attgtaatat tttaatgaaa gatgacaaag 540
 atccccagtg taatatatct ggtcaagact tacctgcagt accccagaga aaagaattta 600
 attttccaga ggctgggttc tcttctgggtg ccttattccc aagtgtgtgt tcccctccag 660
 aactgcgaca gagactacat ggggtagaac tcttaaaaat atttaataaa aaacaaaaaa 720
 aaagggcggc 730

<210> 249
 <211> 466
 <212> DNA
 <213> Homo sapiens

<400> 249
 attgctgccg ctggatcgac tgctttgcct tgtacgacca gcaggaggag ctctgctggc 60
 acatcgagaa ggtccacatc gaccagcgca aaggggagga cttcacttgc ttctgggccg 120
 gttgccctcg aagatacaag ccttcaacg cccgctataa actgctgate cacatgagag 180
 tccactctgg ggagaagccc aacaagtgtg cgtttgaagg ttgcgagaag gccttttcaa 240
 ggcttgaaaa tctcaagatc cacttgcgga gccacacagg cgagaagccg tatttgtgcc 300
 agcatccggg ttgtcagaag gccttcagta actccagtga ccgcgcaaaa caccagcgga 360
 cgcatctgga cactaaacct tatgcttgct aaattccagg atgtaccaa cgctacacag 420
 acccaagttc cctaagaaag catgtgaagg cacattcttc caaaga 466

<210> 250
 <211> 963
 <212> DNA
 <213> Homo sapiens

<400> 250
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gagggcgggc	gtggcgggcc	ccgcggcctt	ctctcagctt	cctttctcct	cacgacggcc	120
tccacagtec	ggagcccggc	ggagcccggg	cctggggggg	agagctgcct	ccacggccgg	180
gcaccagac	cccaccgtcg	cagtcgccac	cacctcagtc	catccttggg	accggcaatg	240
ggcttcgtat	cctccagtcg	acttgtaact	gacttggaca	cggaatacta	agaactcact	300
tctgtcctca	tcccagtcgc	gccggcggtg	accatctcgg	ctcttttggg	cttaactgcc	360
gtcctcttgg	aotctgtctg	actttggggg	caccatggac	caaagtggga	tggagattcc	420
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ctcctttttc	ctgcttctcc	cctccagctc	tgaatcaaat	aggtctcttt	tggtagaccg	660
cgaggatatt	tgagttctga	ggttgtgtct	cctgagtggt	cgaaccatca	ttaatatttt	720
octgatgagg	ttcagttaat	tagtaagagg	aagcagaaat	atcaagggac	ttaagaattg	780
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gcggggcgat	cacgaggtca	ggagttcgag	accagcctta	ccggcatggg	gaaaccctgt	900
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tcg						963

<210> 251
 <211> 894
 <212> DNA
 <213> Homo sapiens

<400> 251						
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caacctgcac	taccggtttc	tgaattggcg	ccgggggagc	cgaggagattc	gagagggtccg	180
agctttccga	tatcaggaga	ggttcaaaca	tatccttgta	gatggagata	ctttaagtta	240
tcatggaaac	tctgggtgaag	ttggctgcta	cgtggcttct	cgaccctga	ccaaggacag	300
caattatttt	gaggtgtota	ttgtggacag	tggagtccgg	ggcaccattg	ctgtgggggct	360
ggtccctcag	tactacagct	tggatcacca	gcctggctgg	ttgcctgact	ctgtagccta	420
ccatgctgat	gatggcaagc	tgtacaatgg	ccgagccaag	ggccgccagt	ttgggtcaaa	480
gtgcaactcc	ggggaccgga	ttggctgtgg	cattgagcct	gtgtcctttg	atgtgcagac	540
cgcccagatc	ttcttcacca	aaaatgggaa	gcgggtgggc	tctaccatca	tgcccattgtc	600
cccagatgga	ctgttcccag	cagtgggcat	gcactccctg	ggtgaggagg	tgcggctgca	660
cctcaacgct	gagctggggc	gtgaggacga	cagcgtcatg	atggtggaca	gttacgagga	720
tgaatggggc	cgggtacatg	atgtcagagt	ctgtgggact	ctgctggagt	acttagggaa	780
gggcaaaagc	atcgtggatg	tggggctggc	ccaggcccgg	caccactca	gcaccgcgag	840
ccactacttc	gaggtggaga	tcgtggaccc	tggagagaaa	tgctacatcg	ccct	894

<210> 252
 <211> 861
 <212> DNA
 <213> Homo sapiens

<400> 252						
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aggagcactt	agcagcttat	tcagtgtccg	attotgatcc	cggcaaggat	ccaagcatgg	120
aatgctgcog	tcgggoaact	cctggcacac	tgctoctctt	tctggctttc	ctgctcctga	180

gttccaggac	cgcacgctcc	gaggaggacc	gggacggcct	atgggatgcc	tggggcccat	240
ggagtgaatg	ctcacgcacc	tgcgggggag	gggcctccta	ctctctgagg	cgctgcctga	300
gcagcaagag	ctgtgaagga	agaaatatcc	gatacagaac	atgcagtaat	gtggactgcc	360
caccagaagc	aggtgatttc	cgagctcagc	aatgctcagc	tcataatgat	gtcaagcacc	420
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gtctcactct	ctgaatcact	catctttaca	cttttttagag	tttgtaaatg	gtgaaagatt	720
tgaaaattaa	ggtatgattt	cagtgaaaag	taccaagtgt	tgtattgtgc	gaaggaaaag	780
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tgaatagtgt	taaaaaaaaa	a				861

<210> 253
 <211> 556
 <212> DNA
 <213> Homo sapiens

<400> 253						
caggctgtta	agacaagagc	ttgtgggtgct	ttgccacctt	caccacccca	gtttgatatc	60
tttgctggca	gctgggattc	gtccccggat	gttgggtgatg	gagttagcct	ccaaggggtc	120
cttggatcgc	ctgcttcagc	aggacaaagc	cagcctcact	agaaccctac	agcacaggat	180
tgactccac	gtagctgatg	gtttgagata	cctccactca	gccatgatta	tataccgaga	240
cctgaaaccc	cacaatgtgc	tgcctttcac	actgtatccc	aatgctgcca	tcattgcaaa	300
gattgctgac	tacggcattg	ctcagtactg	ctgtagaatg	gggataaaaa	catcagaggg	360
cacaccaggg	tttcgtgcac	ctgaagttgc	cagaggaaat	gtcattttata	accaacaggc	420
tgatgtttat	tcattttggtt	tactactcta	tgacattttg	acaactggag	gtagaatagt	480
agagggtttg	aagtttccaa	atgagtttga	tgaattagaa	atacaaggaa	aattacctga	540
tccagttaaa	gaatag					556

<210> 254
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 254						
caaaggccag	taatagtacc	catgagtttc	gtattggcct	acctgagggg	tgggaatccg	60
aaaaaaaggc	agttatcccc	ctggggatcg	ggccaccctt	gactttaatc	tgctagggg	120
ttctgggggg	tattctcatc	tacgggagga	aaggcttcca	aactgcccac	ttttacttaa	180
aggacagtcc	atccccctaa	gtaatatcca	cccctccacc	acctatcttt	ccaatttcaa	240
aggaggtcgg	accaattcca	ataaagcact	ttccaaagca	tgtggcaa	ttacatgcaa	300
gtaggggggtt	tactgaaaaa	tttgaaacac	tgaaaaagtt	ttaccaggaa	gggcaaagct	360
gtactgttga	cttaggtatt	acagcaaaca	gtcccaacca	cccagacaac	aggcacagga	420
atcgatcctt	aattg					435

<210> 255
 <211> 698
 <212> DNA
 <213> Homo sapiens

<400> 255
 cctcatttcc tgatcgaaca gcctcacttg tgttgetgtc agtgccagta gggcaggcag 60
 gaatgcagca gagaggactc gccatcgtgg ccttggctgt ctgtgcggcc ctacatgcct 120
 caccagccat acttcccatt gcctccagct gttgcacgga ggtttcacat catatttcca 180
 gaaggctcct ggaaagagtg aatatgtgtc gcatccagag agctgatggg gattgtgact 240
 tggctgctgt catccttcat gtcaagcgca gaagaatctg tgtcagcccg cacaaccata 300
 ctgttaagca gtggatgaaa gtgcaagctg ccaagaaaaa tggtaaagga aatgtttgcc 360
 acaggaagaa acaccatggc aagaggaaca gtaacagggc acatcagggg aaacacgaaa 420
 catacggcca taaaactcct tattagagag tctacagata aatctacaga gacaattcct 480
 caagtggact tggccatgat tggttagtct cgctctgtca cacaggctgg agggcagtgg 540
 cgggatctcg gttcacccca acctttgcct cacgggttca agggattctc gtgcctcage 600
 cttocaagtg gctgggattg caggtgtgcg ccagtcagcc tggctagttt tagtattttt 660
 tgttacagac ggggtttcac catgttggct gggctggt 698

<210> 256
 <211> 736
 <212> DNA
 <213> Homo sapiens

<400> 256
 gtttgaacag cccggaaacc cgggcgaccc acgcgtacga actccgcccc catggggggcc 60
 ccactttttc gctttgattc cttcttcccc caaagaggte ccagctaccc catcctccag 120
 aagggaaccc attgccccaa cagcgactct tctctctaaa aagaccccag caactctagc 180
 ccccaaagag gccctcattc cccagctat gactgttccc tcccctaaaa agaccccagc 240
 aattccaacc cccaaagaag cccagctac cccatcctcc aaagaggcct ccagtcccc 300
 agcagtgact ccttccactt acaaaggggc cccatcccc aaagagctcc tcattccacc 360
 agctgtgact tctccttccc ccaaagaggc acctactcct ccagctgtga ctctccatc 420
 ccccgaagag ggcccagcaa ctccagcccc caaagggact cccacttccc cacctgtgac 480
 tccttctctc ctcaaagact cccctacttc cccagcttct gtcacatgta aaatgggggc 540
 cactgttcct caagcatcta aagggttcc agcaaagaaa ggccccacag ctctgaaaga 600
 agtacttgtt gccccagctc cagaaagcac gccaatcatc acagctccca ctcggaagg 660
 tccacagacc aaaaagagtt ctgctacttc acctcctata tgcccagatc cctcagctaa 720
 gaatggttct aaagga 736

<210> 257
 <211> 77
 <212> DNA
 <213> Homo sapiens

<400> 257
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 tatcttttaaa aaaaaaa 77

<210> 258
 <211> 499
 <212> DNA
 <213> Homo sapiens

<400> 258
 aatgctcctt tggtaagaac aattatatgg ctaaattaat ctcagccacc tagttctaaa 60
 tgtagagcaa ggattgcaag ggattattta gacaagttca tcaattaagt aaaattagac 120
 atgaaggata taagaatgaa tgataaagca agctaaaaat ggtgaaacaa gggatgtctg 180
 attggaagta gaagatattt atttaggttc taggacatta gtatcagtga ggacagtaat 240
 ttctgcttg tttgtatttc agtgatcaca tacacttctt tacctgataa cgtctctctt 300
 ctctaggctg gttttgggta cggcttgcca atttctcgtc tgtatgccaa gtactttcaa 360
 ggagatctga atctctactc tttatcagga tatggaacag atgctatcat ctacttaaag 420
 gtatcccttg aattcaatag caaaatcctg tttctaaaac cattgctcct tttatagccc 480
 tgagtgtctat ggtccggag 499

<210> 259
 <211> 621
 <212> DNA
 <213> Homo sapiens

<400> 259
 tttcgtgact gtagtcagcc cttagtggat gagagcgct atgcttcaga aacagcaggc 60
 tcccaggatg gacacccgc cccctgaaga acgcttagag aagcaaatg aaaaactgaa 120
 caaccaggaa gaggagacgg agtttaagga actggacggt ctgaggggaag ccttggcaaa 180
 cctccgggga ctgtcagagg aggagaggag cgagaaggct atgcttcgct cccgcattga 240
 agagcagtcc cagctcatct gcatcctgaa gcggagggtca gatgaggccc tggagcgctg 300
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 gctcaaggcc caggggtgagt acagtcggaa actagaggaa cgctttatga ccctagcagc 420
 caaccacgag ttgatgctcc gcttcaagga tgaatacaag agtgagaaca tcaagctgag 480
 ggaggagaat gagaagctga ggctggagaa taacagcctc ttcagccagg ctctgaagga 540
 tgaggaggcg aaagtattac agctcacagt ccggtgtgag gccctcactg gggagctaga 600
 aacgctgaag gagagggtgtg c 621

<210> 260
 <211> 414
 <212> DNA
 <213> Homo sapiens

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<400> 260
agatccgggt gcgagccacg cgtccgtgca ggtgcaggta ctgaaagagc aactttttgc      60
tgggcgatat ccttcaccct tccgctcctg cgcactcatg ggaatgtgtg gcagtagaag      120
cgctgataac ttgtcatgcc cttctccatt gaatgtaatg gaaccagtaa gcttctttcc      180
tcttaaatca ctggggaagg gaatgataca acatttcaga cacatagttt ccctagttta      240
gatgaaatat atgtttatct taaatacata atttgataaa ttattgttga ttggaagtga      300
ctttcacctt tgaaagtcca ttgctgtctg aagccactag aaagccacct gaattgcaat      360
agtgatttat ctttctgact aaaggaggta atgcaccata aaaacatgta cagt          414

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<210> 261
<211> 620
<212> DNA
<213> Homo sapiens

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<400> 261
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acagaccagt atggagacat ctggacattg catgatggag gattccggaa ttataacacc      180
agcatagata tgcaaagggg aaagctagat gacatcatgg agcatccaga aaagtctgac      240
aaggacagtt ctagtgctta caacacagct gagagctgca gaagtactcc gctcactgta      300
gaccgttccc ctgacagttc cttccaagg gtgatcaacc tcaccaataa gaaaaacctg      360
agaagcacia tggcagccac ccagtcctct tccggacaga gcagtaaaga gtcgacctcc      420
accaaagcca aaaccactga gcaaggttgt agcgtgaaa gcaaggagaa ggttttagaa      480
ggcagcaagc ttctgatca agagaaggca gtcagcgaac acatccctta cctctctcct      540
taccacagct cctcatatag atatgcaaac atcccagcac acgcccggca ttatcaaagc      600
tacatgcagt taattcaacg                                620

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<210> 262
<211> 418
<212> DNA
<213> Homo sapiens

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<400> 262
gggtctgggg ctgcctggcc accgtgtcca cccacaagaa gatccaagga ctgccatttg      60
ggaactgcct gcccgtcagt gatggccctt tcaacaatag cactgggatt ctttctttot      120
acatgacagc caaggacccc gtggtggctg atctgatgaa gaaccccatg gcctcgctga      180
tgctgccaga atcagaaggg gagttctgca gaaaaaacat cgttgatccg gaagatcccc      240
gatgtgtcca gttaacgctc actggccaga tgatcgagc gtctccagaa gaagtagaat      300
ttgccaagca agccatgttt tcaaggcacc cagggatgag gaagtggcct cgtcaatatg      360
aatggttctt tatgaagatg aggatagaac atatctggct tcagaaatgg tatggagg      418

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<210> 263
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 263
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 gtggcgcgcg tggacgcggc tttgcctccc ggagaaggat cagtgggtcaa ttggtcagga 120
 cagggactac agaaattagg tccaaattta ccctgtgaag ctgatattca cactttgatt 180
 ctggataaaa atcagattat taaattggaa aatctggaga aatgcaaacg attaatacag 240
 ttatcagtag ctaataatcg gctgggttcgg atgatgggtg tggccaagct gacgttgctt 300
 cgtgtattaa atttgcctca taatagcatt ggctgtgtgg aagggctaaa ggaactagta 360
 catctggaat ggctgaattt ggcaggaaat aatcttatag ccatggaaca gatcaatagc 420
 tgcacagctc tacagcatct c 441

<210> 264
 <211> 832
 <212> DNA
 <213> Homo sapiens

<400> 264
 tatttcgagc ggcagttggg gcggtaccag aggggtgcctg gaaggatacg gccagctcc 60
 acaagagcga ggaggcgaag cgggtgctgc ggtattacct cttccagggc cagcgctata 120
 tctggatcga gaccagcaa gccttctacc aggtcagcct cctggaccat ggcgctctt 180
 gtgacgacgt ccaccgctcc cgccatggcc tcagcctcca ggaccaaag gagaggaagg 240
 ccatttacgg cccaacgtg atcagcatac cgggtcaagtc ctacccccag ctgctggtgg 300
 acgaggcctt cagcatcgcg ctgtggctgg ctgaccacta ctactggtac gccctgtgca 360
 tcttctcat ttcctccatc tccatctgcc tgtcgtgta caagaccaga aagcaaagcc 420
 agactctaag ggacatggtc aagttgtcca tgcgggtgtg cgtgtgccgg ccagggggag 480
 aggaagagtg ggtggactcc agtgagctag tgcccgaga ctgcctggtg ctgtcccagg 540
 aggggtgggct gatgccctgt gatgccgccc tgggtggcgg cgagtgcag gtgaatgata 600
 gctctctgac aggagagagc attccagtgc tgaagacggc actgccggag gggctggggc 660
 cctactgtgc agagacacac cggcggcaca cactcttctg cggaaccctc atcttgcag 720
 cccgggccta tgtgggaccg cagtccttg cagtgggtgac ccgcacaggt atgagccggg 780
 aggctgggct tgagagagat ccgggctcag cacccttgaa gaggtggagt gg 832

<210> 265
 <211> 714
 <212> DNA
 <213> Homo sapiens

<400> 265
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ggacgctgcc	atggctgtgc	tgacggcctc	caaccacgtg	agcaacgtca	ccgtgaacta	120
caacatcacc	gtggagcgga	tgaacaggat	gcagggcctg	cgggtctcta	cagtgcagc	180
cgtgctgtcc	cccaatgcc	cgctggcact	gacggcgggc	gtgctggtgg	actcggccgt	240
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caatgtcacc	cacacctacg	ctgccccagg	tgagtacgtc	ctgaccgtgc	tggcatctaa	420
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acgtacgttc	agcaacaaga	cgctggtgct	ggatgagacc	accacatcca	cgggcagcgc	660
aagcatgtga	ctggtgctgc	ggcggggcgt	gctgcggggac	ggcgagggat	acac	714

<210> 266
 <211> 1872
 <212> DNA
 <213> Homo sapiens

<400> 266						
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ccagaagccc	cttcacgatg	gggccctcgg	gtcgcagcag	aacttggttc	gcatgaagga	120
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gagcgtgtc	aatgggagcc	atgcgatgat	ggacctactg	gttgaacttt	gccttcagaa	240
ccacctgaat	ccatcccacc	atgcccttga	aattcgggtc	tcagaaaccc	aacaaccttt	300
gagttttaag	ccaaataactt	tgattgggac	cctgaatgtg	catactgtgt	ttctgaaaga	360
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tttggtcgtg	aattacctgc	ggacacaaaa	agctgttggtg	cgtgtgagcc	ctgaggttcc	480
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cgggataaag	gagctctacg	cgtgggacaa	cagaagagaa	accttttagga	aatcatcact	660
tggcaatgat	gagacagata	aagagaagaa	aaaattttctg	ggattttttca	aagttaataa	720
aagaagcaat	agtaagggct	gtttaacgac	ccccaaactcc	ccatccatgc	actcacgttc	780
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gatgaagaag	gcgcgagccc	ctcctcctcc	aggttcaggg	ccacctgtgc	aagacaaggc	900
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caagcgcttc	tgatggacgg	gcctcttcct	gacctcggac	ctttcccagc	gtctcttctg	1140
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cccagaattt	acttcctttg	gggtttacat	ataaatgcat	taataacaga	gatttgtttg	1260
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actaggaact	cacaacttat	atatactatc	cattcaatga	tacataggac	ccaatgtctt	1620
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gaaagaagtg	ggagaagaag	gggggtctat	tcattattct	atattatgat	tctcttcatt	1740
attctgttct	cttcattatt	ctattcattt	cttcacccat	ttattcacta	aacagtgaca	1800
tagtacttac	ttgatgctag	gtattacacc	agttttgtgg	gctataagag	tgaataacaa	1860
gcacgtgacc	tt					1872

<210> 267

<211> 684
 <212> DNA
 <213> Homo sapiens

<400> 267
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 aaaacaattt tgaaaaagat ttcaaaaaaa ttttgaagga atcatgctgc ccagttttta 120
 gacttactat aaagctgtga taatcaaggc aatctgggtat ttatgaaagg ataaacacat 180
 agatcaatgg aataaagtcc aaaaccagac tcacataaat agcaattgat ttctgacaaa 240
 ggtgaaaaga caactcaatg gggaatggag agtttttcaa cagatgattt taaaacaact 300
 gaacatccat atgcaaaaaa ataaacctac ctaaaatttca cagcttatac aaaaattaac 360
 ctaaaatgga tcacggatct aaatgtagaa ctaaaatttata aaaatttttta gaagaaaaaa 420
 atccataggc cgggcacggg ggctcatgcc tgtaatccca gcacttcaga ggctgaggcg 480
 ggcatagccg ttgaggtcag ttcaagacca gcctagccta tgggtgaaa tcccaactct 540
 actaaaaata aaaaataaaa aaaaaatggg ctgggagtgg tgggtgcacac ctgtagtccc 600
 agctacttgg gagactgaag cacaagaatc acttgaaccc agcaggcaga ggttgcagtg 660
 agtggagatt gtgccactgc accc 684

<210> 268
 <211> 453
 <212> DNA
 <213> Homo sapiens

<400> 268
 ggtcgacgat ttgcgccgcc gtcggacgag gacgaggagc cgtgggagcc gtggacgcag 60
 ctgcgcctgt cgggccacct gaagccgctg cactacaatc tgatgctcac cgccttcctg 120
 gagaacttca ccttctccgg ggaggtcaac gtggagatcg cgtgccggaa cgccaccgcg 180
 tacgtagtgc tgcacgcttc ccgagtggcg gtggagaaag tgcagctggc cgaggaccgg 240
 gcgttcgggg ctgtccctgt agccggtttt ttctcttacc cgcaaaccga ggtcttagtg 300
 gtggtgctga ataggacact ggacgcgcag aggaattaca atctgaagat tatctacaac 360
 gcgctcatcg agaatgagct cctgggcttc ttctgcagct cctatgtgct ccacggggag 420
 agaagattcc ttgggggttac tcagttttcg cct 453

<210> 269
 <211> 525
 <212> DNA
 <213> Homo sapiens

<400> 269
 ggcaacgagaa ctggtgctta atttaatgcc aattcatgat gtaggtttct aagcagcaca 60
 taaaaggggc tttttaggta gcactgagta ctttactaaa aatacaaaaa ttagccaggg 120
 ggggggggtgc acgtctttta tcccagctac tcaggggcggg ggccaggggg tggggtaggg 180
 tggggggctga gacaggagaa gcacttgaac ccaggaggcg gaggttgagc tgagctgaga 240
 ttgtgctact gtactccaac ctgggcaaca aacagagtga gacactgtct caaataaata 300

aataaataga	taaataaaat	aaaataaaat	aaaaagaact	cgaccctttt	tacaatagct	360
aaaggaaaat	aaaataactta	agaatatact	taaccaagga	ggtgaaagac	ctctacaaag	420
aaaactacaa	aacactgctg	aaagaaatca	cagatgacac	aaacaaaaac	acatcccaag	480
ctcatggaca	ggtagaatca	atactgtgaa	aatgactata	ctgcc		525

<210> 270
 <211> 880
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(880)
 <223> n = a,t,c or g

<400> 270						
cccagtccca	cattgagccc	tgatcccatc,	caagtccata	gacttggcct	ctgaccaaac	60
ctgaccctgc	acttgtcact	taagggtggc	ccatattcag	ctcagaccct	gaaccgagct	120
ctgaccctgg	cttctgactg	aatctgtgac	agactaaggc	ctgaccctgg	ccctatacca	180
cgtctccacc	cgtgtcctca	actgagtgtc	gaccccaaac	ctagacagcc	ctacctgac	240
cttccccccg	gcctgtcccc	gccgcttcat	ctcaaaagtt	gaagggtgagg	agccggtaaa	300
cagggtctgga	gcctgggtctc	agactcagcc	tgagcaagct	cagtctgggg	tcattggggc	360
tgtaaccccg	ggcaggccct	tgtaggggat	gcagggtctc	accctagggg	tataagggat	420
ttctgtgccc	atcagaactt	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	480
nnnnnnnnnn	nnnnnnnnnn	atcttgtgtg	tagcatatgt	gatgaccttg	acttcacctc	540
cctggcgcca	atatcctctt	ctgtaaaatg	gcttatgcat	tacaaagtga	ggtcctgcca	600
gtgactacac	ctagaggcat	taagtgcctt	tgtggactcc	tgccctgcac	ctcacctctc	660
ccagcttttt	aacccctga	ggaaccttct	taccttgagt	ccctcaccgg	ctacaggcca	720
tccatgagca	gatgaactgc	aaggagtatc	aggaggacct	ggccctgcgg	gctcagaacg	780
atgcggtctg	ccggcgccg	tcagagatgt	ttaagggtgag	gctggctcag	ggtcgtggcc	840
tagcatcttt	aagttctggg	atccagtctg	gggtagggag			880

<210> 271
 <211> 1066
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(1066)
 <223> n = a,t,c or g

<400> 271						
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ccccgctgc	tgctctgggt	taagaggtga	gtgagctcac	agccccgagg	cagggcaggg	180
gagggccctc	gagctgaggg	gttggctcca	gggttatggc	cagggtgga	ggaggaggaa	240
ggctctgtgt	catggagaac	tctctggcgc	cccagggcag	gagccagtgg	gtggcttcaa	300

acaaagcagc	atctttgtgg	tgtttcacca	gttcttagtc	ccagttacag	caggtgactg	360
tggtggacga	aaactggact	caacagtttc	ctccattcag	ggatcccagg	ccatggagca	420
aggagggccc	gaatcagtac	ctccctcaga	tcacctggac	agtgtgagac	aaaaagccgc	480
agggaccatc	cctggagggg	gattcagcag	gctcgatcgg	ggtccagggtg	ctggtatttt	540
tcattagcct	ccaggggatt	ctgatgtagc	cagcagcgtc	cttggacaac	agtttgagat	600
ctgctgcttt	tcaaaactgga	ttccttggag	cgctggaaat	ctcagcgatg	tcacagggca	660
ggagagggag	gttgtggagg	gaaaattcag	acttcccgcc	cagcccacca	tttcaccagg	720
cagctctaaa	tttatgtgtt	ttataagcca	aggttcacac	aaaaaagaaa	attcgtctggg	780
gggaaaaaaa	cagtttctat	ggcttaaaaa	aaagtctgaa	gaccaccagt	ctatttcaat	840
actctatttt	gttcatgaag	aagctggtga	ccaaagatac	ccaaagacta	agtcaggggg	900
atgcaggggt	acaggggtgc	ctctcacttt	cccaaagtga	gatccacata	ccacagcaaa	960
atgatttgag	ccagcctgtg	gatgaacaca	tttaaaattt	tatttataaa	tacatttact	1020
gttacatttg	acttctcttt	attaaatata	tttgtgattt	ataaaa		1066

<210> 272
 <211> 659
 <212> DNA
 <213> Homo sapiens

<400> 272						
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gcacacaact	acaaaaatga	gacggagtgg	agagcgaaca	tcgacacagt	gatggcgtgg	120
ttcacagagg	aggacctgga	tctggtcaca	ctctacttcg	gggagccgga	ctccacgggc	180
cacaggtacg	gccccgagtc	cccggagagg	aggagatgg	tgcggcaggt	ggaccggacc	240
gtgggctacc	tccgggagag	catcgcgcg	aaccacctca	cagaccgcct	caacctgac	300
atcacatccg	accacggcat	gacgaccgtg	gacaaacggg	ctggcgacct	ggttgaattc	360
cacaagttcc	ccaacttcac	cttccgggac	atcgagtttg	agctcctgga	ctacggacca	420
aacgggatgc	tgctccctaa	agaagggagg	ctggagaagg	tgtacgatgc	cctcaaggac	480
gcccacccca	agctccacgt	ctacaagaag	gaggcgttcc	ccgaggcctt	ccactacgcc	540
aacaacccca	gggtcacacc	cctgctgatg	tacagcgacc	ttggctacgt	catccatggg	600
gtgagtcgcc	tgctggaggc	accacctcca	ggggtccct	ccccaggctc	tgggtcttc	659

<210> 273
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 273						
acgcgacttc	tcgggtcgac	ccacgcgtcc	gcacatataa	cacatcacgc	accttttgag	60
tggttacctt	ggttctcgcc	tttcttttca	agagaccatt	cttcaacaga	actgtaagga	120
ttcttcttgg	ctgaatcaga	tgtgacgcat	cccacttctg	cgtttgaggt	ctagcacata	180
ccgtccaag	ggctttgacg	tcacagtga	gactcacac	ggaagctgga	cgggcttcgg	240
tggggaagac	ctcgccacca	tccccaaagg	gttgaatact	tattttcttg	tcaacattgc	300
cactattttt	gaatcaaaga	atttcttttt	gcctgggatt	aaatggaatg	gaatacttgg	360
cctatcttat	gccacacttg	ccaagccatc	aagttctctg	gagaccttct	tc	412

<210> 274
 <211> 522
 <212> DNA
 <213> Homo sapiens

<400> 274
 gaattaagag ttactccggg ccaaattggcc ggagttgtca gatctggcag cgtcttcgct 60
 ggggctccag ggagctgctg ctgggggtgga agctctcaca ctctttctcc acgtgccctt 120
 tccagttccc tgacatcgtg gagttctgcg aggccatggc caacgccggg aagaccgtaa 180
 ttgtggctgc actggatggg accttccaga ggaaggtaag gcgtctgac caggtctgga 240
 gctgggattg aggagggcaa gaggtctctg gatgggcaca gagacaccag ctctgggtga 300
 ccagggctca gccaccacag ggttacggcc gagctgctca ggccctggct gagccaaggg 360
 actccatggg ctgtgcagac tgcgtgccat ctgttgccgc aggtgctttg aattggcaaa 420
 gggacagagc cgggcatggg gctctggggg ttgggggaag gactaaggct agagcaaaact 480
 ctcttggtt cagtacttgt gaatcagagg gttaaaga aa 522

<210> 275
 <211> 650
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(650)
 <223> n = a,t,c or g

<400> 275
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 tttcaacatt ttccctttca cctaaaactg tattttttctc tgctaagacc ggctacceta 120
 ctttcatatt cttttcactc ttcttggtc ttttgggct ttttaggaatt tgggatgatt 180
 caggctctga caggcatggg actagattta ttttaggctg ctcttttgct gttgtccaac 240
 aggccaagga gagatttaaa tgatttatcc aatatttgct aaatagtcac gtgtttcatt 300
 tatcccatat atagttcagc ctaatatattg tttttgtttt gatttggtac actagtgcac 360
 acatagagac gtgaagccag aaaatatcct catcacgaaa cattccgtga ttaagctttg 420
 tgacttttga tttgctcggc ttttgactgg accgagtgac tactatacag actacgtggc 480
 taccaggtgg taccgtccc ctgagctgcn ggtgggggac acgcagtacc ggcccccg 540
 tgggatgttt ggggcaattg gctgtgtctn tgctgagctn gctgtcagg aagtgcctct 600
 ggtggccagg aaaatcgga tggtggatca gctgtatctg attaggaaga 650

<210> 276
 <211> 497
 <212> DNA
 <213> Homo sapiens

<400> 276
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 atgtgggtcag caagcctcgc ctttgggtcag gccctggagg gtacagctga cccatagggc 120
 cacttccatg gcaactgggca agtggtgtga ttggaaatga agtcgttgcc cccgatttct 180
 ttggggccag gttgagcttt cctgcccaga gcacggaggc taaagggggg gggctttgga 240
 ctggattggg gctgacctca gcctacacct gcaggaggag gtggagacag aggtggcctg 300
 ggaggaatgt gggcacgtcc tactgtcact gtgtacagc tctcagcagg gtggcttgct 360
 ggtaggtgtg ctgcgctgcg cccacctggc ccccatggat gccaatgggt actcggaccc 420
 ctctgtgcgc ctgtgagtga actggggtag gcaggcggga ggtgaggata aggcggtgac 480
 tcctcacctc tccaggg 497

<210> 277
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 277
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 gcgctgtaat tccctgctgg aggaggagac catcctgcac ttcttctgtc agatcctgct 120
 tgactgcat catgtgcaca cccacctcat cctgcaccga gacctcaaga cccagaacat 180
 cctgcttgac aaacaccgca tggctgtcaa gatcggtgat ttcgccatct ccaagatcct 240
 tagcagcaag agcaaggcct acacgggtgg ggtaccacca tgctatatct cccctgagct 300
 gtgtgagggc aagccctaca accagaagag tgacatctgg gccctgggct gtgtcctcta 360
 cgagctggcc agcctcaaga gggctttcga ggctgcgaac ttgccagcac tgggtgctgaa 420
 gatcatgg 428

<210> 278
 <211> 427
 <212> DNA
 <213> Homo sapiens

<400> 278
 gtccagtgtg gtggaattca ccagggtgtcc ggggcagtgg tagtatctgg gctgctgcag 60
 ggcagtatgg ggctgctggg gagtcccggc cactgtgtcc cccactgtgg gccctgggtg 120
 ctggctccca gcctggttgt ggcagggtctc tctgccaca gggaggtagc ccagttctgc 180
 ttcacacact ggggggttggc cttgtgttac gtgagtctg agaggcgtgg gatgggtgcc 240
 agtgggggtg tatgggggga ctaggggagg gcagaactgc tggctctatc agattcagca 300
 gcgactggaa tagggacata ttttatattt ggaatccaag acttttcctt gattcatctg 360
 gtctccttga atttcacact gttttctgct gtccccaag gtcacttctt attccttcca 420
 tgggagt 427

<210> 279

<211> 561
 <212> DNA
 <213> Homo sapiens

<400> 279
 cccagaatga ccgggtcgac ccacgcgtcc gcacccagct atggaggcag ctgcaggaac 60
 aacttgtttt accgagaaga aacctacact ccaaaagctg agacggacga gatgaatgag 120
 gtggaaacgg ctcccattcc tgaagaaaac catgttttggc tccaaccgag ggtgatgaga 180
 cccaccaagc ccaagaaaac ctctgcggtc aactacatga cccaagtcgt cagatgtgac 240
 accaagatga aggacagggtg cataggggtcc acgtgtaaca ggtaccagtg cccagcaggc 300
 tgcttgaacc acaaggcgaa gatctttgga agtctgttct atgaaagctt cgctagcata 360
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 aggaacggga aggtcccctt ctctgtgaag tctgagagac acggcgtgca gtccctcagg 480
 taactactct gtgatcgggg ctctgtgaaa cggttttcct gtttatgacg gtgttgttga 540
 aattttgaaa aataccacac a 561

<210> 280
 <211> 792
 <212> DNA
 <213> Homo sapiens

<400> 280
 atttttgatg ccatgtggct acattggttt tagaatacta ataaaatcca ttgcttttaa 60
 aataaataaa taaaccccat agcacatcct ccatacaaca tctgttgtcc ctcaagatac 120
 aattgttacc actatcatct aaccattatt ttatgataac tttaaaatat caacttgga 180
 agaaaatatt ccacaaaaca cactctgcct ttttacttta aagagtcctt ggctacctgg 240
 gccaatatta ttctcatttg taggatttag gtccacaga atataatatg tgccttttc 300
 tgtgttccct gcagatttgc aagtaccatc ctttttggg gccttacttt gcacctccag 360
 catctgggaa acaatgtttt cctgttgag actctctttg gtgcagtcac cctcctggcc 420
 aattgtgttg caccttgggc actgaatcac atgagccgtc gactaagcca gatgcttctc 480
 atgttcctac tggcaacctg cttctggcc atcatatttg tgccctcaaga aatgcagacc 540
 ctgcgtgttg ttttggcaac cctgggtgtg ggagctgctt ctcttggcat tacctgttct 600
 actgcccaag aaaatgaact aattccttcc ataatacagg gaagagctac tggaaactact 660
 ggaaactttg ctaatatattg gggagccctg gcttccctcg tgatgatcct aagcatatat 720
 tctcgacccc tgccctggat catctatgga gtctttgcca tctctctctg ccttgttgtc 780
 ctctccttc cg 792

<210> 281
 <211> 1047
 <212> DNA
 <213> Homo sapiens

<400> 281
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atcagctagt	gaatgtgata	caataaccagg	gaggcagtgc	atggcttcct	gtttcttcct	120
gcttaagcaa	tttgatgatg	ttttgattta	cctcaactca	tttaagagcc	acttctataa	180
tgatgacatc	tttaacttta	attatgcccc	agccaaagct	gcaacaggca	ataccagtga	240
gggcgaagag	gcgttcctct	tgatccaaag	tgagaagatg	aaaaatgatt	acattttacct	300
cagctgggta	gctcggggct	atattatgaa	taagaaacca	agactagcct	gggaacttta	360
tcttaagatg	gaaacctccg	gcgagtcctt	cagtctctta	cagctcattg	ctaatactg	420
ctacaagatg	ggccagtttt	actattctgc	caaagctttt	gatgtccttg	agaggctgga	480
tcctaaccct	gaatattggg	aaggcaaacg	gggtgcctgt	gtgggcattt	tccagatgat	540
catagctggg	agagaaccca	aagagaccct	tcgagaagtg	ctccattttac	tgagaagcac	600
aggtaacacc	caagtagaat	acatgatccg	gatcatgaag	aaatggggcca	aagaaaacag	660
agtgtccatc	ctaaaatagc	gccagtgcac	taggaaccag	cttctacttt	gacataaaac	720
tggaatcat	tttcaactcca	gctttaatct	gtgatacagg	gctctgtttt	attgacattt	780
tccttccttg	ctctttaagc	ctcaagggtca	gagactgact	tgctgagact	tagtctcctg	840
gctgaacaga	gtgccatagt	ctgtgaccct	gtatgatcct	agtagcaata	agattttgga	900
cttatctggt	gcctttcttc	caaaaatgct	cagagtactt	ttatgcaatt	tactgacttt	960
aaggaaaaca	gtataacttt	tttttgttag	catttttatgg	cattgtctcc	tggtgcaat	1020
aacaaacatc	tttgatgttc	agaatc				1047

<210> 282
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 282	
ctttaaaagt	ttctgatgaa ttagtgcagc aatatcaaat taaaaaccag tgtctttcag 60
caatagcatc	tgatgcagaa caagaacctt aaattgatcc atatgcattt gttgaaggag 120
atgaggaatt	cctttttcct gataaaaaag atagacaaaa tagtgagaga gaagctggaa 180
aaaaacacaa	ggtaagagaa atcacagtac accaaagggt cactgttgat tttgtagcac 240
tgcatatagt	aacactctta ctaccacagt tatctcactt cttttgtctt agaatagaaa 300
gagtaatcat	ttatttagaa aaacctattt ttgcccggtc gcggtggctc atgcctg 357

<210> 283
 <211> 536
 <212> DNA
 <213> Homo sapiens

<400> 283	
ctggggtgcc	ccgcaacctg ccttcagacc tggagtatct gctgttgctc tacaaccgca 60
tcgtcaaact	ggcgctgag gacctggcca atctgaccgc cctgcgtgtg ctcgatgtgg 120
gcggaaattg	ccgcccgtgc gaccacgtc ccaaccctcg catggagtgc cctcgtcact 180
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tgctggacct	gagtgagaac ttctcttaca aatgcatcac taaaaccaag gccttcagg 360
gcctaacaca	gctgcgcaag cttaacctgt ccttcaatta ccaaaagagg gtgtcctttg 420
cccacctgt	ctctgggccc cctttccttc ggggaagcct gggtcgcccc ttgaaggag 480
ctgggacatg	gcacggcaat ctttctttcc cgctccactt cgaatggggg aagacc 536

<210> 284
 <211> 440
 <212> DNA
 <213> Homo sapiens

<400> 284
 gtatcttatt tgcggcgctg atctggagtt cgttcgatga gaatatagaa gcttcagccg 60
 gaggcggcgg tggttcgtcc atcgacgctg tcatgggtga ttcaggtgcg gtagttgagc 120
 agtacaaacg catgcaaagc caggaatcaa gcgcgaagcg ttctgatgaa cagcgcaaga 180
 tgaaggaaca gcaggctgct gaagaactgc gtgagaaaca agcggctgaa caggaacgcc 240
 tgaagcaact tgagaaagag cggttagcgg ctcaggagca gaaaaagcag gctgaagaag 300
 ccgcaaaaaca ggccgagtta aagcagaagc aagctgaaga ggccggcagc aaagcggcgg 360
 cagatgctaa agcgaaggcc gaagcagatg ctaaagctgc ggaagaagca gcgaagaaa 420
 cggctgcaga cgcaaagaaa 440

<210> 285
 <211> 119
 <212> DNA
 <213> Homo sapiens

<400> 285
 gcgatggaaa tcgtccacga gccgcgcgac ctcgagcgtt acatgcgcga ggccgtgaag 60
 gtgtcgaaacg attcgccggt gctgctcgac cgcttcctga acgacgcgat cgagtgcga 119

<210> 286
 <211> 398
 <212> DNA
 <213> Homo sapiens

<400> 286
 aaacagggga tttaagtgtg tcttttgtgt ttgcaaggca ctaacaccac tcccgtctgt 60
 atttaaattgc tgtccccagg ttacgactat ggctatgtct gcgtggagtt ttcactcttg 120
 gaagatgcc a tcggatgcat ggaggccaac caggttgctt tatacttcgg tcaaatgatg 180
 ctggaaggat atatTTTTTT atatatgggg agggagggtt tcaaatgatt ttactttgga 240
 aaggtacaag aagttctatct gtggagcata ctgtattcca accatcgggt gtgaggaaaa 300
 tctttaaaaa ggctggaaaag ctttctctag aaaacttaat gggcacagag tgcattttaa 360
 aagctagagc ccagttgctt ttggactaga ttccaaaa 398

<210> 287
 <211> 1177
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(1177)
 <223> n = a,t,c or g

<400> 287
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 gcgcttcaca cagccctcca agatgaggcg ccgggtgatc gcacggcccg tgggtagctc 120
 cgtgcggctc aagtgcgtgg ccagcgggca ccctcgcccc gacatcacgt ggatgaagga 180
 cgaccaggcc ttgacgcgcc cagaggccgc tgagcccagg aagaagaagt ggacactgag 240
 cctgaagaac ctgcggccgg aggacagcgg caaatacacc tgccgcgtgt cgaaccgcgc 300
 gggcgccatc aacgccacct acaagggtga tgtgatccag cggaccggtt ccaagcccg 360
 gctcacaggc acgcaccccg tgaacacgac ggtggacttc ggggggacca cgtccttcca 420
 gtgcaagggt cgcagcgacg tgaagccggt gatccagtgg ctgaagcgcg tggagtacgg 480
 cgccgagggc cgccacaact ccaccatcga tgtgggcggc cagaagtttg tgggtctgcc 540
 caccgggtgac gtgtgggtcgc ggcccagcgg ctccctacct aataagctgc tcatcaccgc 600
 tgcccggcag gacgatgcgg gcatgtacat ctgccttggc gccaacacca tgggctacag 660
 cttccgcagc gccttctctca ccgtgctgcc agacccaaaa ccgccagggc cacctgtggc 720
 ctccctcgcc tgggccacta gcctgcccgt gcccggtggc atcggcaccc cagccggcgc 780
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 cggagacaag gaccttccct cgttggccgc cctcagcgct ggccctgggt tggggctgtg 960
 tgaggagcat ggggtctcgg cagcccccca gcacttactg ggcccaggcc cagttgctgg 1020
 ccctaagttg taccctaaac tctacacagg acattccaca ccacacacat acacacaccc 1080
 cccaccctcc tgccaattaa acagtagcca ttcccnaaa atnnnnnnnn nnnnnnnnn 1140
 nnnnnnnnnn nnnnnctcgg ccccgccta ttcaccg 1177

<210> 288
 <211> 100
 <212> DNA
 <213> Homo sapiens

<400> 288
 tgaattttca ttttacaggg aagtgtttgt ttatgtcagg gctcagtgag gtccagctga 60
 cccatatgga tgatcacact ctaccagggt attgaagctc 100

<210> 289
 <211> 406
 <212> DNA
 <213> Homo sapiens

<400> 289

cggcacgagc	ggcacgagag	tcagaggggtt	ttaattttact	tgtgaagctc	acactattga	60
aactaattgc	aatgcttgac	tttattttct	ttagagtcca	agaaagagaa	aaacaaggca	120
tagcacaaat	ccccctctag	agtgtcatgt	tggttgggta	atggattcca	gagaccatgg	180
gccaggaaca	tcctctgtca	gcacttcaaa	tgcttcacct	tcagaaggcg	caccactagc	240
aggaagttat	ggatgtactc	ctcattcatt	cccaaagttc	cagcatcctt	ctcatgaact	300
tttgaaggaa	aatggcttta	cccaacaagt	gtaccacaag	tatcgtcgaa	gatgcctaag	360
tgagagaaaa	cgcttgggaa	ttggtcagtc	ccaagaaatg	aatacc		406

<210> 290

<211> 359

<212> DNA

<213> Homo sapiens

<400> 290

cccggcagcg	gcggcagcgc	ggggggccga	gacggcagtg	cctaccaggg	cgcgctgttg	60
cctcgagAAC	agttcgcggc	cccgttggg	cgcccggtgg	ggacctcgta	ctccgccacc	120
taccggcct	acgtgagccc	cgacgtggcc	cagtcctgga	ctgccgggcc	cttcgatggc	180
agcgtcctgc	acggcctccc	aggccgcagg	cccaccttcg	tgtccgactt	cttggaggag	240
ttcccggtg	agggtcgtga	gtgtgtcaac	tgccggggccc	tgtccacacc	gctgtggcgc	300
cgagatggca	ccggccacta	cctgtgcaat	gcctgcggcc	tctaccacaa	gatgaatgg	359

<210> 291

<211> 954

<212> DNA

<213> Homo sapiens

<400> 291

cccagatcat	cgacatggtg	cgttgtggtg	gtggtacagc	tgtggagtct	tacctgtcac	60
agtgtcaaga	aatgaagggg	atgaacggaa	ccaggtgctg	accctgtatc	tgtggatacg	120
gcaggagtgg	acagatgcct	acctacgatg	ggaccccaat	gcctatggtg	gcctggatgc	180
catccgcac	cccagcagtc	ttgtgtggcg	gccagacatc	gtactctata	acaagtactg	240
cctatctggg	cccctcctct	ctcttaccct	tctctagact	tgcccttagc	tgtggggggtg	300
tagtgatccc	ctctccctac	cacataacct	ggttgccacg	ctgccctgga	agcttttccc	360
caggaccctt	ctaagctgcc	aagcaactcag	cccctccatg	gcacccccac	tttaggctat	420
cccaggccag	cccaggctga	acgtctcctc	ggaacctact	gtgtggtcca	gggcagatgt	480
ctgaatcaca	agggcctctc	tagggcacac	ttttagctct	aagtctctca	gggctcccc	540
aagagcctgt	ctaaggggtct	ctttcctcca	ggacatagcc	ctctggaaca	ctgctttatg	600
tctccttgac	cagttccgtg	tctcccagcc	agcacatagc	tctgcatatt	ttctctgggg	660
cccttctaca	agttttgcag	atgtccccca	agggaaagtca	ctgtgtgtcc	cggagctacc	720
tctgggttct	gcagaggcct	ttttatacat	cctctggcta	cgtctgtgtc	ccttctggcg	780
ccttcaggca	ccaccccttc	caggcctcga	aaggcagcgg	gtctctctag	gtgcactcca	840
ccctctgtgt	tgctttgttc	tgaaaacaag	aatcaaatta	acgaaaaaaa	aacaagcaca	900
agttttattha	tttattttgag	acacagcctg	ggcaagagag	tgagacttca	tctc	954

<210> 292
 <211> 595
 <212> DNA
 <213> Homo sapiens

<400> 292
 tacgcactga ctggtgcgtt gggtattgtc accgggatgg tgatgggaaa tatcgccgat 60
 tatttcaatc tgccgtgttc cagtatgagt aataccttca ccttcctcaa cgccggcatt 120
 ttaatctcta tcttcctcaa cgcctggctg atggaaatcg tcccgttgaa aacgcagtta 180
 cgttttggtt ttctcctgat ggtgctggcg gttgcccgtt tgatgttcag ccacagcctg 240
 gcgctgttct cggcggcgat gttcattctc ggggtgggtc gcggcatcac catgtcgatt 300
 ggtacattcc tggtaacaca aatgtatgaa gggcgtcagc gcggttcccg cctgttattt 360
 accgactcct tottcagtat ggctgggatg attttcccaa tgatcgccgc gtttctactg 420
 gcgcgcagca ttgagtggta ctgggtttat gcctgcacgc ggctgggtga tgtcgctatt 480
 tttattctga ccttcggctg tgagttcccg gcgctgtgca gccatgcgac taagttgggt 540
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<210> 293
 <211> 552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(552)
 <223> n = a,t,c or g

<400> 293
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 gttctccggc ggctcagcgtc agcgtatcgc catcgcccgt ggtctgatgc tcgaccggga 180
 tgtggtgatt gccgatgaac cggtttccgc gctggatgtt tcagtgcgcg cgcagggtgt 240
 gaatctgatg atggatttgc agcaggagtt ggggctgtct tatgtcttta tctcccacga 300
 cctgtcgggtg gtggagcaca ttgctgatga agtcatggtg atgtacctgg gccgctgcgt 360
 ggagaaggga acgaaagacc aaatcttcaa taaccgcgcg catccgtaca ctcaggcgct 420
 actttccgag acgcccgcgc tgaaccggga cgatcgccgc gagcgcacatca agctcagcgg 480
 tgaactacca agccactga atccaccgcc ggggttgcgc ttcaacgccc gctgttgtcg 540
 gcgnttcggc cc 552

<210> 294
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 294
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gggtaaaaacg gtgtatcact cccccggg gcgagatgc cgcgagttta cgcgtgacgc 180
catacccgat aaagacgctc aggggtggcg ggtgtatctc ctttcgggcc cgacgatgat 240
gatgccaggc caggtcacg ggcatatgga acacagcaac tggcgatga ttaacttgcc 300
ggttggcccg ttggtggacg gcaaaccgat ttatacgctc tacatcgcg ttcgatcga 360
ttttcatctt cattacataa atgatttgat gaataaactt attatgaccg catcggtaat 420
catcat 426

<210> 295
<211> 340
<212> DNA
<213> Homo sapiens

<400> 295
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cgagtatcg ccgccaggat tgcattgcgc acgggacgaca tctggcaggc ttcattcacg 120
cctgctatcc ccgtcagcct gagcttgccg cgaagctgat gaaagatgtt atcgctgaac 180
cctaccgtga acggttactg ccaggcttcc ggcaggcgcg gcaggcggtc gcggaaatcg 240
gcgcggtagc gagcggtatc tccggtccg gccgcacctt gttcgctctg tgtgacaagc 300
cggaaaccgc ccagcgcggt gccgactggt tgggtaaaat 340

<210> 296
<211> 281
<212> DNA
<213> Homo sapiens

<400> 296
cgggcagcag cagcgctgg cgctggcccg cgcgctgac ctcaagccga aagtgtgtgt 60
gtttgatgag ccgttgagta acctcgacgc caacctgcgt cgcagcatgc gcgacaagat 120
ccgcgagttg caaaagcagt ttgatatac ctcgctgtac gtcacccacg atcagagcga 180
agccttttgc gttttctgata ctgtgctggt gatgaacaag gggcacatca tgcagatcgg 240
ctcacgcgag gatctccggg tacggagatt gaattggtaa t 281

<210> 297
<211> 155
<212> DNA
<213> Homo sapiens

<400> 297

tggcgggtgca	ttacctagag	cgggtgagaa	ttgccgaaca	tgcgcataag	tttcccggac	60
agatttcagg	tggtcagcag	caacgcgttg	ccattgcgcg	ttcgctgtgt	atgaagccga	120
aaattatgtt	gtttgatgag	ccaacgtcgg	cgctc			155

<210> 298

<211> 217

<212> DNA

<213> Homo sapiens

<400> 298

gctccctatg	acgccgaaaa	ttattttgat	tatgacaatc	tgaataacgg	accttctttg	60
cagcactggg	ttggcgctga	ttcactgggg	cgtgacattt	tcagccgtgt	cctgggttgg	120
gcgcaaattc	cgctggcggc	gggcgtgttt	gccgtgttta	tcgggtgcggc	gatcggggacg	180
ttgctggggc	tgctcgctgg	atattatgaa	ggctggt			217

<210> 299

<211> 568

<212> DNA

<213> Homo sapiens

<400> 299

aggatttctg	tctgatcgct	gaccttgacc	cgatcgatga	gcttgtggac	ttcccgatcg	60
tttacgcttc	tgcgctgaac	ggtatcgcg	gtctggacca	cgaagatatg	gcggaagaca	120
tgaccccgct	gtaccaggcg	attgttgacc	acgttctctg	gccggacgtt	gaccttgacg	180
gtccggttcca	gatgcagatt	tctcagctcg	attacaacag	ctatgttggc	gttatcggca	240
ttggccgcat	caagcgcggt	aaagtgaagc	cgaaccagca	ggtcactatc	atcgatagcg	300
aaggcaaaaac	ccgcaacgcg	aaagtcggta	aagtgcgtgg	ccacctcggt	ctggaacgta	360
tcgaaaccga	tctggcggaa	gctggcgata	tcgttgcgat	cacgggcctt	ggcgaactga	420
acattttctga	caccgtttgc	gacacgcaaa	acgttgaagc	gctgccggca	ctctccgttg	480
atgagccgac	cgttttctatg	ttcttctgcg	ttaacacctc	gccgttctgc	ggtaaagaag	540
gtaagttcgt	aacgtctcgt	cagatcct				568

<210> 300

<211> 366

<212> DNA

<213> Homo sapiens

<400> 300
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 ggcctgaaat tcggtgacta cggctccatc gattacggcc gtaactacgg tntagcatac 120
 gacatcgggtg cgtggactga cgtcctgcca gaattcgggtg gtgacacttg gactcaaacc 180
 gacgtgttca tgactcaacg tgcaactggt gttgcaacct atcgtaacaa cgacttcttt 240
 ggtctggttg atggtctgaa ctttgctgct cagtaccaag gcaaaaacga tcgtagcgat 300
 ttcgataact acactgaagg taacggccac ggcttcgggt tctctgctac ctatgaatac 360
 gaaggg 366

<210> 301
 <211> 199
 <212> DNA
 <213> Homo sapiens

<400> 301
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 tcactattac cgtgttgacg ctggctgcgg ttaatacgtc gggattccg gtcgatctgc 120
 ccacggcgct gctgttgagc gtggtggctt ctctgtgtgc ctgtggcgca tccggcggtg 180
 cgggggggtc tctgctgct 199

<210> 302
 <211> 140
 <212> DNA
 <213> Homo sapiens

<400> 302
 gccaacgcgc agcaagggtc gccagtggt atcacctga agctaaataa ccttgctgat 60
 aaaggcctgg ttgatcgtct gtatgcggcc tccagctcgg gcgttcgggt taatctgctg 120
 gttcgcggaa cgtgttcgct 140

<210> 303
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 303
 cgcgcgaatg acgctcatcc ccggcacaca tctgctggaa aacatccaca acatctgggt 60
 gaacggggta ggacgaata gcgcgccgtt ctggcggatg ttgcttaaca gctttgtgat 120

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ggcgttcagc attacgctcg gcaaaattac cgtctcgatg ctctcgcat ttgccattgt 180
ctggtttcgt tttccgctac gtaacctctt cttctggatg atttttatca ccctgatgct 240
gccggttgaa gtacgtatct tcccgaaggc ggaagtcac gccaacctgc agatgctcga 300
cagctacgcc ggtttaacgc tgccgctgat ggcctcggcg accgctactt tcctgttccg 360
caagttaaat atgtcggggc cggacaaggc ggtgccagcc gcgcggatct ccgggtacgg 420
acctagagtt cgtaagcaag a 441

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<210> 304
<211> 402
<212> DNA
<213> Homo sapiens

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```

<400> 304
ctgtgcgaaa tgtttgctg atgcggatga atgcccctcc ggggcgtttg aacggattgg 60
tcgcgatatc agccttgacg ctctggaacg ggaagtgatg aaagatgaca ttttctttcg 120
cacgtccggc ggcggcgctca cgctttctgg cggcgaagtg ttaatgcagg cggagtttgc 180
taccggtttt ttacagcgac tgccgctgtg ggggtgtgtc tgcgccattg aaactgccgg 240
agacgcacca gccagcaagc tattaccgct ggcgaaattg tgcgatgaag tgttgttcga 300
tttaaaaatt atggacgcga ctcaggcgcg ggatgtggtg aagatgaacc tgccacgcgt 360
gctggagaat ctgcgtttgc tggatgagtga gggcgctcaac gt 402

```

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<210> 305
<211> 346
<212> DNA
<213> Homo sapiens

```

```

<400> 305
tacctgttat tgtttgtctg cttccttctg atgtctctgc tggttgggct ggtgtacaaa 60
tttaccgccc aacgcgcggg caaacagtcg ctggatgatt tgatgaacag ttcgctgtat 120
ctgatgcgca gcgaattgcg tgagatcccc ccacacgact ggggtaaaac tctgaaagag 180
atggatttaa atctctcttt cgatctgcgt gtcgagccac tgagtaaata ccatcttgat 240
gatatttcca tgcaccgact gcgtggcgcg gaaattgtcg ccctggacga tcagtacacg 300
tttttgcagc gtatcccgcg cagccactac gtgctggcag ttggtc 346

```

```

<210> 306
<211> 207
<212> DNA
<213> Homo sapiens

```

```

<400> 306

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```

gttgaattat tcttcagcga tgaaggcgat gatgtggtga ttgaagtcgc cgatcagggc      60
tgcggcggttc cagagtctct acgagacaaa atatttgagc aggggggtcag tacgcgtgct      120
gacgagcccg gtgaacatgg cattgggttg tacttgattg ccagctacgt aacgcgctgc      180
ggtggtgtta tcaactctga agataat                                           207

```

```

<210> 307
<211> 214
<212> DNA
<213> Homo sapiens

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```

<400> 307
tcgaagccat tatcgccccc gatgccaacg ccctgccgcg tgccgcacaa gccgcagaaa      60
acttgaaaaa tgacaaagta gcgattgtcg gattcagtac gccaaatgtg atgcgcccg      120
atgtagagcg cggcacggtg aaagaatttg gcctgtggga tgtggttcag caaggcaaaa      180
tatcagtgtg tgtggcggat gcattacagt aaaa                                           214

```

```

<210> 308
<211> 129
<212> DNA
<213> Homo sapiens

```

```

<400> 308
tacatcgtag tgacggggaa aacacattgc ggtacgccac ttactaccgt tacaggagac      60
gcaacgcaat cgggttatct gacgctgaac ctgcctgaaa tgtgggaagt gtcaggttat      120
aaccgtgtt                                           129

```

```

<210> 309
<211> 358
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(358)
<223> n = a,t,c or g

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<400> 309
gccggttttg ccgcatcaat ggtgcttagc gatgactcaa cgtaccagtg cgccgactgc      60
aaatctgccc gccgggccag taaggagtac ccagttcat caagaagctg gcttgccact      120
ttcggcaacg cgaccggatt aagcttcaat gactttgtct ggttatttgt aagtgcgctt      180

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aaccgtgcct	caataatattt	cattttcccc	gcgacatcgt	tgagctgctg	ccgggttttg	240
ctggcattaa	tatcgggttc	cacacattca	actgaagaag	taatcccggt	ctgatatagc	300
tggcgatcgg	tcgcgataat	ggcgnctctgc	tcttttttcta	tttgcctgcaa	gaccgtgg	358

<210> 310
 <211> 253
 <212> DNA
 <213> Homo sapiens

<400> 310						
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gtcatcaact	gggggatgtt	accgctgcaa	atggcggaag	taccaacctt	tgaagtgggg	120
gattacattt	acatccctgg	cattaaagcg	gcgctggata	atccgggtac	gacgtttaaa	180
ggttatgtga	tccatgaaga	tgccgcggta	acggaaatta	cgctctatat	ggaaagtcag	240
gaagccagaa	cag					253

<210> 311
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 311						
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tgaacaggcg	gcgagctgcc	agcgtgtgat	tggcgggtctg	gcgaatattg	ccgaggagta	120
cgcgactaaa	cgctatcggt	ctaacgcat	caactggggg	atgttaccgc	tgcaaatggc	180
ggaagtacca	acctttgaag	tgggggatta	catttacatc	cttggcttta	aagcggctaa	240
gtatagtccg	ggcacggcgt	ttacagtcta	tgcgatctcc	gggtacggac	ctcgaatctg	300
ataa						304

<210> 312
 <211> 344
 <212> DNA
 <213> Homo sapiens

<400> 312						
actctagagg	atctgctgat	ggcgttagat	ggagagcaac	atcttcagca	acaggatatcg	60
gaaaaagtat	tagccgataa	tgtgttaatt	gccccctggt	ctgttaaacc	tgatgcgaca	120
ttctggtcgg	ccttaatcca	ggatcgctat	aacgtgatga	cctgtattga	aaaagacgcc	180
tgcgctctgg	tcgagcaaga	tctgaatagt	gatggtcagg	cggagcggat	cctgtttgct	240
tttaatgatg	acagagtcac	tgtctatggc	tttgactcag	acagaaaaga	atgggacgcg	300

cttgatatga gtttacttcc gaacgaaata acgaaagaaa aatt

344

<210> 313
 <211> 630
 <212> DNA
 <213> Homo sapiens

<400> 313
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 cttcggatcc gccagcattt tcagcgaggt gcgctacgtg aaggagccat acatccagtc 180
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 gttgcacgcc gcctgcaagg ccaccactt cttcaagcgc aacccccacc ctgacgctgc 420
 caacccttg cagctcaagt cctcggctga ctacctggc gagacgaagg tgcgccatt 480
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 tgtggccagt cggctaacct tccctgaccg ggaggcgtg gcggagcacg ccgacctcaa 600
 gagcatggtg gagctgataa gcgcctgctc 630

<210> 314
 <211> 2285
 <212> DNA
 <213> Homo sapiens

<400> 314
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 acgtgaaga cgcacatgcg aagccacacg ggggagaaac cgtacgaatg cgatcactgt 120
 ggtaaggcct tcagcatagg ctccaacctg aatgtgcaca ggcgatcca caccggggag 180
 aagccctacg aatgccttgt ctgcggggaa gccttcagcg accactcatc cctcaggagc 240
 cacgtgaaaa ctaccgggg agagaagctc tttgtgtcat ccgtgtggaa aaggctccag 300
 tgagcgcgcc tgcttttagag acacaggatg attcagaccg gaaacagacc tcgtgggtgt 360
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 caagccgtgg ctttaaatgt caaaatgact tcagaccact tctagccttc tgggccctag 660
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cgagagaagc	cccaacgaga	ttttccgggtg	aatacgggac	tgcacgtact	ctatcatcat	1500
gaaaacagag	ccccgttcat	aaatttttca	tctttatttt	taagggtata	ctcctctaaa	1560
taacccttaa	gcctcatcaa	gaaagggttg	tttatagtat	ttttactata	gcttcatcct	1620
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<212> DNA

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 <211> 2366
 <212> DNA
 <213> Homo sapiens

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 <211> 1925
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 <213> Homo sapiens

<220>
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 <223> n = a, t, c or g

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 <211> 1181
 <212> DNA
 <213> Homo sapiens

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<210> 327
 <211> 1842
 <212> DNA

<213> Homo sapiens

<400> 327

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<210> 328

<211> 1293

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(1293)

<223> n = a,t,c or g

<400> 328

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 <212> DNA
 <213> Homo sapiens

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 <211> 2105
 <212> DNA
 <213> Homo sapiens

<400> 330
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<210> 336
 <211> 1126
 <212> DNA
 <213> Homo sapiens

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<210> 337
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 <212> DNA
 <213> Homo sapiens

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<400> 337
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<210> 338

<211> 1796

<212> DNA

<213> Homo sapiens

<400> 338

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<210> 339

<211> 1771

<212> DNA

<213> Homo sapiens

<400> 339

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 <213> Homo sapiens

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 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

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<210> 347
 <211> 918
 <212> DNA
 <213> Homo sapiens

<400> 347

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<400> 348

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<212> DNA
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<210> 350
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<212> DNA
<213> Homo sapiens

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<210> 352
 <211> 1194
 <212> DNA
 <213> Homo sapiens

<400> 352

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<210> 354
 <211> 2401

<212> DNA
<213> Homo sapiens

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<211> 2186
<212> DNA
<213> Homo sapiens

<400> 355

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 <211> 1142
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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 <223> n = a, t, c or g

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<212> DNA

<213> Homo sapiens

<400> 372

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<212> DNA

<213> Homo sapiens

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<212> DNA

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 <223> n = a,t,c or g

<400> 389

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 <212> DNA
 <213> Homo sapiens

<400> 390

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<211> 1458

<212> DNA

<213> Homo sapiens

<400> 391

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<210> 392
 <211> 1667
 <212> DNA
 <213> Homo sapiens

<400> 392

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<210> 393
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 <212> DNA
 <213> Homo sapiens

<220>
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 <223> n = a, t, c or g

<400> 393

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<210> 394

<211> 1283

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(1283)

<223> n = a,t,c or g

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 <212> DNA
 <213> Homo sapiens

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2149

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<211> 1895

<212> DNA

<213> Homo sapiens

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<211> 2416

<212> DNA

<213> Homo sapiens

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<211> 1495

<212> DNA

<213> Homo sapiens

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<210> 406
 <211> 2001
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

<400> 407

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 <212> DNA
 <213> Homo sapiens

<400> 408

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2234

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<212> DNA
<213> Homo sapiens

<400> 413
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<211> 1849
<212> DNA
<213> Homo sapiens

<400> 414
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<210> 415

<211> 2555

<212> DNA

<213> Homo sapiens

<400> 415

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<210> 416
 <211> 2950
 <212> DNA
 <213> Homo sapiens

<400> 416

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<210> 417
 <211> 850
 <212> DNA
 <213> Homo sapiens
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 <222> (1)...(850)
 <223> n = a,t,c or g

<400> 417
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<210> 418
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 418
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<210> 419
 <211> 949
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> n = a, t, c or g

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<210> 420
 <211> 986
 <212> DNA
 <213> Homo sapiens

<400> 420
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<210> 421
 <211> 1209
 <212> DNA
 <213> Homo sapiens

<400> 421

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 <213> Homo sapiens

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<210> 426
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<212> DNA
<213> Homo sapiens

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<211> 1579

<212> DNA

<213> Homo sapiens

<400> 427

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<211> 413

<212> DNA

<213> Homo sapiens

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<210> 429

<211> 1567

<212> DNA

<213> Homo sapiens

<400> 429

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<211> 728

<212> DNA

<213> Homo sapiens

<400> 430

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<212> DNA

<213> Homo sapiens

<400> 431

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<210> 432

<211> 1908

<212> DNA

<213> Homo sapiens

<400> 432

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 <212> DNA
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 <211> 478
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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 <211> 1968
 <212> DNA
 <213> Homo sapiens

<400> 436						
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 <212> DNA
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<400> 440

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<400> 441

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<400> 448

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 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 449

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<400> 450

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<211> 2674

<212> DNA

<213> Homo sapiens

<400> 451

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 <211> 601
 <212> DNA
 <213> Homo sapiens

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<210> 453
 <211> 474
 <212> DNA
 <213> Homo sapiens

<400> 453	
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<210> 454
 <211> 1838
 <212> DNA
 <213> Homo sapiens

<400> 454

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<210> 455
 <211> 1790
 <212> DNA
 <213> Homo sapiens

<400> 455

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<210> 456

<211> 1293

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (1293)

<223> n = a,t,c or g

<400> 456

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<210> 457
 <211> 1155
 <212> DNA
 <213> Homo sapiens

<400> 457						
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<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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 <212> DNA
 <213> Homo sapiens

<400> 473

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<211> 1374

<212> DNA

<213> Homo sapiens

<400> 474

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<210> 475

<211> 3076

<212> DNA

<213> Homo sapiens

<400> 475

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<211> 959

<212> DNA

<213> Homo sapiens

<400> 476

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<211> 3652

<212> DNA

<213> Homo sapiens

<400> 477

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3652

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 <213> Homo sapiens

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 <211> 1297
 <212> DNA
 <213> Homo sapiens

<400> 479

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<400> 481

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 <212> DNA
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<400> 482

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<212> DNA

<213> Homo sapiens

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<211> 1148

<212> DNA

<213> Homo sapiens

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<211> 1256

<212> DNA

<213> Homo sapiens

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<211> 2547

<212> DNA

<213> Homo sapiens

<400> 486

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<211> 4797

<212> DNA

<213> Homo sapiens

<400> 490

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<212> DNA

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<212> DNA

<213> Homo sapiens

<400> 519

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 <211> 1041
 <212> DNA
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<400> 521

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<211> 2014

<212> DNA

<213> Homo sapiens

<400> 523

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<211> 2151

<212> DNA

<213> Homo sapiens

<220>

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<400> 534

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<211> 704

<212> DNA

<213> Homo sapiens

<400> 536

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<211> 1058

<212> DNA

<213> Homo sapiens

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 <213> Homo sapiens

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<211> 649

<212> DNA

<213> Homo sapiens

<400> 549

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<210> 550

<211> 696

<212> DNA

<213> Homo sapiens

<400> 550

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<211> 1037

<212> DNA

<213> Homo sapiens

<220>

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<211> 813
 <212> DNA
 <213> Homo sapiens

<400> 552

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 <212> DNA
 <213> Homo sapiens

<400> 553

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 <212> DNA
 <213> Homo sapiens

<400> 554

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 <211> 1040
 <212> DNA
 <213> Homo sapiens

<400> 555

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 <212> DNA
 <213> Homo sapiens

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 <211> 971
 <212> DNA
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<400> 557

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<212> DNA

<213> Homo sapiens

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 <213> Homo sapiens

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<211> 2003

<212> DNA

<213> Homo sapiens

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<211> 1206

<212> DNA

<213> Homo sapiens

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<223> n = a,t,c or g

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<212> DNA

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<400> 587

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<212> DNA

<213> Homo sapiens

<400> 588

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<212> DNA

<213> Homo sapiens

<400> 591

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<211> 816

<212> DNA

<213> Homo sapiens

<400> 596

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<211> 1575

<212> DNA

<213> Homo sapiens

<400> 597

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 <212> DNA
 <213> Homo sapiens

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<211> 802

<212> DNA

<213> Homo sapiens

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 <211> 1927
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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<400> 604

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<212> DNA

<213> Homo sapiens

<400> 629

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<400> 630

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<400> 631

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<211> 3149

<212> DNA

<213> Homo sapiens

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 <211> 1841
 <212> DNA
 <213> Homo sapiens

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<400> 634

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<400> 635

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<400> 636

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<210> 637
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 637

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<210> 638

<211> 1131

<212> DNA

<213> Homo sapiens

<400> 638

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<210> 639

<211> 1844

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(1844)

<223> n = a,t,c or g

<400> 639

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<210> 640

<211> 1210

<212> DNA

<213> Homo sapiens

<400> 640

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 <211> 1108
 <212> DNA
 <213> Homo sapiens

<400> 641

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<210> 642
 <211> 2418
 <212> DNA
 <213> Homo sapiens

<400> 642

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 <211> 1166
 <212> DNA
 <213> Homo sapiens

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<210> 644
 <211> 1024
 <212> DNA
 <213> Homo sapiens

<400> 644						
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 <211> 1498
 <212> DNA
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 <212> DNA
 <213> Homo sapiens

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<211> 2231

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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 <212> DNA
 <213> Homo sapiens

<400> 651

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 <211> 457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(457)
 <223> n = a,t,c or g

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 <212> DNA
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 <211> 1725
 <212> DNA

<213> Homo sapiens

<400> 654

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<210> 655

<211> 748

<212> DNA

<213> Homo sapiens

<400> 655

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<210> 656
 <211> 977
 <212> DNA
 <213> Homo sapiens

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 agagtctcgt gctgaaagge tgttccaacg tcagtaacgc cacctgtcag ttcctgtctg 600
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<210> 657
 <211> 746
 <212> DNA
 <213> Homo sapiens

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 aaatgtcaga cagacttacg atgatggagc tgcaaccgca ctaatgtcaa cagtgaacct 600
 ttgagggagc cagcacccctc tgaagatgtg attgatatta agccagaacc agatgatctc 660
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 acacttacat atggttcttc tcgccc 746

<210> 658
 <211> 559
 <212> DNA
 <213> Homo sapiens

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 gggcagcgga agcgcccca 559

<210> 659
 <211> 538
 <212> DNA
 <213> Homo sapiens

<400> 659
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 acaggacaga gacagctgcc cgggaggatg ggagaacaga aagaggagg aaacgccgag 180
 cactgacctg ggggagggga gtaaagagaa gtgaaggggg attggaaggg aactggagaa 240
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<210> 660
 <211> 735
 <212> DNA
 <213> Homo sapiens

<400> 660
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 accccaacgag gcgctcagca cccagggaag gcgcgtgtgt ccccgatgct ggctcctccc 180
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actgcattta	tgccctctgtg	gatgtgaagg	ctatttctag	aaatctcttc	ctttgcagaa	300
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<210> 661
 <211> 978
 <212> DNA
 <213> Homo sapiens

<400> 661

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<210> 662
 <211> 1118
 <212> DNA
 <213> Homo sapiens

<400> 662

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acaacaattt	ataatacttt	ataccacaag	ggtaaaactag	taagctgctt	tctaaaatta	1080
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<210> 663

<211> 556

<212> DNA

<213> Homo sapiens

<400> 663

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<210> 664

<211> 373

<212> DNA

<213> Homo sapiens

<400> 664

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cctcgatctt	catcgcgctg	gttagtccgt	ctcgctgctt	tgttctgttt	cctcctctct	360
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<210> 665

<211> 411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
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 <223> n = a,t,c or g

<400> 665
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 ctgaattatc caatgaggag aggaatcttc tctcagatgc tcataccaat gctgtatgag 180
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 gcgatgatgt actgtctctt ttggaaaagc tcttgatccc caatgcttca catgcataga 360
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<210> 666
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 666
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 gggagaggag gagattagcc cacaactga ataagtcagt atcaaagaag ttgctgtcac 180
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 cttacggcag ggatcattgg gaaaggtgta cttaggtaag aaagtctcag gctctgatgc 300
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<210> 667
 <211> 1991
 <212> DNA
 <213> Homo sapiens

<400> 667
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 <212> DNA
 <213> Homo sapiens

<400> 668						
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<210> 669
 <211> 539
 <212> DNA
 <213> Homo sapiens

<400> 669
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<210> 670
 <211> 682
 <212> DNA
 <213> Homo sapiens

<400> 670
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 gagaagatcg gagagggcac ctatggggtg gtgtacaagg ccaagaacag ggagacaggg 360
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 cccctggctt ggaagtgcct tt 682

<210> 671
 <211> 536
 <212> DNA
 <213> Homo sapiens

<400> 671

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<210> 672
 <211> 1038
 <212> DNA
 <213> Homo sapiens

<400> 672

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<210> 673
 <211> 676
 <212> DNA
 <213> Homo sapiens

<400> 673

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<210> 674
 <211> 418
 <212> DNA
 <213> Homo sapiens

<400> 674						
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<210> 675
 <211> 1423
 <212> DNA
 <213> Homo sapiens

<400> 675						
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<210> 676
 <211> 621
 <212> DNA
 <213> Homo sapiens

<400> 676
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 caccacatag tgaagtggaa cttgttaacc agtgaaacaa ctcaaatagt aaagcttcct 360
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<210> 677
 <211> 1258
 <212> DNA
 <213> Homo sapiens

<400> 677
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<210> 678
 <211> 1289
 <212> DNA
 <213> Homo sapiens

<220> .
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 <222> (1)...(1289)
 <223> n = a,t,c or g

<400> 678

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<210> 679
 <211> 539
 <212> DNA
 <213> Homo sapiens

<400> 679

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<210> 680

<211> 349

<212> DNA

<213> Homo sapiens

<400> 680

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<210> 681

<211> 329

<212> DNA

<213> Homo sapiens

<400> 681

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<210> 682

<211> 574

<212> DNA

<213> Homo sapiens

<400> 682

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<210> 683
 <211> 627
 <212> DNA
 <213> Homo sapiens

<400> 683						
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<210> 684
 <211> 1271
 <212> DNA
 <213> Homo sapiens

<400> 684						
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gaagtccccg	tctccagttc	agggcaagaa	gagtcgcgca	ctcctatgca	tagaaaaagt	180
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<210> 685
 <211> 685
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(685)
 <223> n = a,t,c or g

<400> 685						
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<210> 686
 <211> 962
 <212> DNA
 <213> Homo sapiens

<400> 686						
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ct						962

<210> 687
 <211> 676
 <212> DNA
 <213> Homo sapiens

<400> 687						
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<210> 688
 <211> 639
 <212> DNA
 <213> Homo sapiens

<400> 688						
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<210> 689
 <211> 116

<212> DNA

<213> Homo sapiens

<400> 689

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<210> 690

<211> 509

<212> DNA

<213> Homo sapiens

<400> 690

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<210> 691

<211> 1362

<212> DNA

<213> Homo sapiens

<400> 691

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<210> 692
 <211> 503
 <212> DNA
 <213> Homo sapiens

<400> 692						
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 <211> 1671
 <212> DNA
 <213> Homo sapiens

<400> 693						
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<210> 694

<211> 898

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(898)

<223> n = a,t,c or g

<400> 694

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<210> 695

<211> 630

<212> DNA

<213> Homo sapiens

<400> 695

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<210> 696
 <211> 879
 <212> DNA
 <213> Homo sapiens

<400> 696

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<210> 697
 <211> 719
 <212> DNA
 <213> Homo sapiens

<400> 697

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tgcttctgct	acgaggattg	agcgtctcca	cccatcttct	gtgcttcacc	atctacataa	180
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taattttaaa	ttatgatata	aggaaaaatt	tgtaataact	attatgaatt	ctgccaatta	540
ctgtaatctg	gggatagtat	aacagcacta	taaatgtttt	tgtatgtgac	catttggttg	600
acaagatcca	tgtgtggatg	aaatgttagg	aaaagggagg	cccagtgga	gtgggctcac	660

acctgtaatc ccagtaggct agggagggtg aagcaagagg atggcttgag tctagaagt 719

<210> 698
 <211> 420
 <212> DNA
 <213> Homo sapiens

<400> 698
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 catgtctgtg gtaccgcca atcgctcgca gaccggctgg ccccgggggg tcaactcagtt 180
 cggcaacaag tacatccagc agacgaagcc cctcacctg gagcgacca tcaacctgta 240
 agtgcggcgc ggccttggcg ggcatttctc tcgtgaaagc tcctatagac tctccgacgc 300
 gccccggct tttcggcgcg cttcacgcct ctgcacctcc ccgcctcaa ctcgcgtgg 360
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<210> 699
 <211> 422
 <212> DNA
 <213> Homo sapiens

<400> 699
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 ggaagaccgc tgccctgtga tctgagggcc aaagtgttga agattgctct gaatgttgca 180
 ggaaaagggt atagtttggc atcatgggat ggtatttttag acttgccaga acagaacact 240
 attcacaag attgcctgca gtttattgac cagctttcag tgccagagga gaaggcagca 300
 gaattacttt tggatattga atctgtaatt accttttatt gtaaatcacg taacattaaa 360
 tatagcacat cccttagctg gatacatcta ctgaaacctat tgggtgcatct tcaactgcca 420
 cg 422

<210> 700
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 700
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 gaactgaggt gtccaacaca tgagtgagge cttcctggat ctctagctct cgtcaagcct 120
 tcccaacacc acgaggaaca aaaatgagcc atccaaatga gctttaccga aattcctgac 180

ccacggtgtc	aagagcaatg	aaagggttgt	cgtttggtc	tttcegccat	cttttcgtgc	240
cgccacaatg	gtgcacatga	atgtcctgcc	tgatgctctc	aagagcatca	acaatgccga	300
aagaagaggc	aaaccccagg	ttcttattag	gctgtgctcc	aaaatcatca	tctggtttct	360
cactgtaatg	gtgaagtatg	gttacattgg	caaatttgaa	cccacgcgtc	cg	412

<210> 701
 <211> 977
 <212> DNA
 <213> Homo sapiens

<400> 701

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ccgagccccc	tcccttgccc	cagcccgact	ccctcctcct	tcccgaaacca	tccggctcgg	180
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cagcgcgccg	gcaccatcaa	gcatggatcg	gcgctggacg	tgctcctctc	catgggggtc	360
cccagagccc	gcgcacaaaa	agccttgcca	tccacgggag	gaagaagtgt	tcaggcagca	420
tgtgactggg	tattctccca	tgtcgggtgac	cccttcctgg	atgacccct	gccccgggag	480
tacgtcctct	acctccgtcc	caccggcccc	ttagcacaga	agctttccga	cttttggcag	540
cagtcgaagc	agatctgcgg	gaagaacaag	gcacacaaca	tcttccccca	catcacactc	600
tgccagttct	ttatgtgcga	ggacagcaag	gtggatgccc	tgggggaagc	cctgcagacc	660
acggtcagtc	gctggaaatg	taagttctcg	gccccgctgc	ccctggagct	ctatacgtcg	720
tccaacttca	tcggcctctt	tgtaaaggaa	gacagtgcgg	aggtcctcaa	gaagtttgct	780
gctgactttg	ctgcagaggc	tgcatccaaa	accgaagtgc	atgtggaacc	tcataagaag	840
cagctacatg	tgaccctggc	ttaccacttc	caagccagcc	acctaccac	cctagagaaa	900
ctggcccaga	acattgacgt	caagctaggg	tgtgactggg	tggtaccat	attttctcgg	960
gatatccgat	ttgctac					977

<210> 702
 <211> 406
 <212> DNA
 <213> Homo sapiens

<400> 702

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ttagtcttct	ggaggctatg	atttttgcct	tactcccaaa	gccacggaag	aacgttgctg	180
gtgaaatagt	cctcatcaca	ggtgctggaa	gtggactcgg	aaggctctta	gccttgacgt	240
ttgccgggct	gggatctggt	cttgttctct	gggatataca	taaggagggg	aatgaggaaa	300
catgtaagat	ggctcgggaa	gctggagcca	caagagtgc	cgctataacc	tgcgattgca	360
gccaaaagga	aggagtgtat	agagttagccg	accaggttaa	aaaaga		406

<210> 703

<211> 987
 <212> DNA
 <213> Homo sapiens

<400> 703

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tcaagtgtcg	tatatagggg	acaagtattg	atgttcaata	tgattcaaac	tattactgtt	180
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gaaagagctt	cttaacttct	tgcattgaga	agcatcctct	aagttctcat	ctaaacactt	420
ccagtactca	tcccggggccc	cccagcagac	ctgtctttcc	ttcatagatg	gggctgccat	480
tcctactgcg	atgaagctct	ctgcccggcc	acgtccggct	tcctttcgat	gtcgacggga	540
ggaaactgtc	acgcaggcca	ccaaccggcg	gtggaggggcg	cggtgccgag	tcctgccact	600
gcagggtcgc	cccgtgggt	caagctctag	aagcgtagac	ctcccagcc	gcaaaaagca	660
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cctcagcctg	cctcccaggt	agctgggact	acaggcgcac	aacaccatcg	cttcttggat	900
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<210> 704
 <211> 473
 <212> DNA
 <213> Homo sapiens

<400> 704

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tgaatcctgc	tcagagaaaa	ctctacagag	atgtcatgct	ggagaccttc	aagcacctgg	180
cctcagtaga	taatgaggct	cagcttaaag	ccagtgggtc	tattttctcag	caggatactt	240
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cctccctttt	aggaaaaaat	tgggaagaac	atagcgttaa	agacaagcac	aacaccaagg	360
agagacattt	gagcagaaat	ccaagggtgg	agagaccatg	taaaagcagt	aaaggtaata	420
aacgtggaag	aaccttcaga	aagactcgaa	attgtaatcg	tcactctcgc	agg	473

<210> 705
 <211> 435
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(435)
 <223> n = a,t,c or g


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<400> 705
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aatttcagca cgtcctggca cactgggctg tgggaggtct gtgagcaaat ggaagaacat    180
gagaggaact tgtaaatgct ggaaatacaa aatcagctcc atcgcaggct tcagggtctg    240
catctgcctt cctgtaatcc caccatctt tntagtgtgt atgtgggttt tttgtttgtt    300
ttgagacaaa gtcttgcttt gtgcgccagg ctggagtgcg gtggcacaat ctcagctcac    360
tgcaagctct gcctcccggt ttcaagcaat tctcctgcct cagcctcctc agtagctggc    420
attataggcg cgtgc                                     435

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<210> 706
<211> 894
<212> DNA
<213> Homo sapiens

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<400> 706
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tgcgctcagt tccagctatt cttcagatgc tctggatttt gagacggagc acaaattgga    180
ccctgtattt gattctccac ggatgtcccg ccgtagtttg cgcctggcca cgacagcatg    240
caccctgggg gatggtgagg ctgtgggtgc cgacagcggc accagcagcg ctgtctccct    300
gaagaaccga gcggccaggc gagcacgcgt gcacttcctc tccatctgat ctctaaccac    360
agttaaaacc aagcttccat acttttttgt ctgtaaagcc gcaccctgtc tcgagcttaa    420
ggatatgtgt gtgtatgtgc gtgtacagac acacaaacct gccatataaa gtggtagttt    480
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gggtctggaag ctttgtggtc ctgtgggtgg agctcagcta cagctgtcct accacatgtg    660
taaagaggaa ggaatcttac agattacaca tgctgtcgtg gacgatctcc gtgtccagtt    720
cattcttttt tctggagacg gagtctcgtc cttgtcgcgc aggggtggaat gcagtggcac    780
gatctcagct cactgcctcc tctgtctccc gggttcaagc gattctactg cagcagcct    840
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<210> 707
<211> 410
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1) ... (410)
<223> n = a,t,c or g

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<400> 707
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aaactctggc	ctcgactgaa	caaaatgagg	tcccaagagt	ggttacttct	ggggaacaag	240
aagctatttt	aagaggaaat	gctgctgatg	cagagtcttt	cagacagagg	tttaggtggt	300
tttgttactc	agaagtagct	ggaccagga	aagctctgag	tcaactctgg	gagctctgca	360
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<210> 708
 <211> 650
 <212> DNA
 <213> Homo sapiens

<400> 708						
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agaagggaga	ggagcgaaca	tggcagcgcg	ttggcggttt	tgggtgtgtct	ctgtgaccat	120
ggtggtggcg	ctgctcatcg	tttgcgacgt	tccctcagcc	tctgccc aaa	gaaagaagga	180
gatggtgtta	tctgaaaagg	ttagtcagct	gatggaatgg	actaacaaaa	gacctgtaat	240
aagaatgaat	ggagacaagt	tccgtcgctt	tgtgaaagcc	ccaccgagaa	attactccgt	300
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ccaactacgc	tttaaaatta	aataactcat	ataacgttaa	ccattttctca	atcccagaag	420
ggccaagtta	gtgcagtagg	tacttaaata	atgtgtatac	cttactcagg	atgtctatgg	480
tagcaatact	actgctcttt	tatagtcaat	tcttgattat	ccgtatcagt	gggggaagca	540
tggataaata	attgtggtag	ccatcataaa	agtaacttaa	agatcaaaca	gtcatcttat	600
aaattagtat	caacttggcg	gggcatgggg	gctcatgcct	gtaatccccg		650

<210> 709
 <211> 534
 <212> DNA
 <213> Homo sapiens

<400> 709						
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tccaactaaa	gctttacctg	agaaagccaa	aagaagtata	aggcctactg	tacctcatga	180
tgaagactct	tcagatgata	ttgctgtagg	tttaacttgc	caacatgtaa	gtcatgctat	240
cagcgtgaat	catgtaaaga	gagcaatagc	tgagaatctg	tggtcagttt	gctcagaatg	300
tttaaaagaa	agaagattct	atgatgggca	gctagtactt	acttctgata	tttggttggtg	360
cctcaagtgt	ggcttccagg	gatgtggtaa	aaactcagaa	agccaacatt	cattgaagca	420
ctttaagagt	tccagaacag	agccccattg	tattataatt	aatctgagca	catggattat	480
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<210> 710
 <211> 478
 <212> DNA

<213> Homo sapiens

<400> 710

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cggggccttc	ctgtccggaa	ccttcatagc	caccgtcggc	atagacttca	gggtgagggtg	420
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<210> 711

<211> 585

<212> DNA

<213> Homo sapiens

<400> 711

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cgaagcaaaa	agaccagttt	tcattcttga	atgggttcga	tttcttgata	aagtcttgggt	180
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ggaacttgag	agtattacac	gaatgggaaa	tttagtggca	aaactcaaac	ctcgttttaa	360
tccagctcat	tgccatatct	ctttatgttt	gtacctgggc	agctcattgt	aactggagaa	420
aaacatggct	atatgactgg	tgtcacttta	aatttatcat	cgtcaccctg	tgcaagtgat	480
ctctctatgc	tgccatacaa	tcccagtgct	ttcacttata	tctttgagga	gtcaataata	540
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<210> 712

<211> 391

<212> DNA

<213> Homo sapiens

<400> 712

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aaagcgtgta	tcagcaaacc	aaagcacttc	tgtgcaagaa	ttttcttaag	aatgggagga	180
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gggtagataa	atttaatagc	tcttctttta	tggttggtga	tacaccaata	tctaatttaa	360
cccagcagat	aatgaataaa	acagcacttg	c			391

<210> 713
 <211> 524
 <212> DNA
 <213> Homo sapiens

<400> 713
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<210> 714
 <211> 2468
 <212> DNA
 <213> Homo sapiens

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<210> 715
 <211> 924
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(924)
 <223> n = a,t,c or g

<400> 715						
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aatactttgc	acttttgatt	gtgtattatg	gataccaagg	aagagaagaa	ggaacggaaa	360
caaagttatt	ttgctcgact	gaaaaagaaa	aaacaagcca	aacaaaatgc	agagacagcc	420
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ccagacaagt	gcaacattgc	tgtggaagag	gaatatatga	ctgatgagaa	aaaaaagaga	540
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<210> 716
 <211> 679
 <212> DNA
 <213> Homo sapiens

<400> 716

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ccttccgggt	ggtgggagag	aagcagctcc	cgcaggagat	tattttcctg	gtctggtcgc	180
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caagttttca	tcgagtttgg	agttttccac	caaagtga	tacaggaaag	gaggtgacgt	300
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<210> 717

<211> 821

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (821)

<223> n = a,t,c or g

<400> 717

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cggacgcgac	ggaggtcgta	gtagtagtga	gtacgtgctg	aggagcaaag	gagtaaccaa	360
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ccgaagacct	ctgggtatct	tacctgggac	gcgtgtacga	cctaacgtca	ttggcacagg	540
aatacaaggg	gaacctgctg	ctgaaaccca	tcgtggaagt	tgacggccag	gatatcagcc	600
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ggaaatggag	agcggggatg	ggaaggaaa	gcggaggcta	gccagagcct	aatggctgct	720
ctgacaccct	cgccccaaac	cctccttta	agatccgcaa	gcacgaattc	caccacatgg	780
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<210> 718

<211> 480

<212> DNA

<213> Homo sapiens

<400> 718

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cggagactgg	gaaatggatt	cagtgtcatt	tgaagatgtg	gctgtggcct	ttactcagga	240
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caaaaatcct	gggagaaatc	taagcagtca	tgtggtagag	agactgtttg	aaattaaaga	420
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<210> 719
 <211> 467
 <212> DNA
 <213> Homo sapiens

<400> 719						
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caggggcctc	agggtttttg	cctctgccc	gctccgcct	cttcaagata	atcgtgatcg	180
gcgactccaa	tgtgggcaag	acatgcctga	cctaccgctt	ctgcgctggc	cgttccccg	240
accgcaccga	ggccacgata	gggtggatt	tccgagaacg	agcgggtggag	attgatgggg	300
agcgcatcaa	gatccagcta	tgggacacag	caggacaaga	acgattcaga	aagagcatgg	360
ttcagcacta	ctacagaaat	gtacatgctg	ttgtcttcgt	gtatgatatg	accaacatgg	420
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<210> 720
 <211> 490
 <212> DNA
 <213> Homo sapiens

<400> 720						
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gagtctgatg	ttctgcattt	ccagtgtgaa	cagcaaggag	atgtggtctt	gcagaaaatg	180
aatcttttga	gacagcagaa	tttattttgt	gatgtatcaa	tttacattaa	tgacactgag	240
ttccaggggc	acaaggtgat	tttggctgct	tgtctcactt	ttatgagaga	tcagttttta	300
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gtcaagttct						490

<210> 721
 <211> 706
 <212> DNA
 <213> Homo sapiens

<400> 721

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tttgaaaagc	agcagtggcc	cccacatggc	catgctccat	gccgccccgc	cgcccgtggg	180
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tggctcttat	ctgcctcctg	tggcaagtgc	cccgtcctcc	cacctggggc	caggtgcagc	300
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cagaggccag	gcagcagagg	gactcctgcc	agcttgtcct	tgtggaaagc	atccccagg	420
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agcagctgct	gggcaggaac	atttccctgg	ctgtggccac	cagcagcccc	acactggcca	660
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<210> 722

<211> 677

<212> DNA

<213> Homo sapiens

<400> 722

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gcgtggaaga	cctcgccccg	ctcccccttct	gggcccggc	tccgcttaag	tgaaggcctg	180
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ctcctccatt	cttgaagaaa	gaagaagatg	ccactgccat	ttgggttgaa	actgaaacgc	480
acccggcgct	acacgggtgc	cagcaagagt	tgcttggttg	cccggatcca	actgcttaat	540
aacgagtttg	tggagtccac	cctgtccgtg	gagagcactg	gccaggaaag	cctcgaggcc	600
gtggcccaga	ggctggagct	gcggggaggtc	acttacttca	gcctctggta	ctacaacaag	660
caaaatcagc	gccggtg					677

<210> 723

<211> 600

<212> DNA

<213> Homo sapiens

<400> 723

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ctaccagcaa	ttttgagaac	ttgcaaaaac	agcttgcaag	gaaaatgaag	cttcttattt	180
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aaactgcttt	tatccgaaaa	ctgcacccga	cagacaactt	tgcacaaagt	tcctgctttg	360
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tgagtggaga	actaagggcc	agacgagcag	aggacggcat	cgtcctggac	ttgcctcttt	540
atccagccca	ccccaggac	ttccatgaag	tagaggactt	gataaagact	gccataggca	600

<210> 724
 <211> 530
 <212> DNA
 <213> Homo sapiens

<400> 724						
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cagagattca	ccaagatcac	ccaataccta	attcgaatta	gaaaacttac	actaaagcga	480
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<210> 725
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 725						
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cgcgaagcgg	acattggtgg	atcccagcgc	tgtgtgtatt	gcggggaggg	acacctgtgg	240
caccgttaag	ggcagtcct	gatctgaaga	tccgagaact	tccaaaagaa	actgacgttg	300
ggtcagagag	agttgttgag	taaaagttag	tgaagcgaag	agggttcttc	agacaggaaa	360
aagtacgtac	aagggccctg	ggacaagaga	gcattgttctg	tcagagtcac	aaacacaagt	420
ggtccttt						428

<210> 726
 <211> 859
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1) ... (859)

<223> n = a,t,c or g

<400> 726

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aagaagagtt	ttattggcca	aaataaatca	ttctttggtc	ctttggagct	ggtggagaaa	300
ctttgtccag	aagcatcaga	tatagcgact	agtgtcagaa	atcttccaga	attaaagaca	360
gctgtgggaa	gagggcgagc	gtggctttat	cttgactca	tgcaaaagaa	actggcagat	420
tatctgaaag	tgcttataga	caataaacat	ctcttaagcg	agttctatga	gcctgaggct	480
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<210> 727

<211> 450

<212> DNA

<213> Homo sapiens

<400> 727

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tctcctcagc	cccgacgctg	cgcccgcttt	gtgctcattt	ttctctgggg	aaactgaggg	240
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ctgagccgcg	gcattcccg	gccccgctag	ggctgcaggg	tctcaggatg	gcagcctcgg	360
cgaggtgtc	tgtgacctt	gaggatgtgg	ctgtgacatt	caccaggag	gagtggggac	420
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<210> 728

<211> 439

<212> DNA

<213> Homo sapiens

<400> 728

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atgccctgct	gtagtcacag	gagctgtaga	gaggacccc	gtacatctga	aagccgggaa	180

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acctctatag	gaaaaaaatg	gagtgaccag	aacattgaat	atgagtacca	aaaccccaga	360
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<210> 729
 <211> 236
 <212> DNA
 <213> Homo sapiens

<400> 729						
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<210> 730
 <211> 807
 <212> DNA
 <213> Homo sapiens

<400> 730						
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<210> 731
 <211> 944
 <212> DNA
 <213> Homo sapiens

<400> 731

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gcataattca	gcacggatgg	aaagatggag	atgaacctct	aacacagtgg	aaaggaaccg	780
ttctggatca	gctcctttga	ataaacctgc	ccaccaccaa	gaaccatac	atgactttct	840
tttcattgta	tcaaacgaat	gtgtccaccg	gtgtgagcac	cagcaactca	cttcttctct	900
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<210> 732

<211> 761

<212> DNA

<213> Homo sapiens

<400> 732

ccgagacctc	ggtgtggccc	ttgaggcatt	tcaatgggcg	agggccggcg	actgtggatc	60
tggagctgga	cgcgctggag	gggaaggagt	tgatgcagga	cggcgcgtec	ctgagcgaca	120
gcaccgagga	cgaggaggag	ggggcgagcc	tgggcgacgg	cagcggggcg	gaaggcggca	180
gctgcagcag	cagcaggcgg	tcgggcccgg	atggcgggga	cgaagtggag	ggcagcggtg	240
tgggagctgg	cgaaggagag	actgtccagc	acttcccgcct	cgcgcggccc	aagtctctaa	300
tgcagaagct	ccaatgctcc	ttccagacct	cctgggtcaa	ggactttccc	tggctgcgct	360
attccaagga	tactggtctt	atgtcttgcg	gctggtgcc	aaagacccct	gcagatgggg	420
gaagcgtgga	ccttccccca	gtggggcatg	atgagctttc	gcgagggacc	cgcaactaca	480
agaaaacctt	cctcctgagg	caccacgtct	ctaccgagca	caaactccac	gaagccaacg	540
cccaggagtc	agaaatacca	tcagaggagg	ggtactgtga	ctttaatagt	aggccaaatg	600
agaactctta	ttgctatcaa	cttctgcgac	aactaaatga	acagagaaag	aaaggtattc	660
tttgtgatgt	cagcattgtg	gtaagcggaa	aaatcttcaa	agctcataag	aacatcctgg	720
ttgcaggcag	ccgtttcttt	aagactttat	attgcttttc	a		761

<210> 733

<211> 523

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(523)

<223> n = a,t,c or g

<400> 733
aattcccggg tgcacgattt cgtgcggggag cagagatctg cgggcgnttg cagcttgccg 60
tagggaggcg tgggtggtctg aagcctccga gcagccgcgg ccatggcgga tgtaaccgcc 120
cgtagtctgc aatacgagta caaggcgaac tcgaatcttg tgctccaagc tgaccgttct 180
ctcattgacc ggaccgcggg ggatgaaccc acaggagagg tgctgtccct tgttggggaag 240
ctggaggggca cccgtatggg agacaaggct caacggacca aaccgcagat gcaggaggaa 300
agaagagcca agcgaagaaa gcgtgatgag gaccggcatg acatcaacaa gatgaagggt 360
tatactctgc tgtcggaggg cattgatgag atgggtgggca tcatctacaa gccccaaact 420
aaagagactc gggagaccta tgaggtgcta ctcagcttca tccaggctgc tcttggggac 480
cagccacgtg atatcctttg tggggcagct gatgaagttc tag 523

<210> 734
<211> 1341
<212> DNA
<213> Homo sapiens

<400> 734
tttttttttt ttaaccagat tatttcactt attattttatt ttatcttcca atttcctctt 60
gccagactcc catccaaaga gtcataagca gccttcttcc caccctctta catgaaatac 120
atccccacct gaacaaaggc acacggacag gaggaagggg aataggactt cgcaaaactg 180
gacacggcat cgcttcagat cttggactct gaggttccgt tgttactggg ttcacagtta 240
caggcttcgg atgggtctgca cgtgctgttt caagactaat ggtagtctct attgcttctg 300
ttatgtcctt atccaacctg ttcagcctgt cctctgactc aaatatggag taatcaatgg 360
tgaaatctgc actaaagtca tcataactgg ggggtgactgt ataataatag accacctgat 420
aatattcatc ctctcccagt ctttcttcat cctcatatcc ttgtcccagg ataagtggca 480
cagcaaagat ggctacaaag aggacatcca ttctggattc tgcactattg catcaccacc 540
cagagttgcc tttctctctg aggttcatc agtctctttt cgtcacagtg gaaatgttct 600
gaggaagggg tgagcatttt tctagactga aaagaatccc tttcttctgt ctgtctggag 660
cagccatggg ggctgcgggtg ttttccggct gcactttcgt cgcgttcggc ccggccttcg 720
cgcttttctt gatcactgtg gctggggacc cgcttcgctg tatcatcctg gtcgcagggt 780
gagtagaggg cccgggagac gcgggagagc gtcgaagaga gaggtgcgga aggggctgga 840
ggaactgggg caagcctggg agcctgaatt ggggacgata agtcggaggt gaagtttggg 900
cggaggtgag ggggttgggtc tgggagattt gtcttttccc gcagttgggt tccaccttcc 960
aaggatctca cagattcctc ctatattcct cccagcgacg tcagagaagg cccaaggccg 1020
agactcgtga gggggctgtg ctgacctagg caggccgagt cagggtgcctt aggggaggat 1080
ccaggaacgg atacctgcc cttccgtgct cgcacactct ggctgtcatc gctctgaaga 1140
ctctttaatt agatttctcc cctttccagt gcgttcaact ttctacagat gagtctcctg 1200
gtggagacag ttacctacc tgggtccatgt ctccttaacc atccggaagg ctaacttcca 1260
cttttcaage agctttggct ggtttcctc cttgatttct ctggctccca ctactattgc 1320
ttgtctcaact gccctgtat t 1341

<210> 735
<211> 703
<212> DNA
<213> Homo sapiens

<400> 735

tttcgtgaga	ggcccagggtg	aggagcaagc	gcccgcgttc	cggaagcccg	ctcccggggc	60
catgggggca	cagggtagggc	tgccgcccgg	agagccctgc	cgagaaggat	atgtgctgtc	120
tctggctctgt	ccaaactcct	cccaggcttg	gtgtgagatc	acaaatgtgt	cacagctgct	180
ggcttctcct	gtgctctaca	cggacctgaa	ttacagcata	aacaacttga	gcatttccagc	240
aaatgtagaa	aacaaatata	gtctttatgt	gggcttggtg	ctggcagtaa	gctcaagtat	300
ttttattggc	tccagcttca	tactgaaaaa	gaagggcctc	ttgcaactgg	ccagcaaggg	360
ctttactaga	gctggacaag	gtggacattc	ttacctgaag	gaatggctct	ggtagggtagg	420
attgctgtca	atactgtcct	ggaatgcaag	ggaaaaagtt	gacctttgaa	atattacatt	480
ttaaccacag	acttcttgta	ttttcttcac	cataacaata	gagaaaagta	cttttctttc	540
atattttccc	acctccta	ttgaacaact	attgtagctg	catattttct	caagaaagag	600
tacagtttcc	ttgccaggac	aacacggata	agtgaaggc	ttctgtggct	gcttggtact	660
gaacaaatgg	agaagaaatg	aagggtgtca	gcactctcct	tcc		703

<210> 736

<211> 401

<212> DNA

<213> Homo sapiens

<400> 736

tttcgtctgg	cgtggacgtt	tgtgggtggg	cgtgttggtc	cgcgctctca	gaactgtgct	60
gggaaggatg	gtagggcgac	tggggctcac	ctccgcaccg	ttgtaggacc	cggggtaggg	120
ttttgagccc	gtgggagctg	ccccacgcgg	cctcgctctg	ccaacggctg	gatggcggag	180
acgaaggacg	cagcgcagat	gttgggtgacc	ttcaaggatg	tggctgtgac	ctttaccggg	240
gaggagtggg	gacagctgga	cctggcccag	aggaccctgt	accgagaggt	gatgctggag	300
acctgtgggc	ttctggtttc	actagggcat	cgggttccca	aaccagagtt	ggtccacctg	360
ctaaagcatg	ggcaggagct	gtggatagtg	aagagaggcc	t		401

<210> 737

<211> 933

<212> DNA

<213> Homo sapiens

<400> 737

agcggcgcgt	cgcgcgtgtt	gtgtgtcccc	gggtgcaccg	agcgtgttgt	gtgtccgtgc	60
ggcgcggcgc	tcgtgtggct	ccctcgcgcc	caccacgctg	gccccggggc	ccgggtcgc	120
ccttcccagg	cgcgggtgc	agcagagttt	cagaacaagc	ttcctggaac	ccatgaccca	180
tgaagtcttg	tcgacattta	taccgtctga	gggtagcagc	tcgaaagtag	aagaaagtgt	240
tgccagggac	ggcagtatct	ctttgtgtga	ccctggcggc	ttatgggacg	ttggcttcag	300
acctttgtga	tacaccatgc	tgcgtgggac	gatgacggcg	tggagaggaa	tgaggcctga	360
ggtcacactg	gcttgccctc	tcctagccac	agcaggctgc	tttgctgact	tgaacgaggt	420
ccctcaggtc	accgtccagc	ctgcgtccac	cgtccagaag	cccggaggca	ctgtgatctt	480
gggctgcgtg	gtggaacctc	caaggatgaa	tgtaacctgg	cgcctgaatg	gaaaggagct	540
gaatggctcg	gatgatgtct	tgggtgtcct	catcaccac	gggaccctcg	tcatactgc	600
ccttaacaac	cacactgtgg	gacggtacca	gtgtgtggcc	cggatgctcg	cgggggctgt	660
ggccagcgtg	ccagccactg	tgacactagc	cagtgaagtct	gctcctttgc	ctccctgcca	720
tgggtgcggtc	cctcctcatc	tctccacccc	tgaagccccc	accattcatg	ctgcctcttg	780

ttactcttag	cataaaatgg	gccttaactg	cagaaatgtc	aaatcagaac	agtagctgcc	840
ttagtaatgc	ccagtgatgg	gggaccctt	gtgcccttgg	aaaacctcac	tccaagtaga	900
ggctgtatct	ggagtgagt	tctacagaga	ggg			933

<210> 738
 <211> 420
 <212> DNA
 <213> Homo sapiens

<400> 738						
ctgggggtcgg	cggagacagc	tggtgtctga	agccgctcgc	gcccaggggtg	accctgtttg	60
cagcacgatg	tctgaagaag	aggcggctca	gatccccaga	tccagtgtgt	gggagcagga	120
ccagcagaac	gtggtgcagc	gtgtgggtggc	tctgcccctg	gtcagggcca	cgtgcaccgc	180
ggtctgcgat	gtttacagt	cagccaagga	caggcaccgc	ctgctgggct	ccgcctgccg	240
cctggctgag	aactgcgtgt	gcggcctgac	caccctgtgc	ctggaccacg	cccagccgct	300
gctcgagcac	ctgcagcccc	agctggccac	tatgaacagc	ctcgctgca	ggggcctgga	360
caagctggaa	gagaagcttc	cctttctcca	gcaaccttcg	gagacggtgg	tgacctcagc	420

<210> 739
 <211> 1248
 <212> DNA
 <213> Homo sapiens

<400> 739						
tttcgtagcg	agtaaagaag	cagatttgc	ctccctcccg	cttcctccct	cccatcttcc	60
caccggtgct	gtgccagggc	cacagagcag	ctgcaggcct	tgggagagga	cccacacagc	120
ctcctgtagg	tggcaacagt	gccacctgtt	tgactcatag	ggctgaaccg	aggactgaaa	180
aaggaggagg	gcagaccact	cggagaggag	ctgggaagca	gtgcagagag	gagagcggag	240
cggagctgcc	gctgagcaaa	ggccttcacc	atggccgagt	cccccggtg	ctgctccgtc	300
tgggcccgt	gcctccactg	cctgtatagc	tgccactgga	ggaaatgccc	cagagagagg	360
atgcaaacca	gcaagtgcga	ctgtatctgg	tttggcctgc	tcttctccac	cttcctcctt	420
tccctgagct	ggctgtacat	cgggctcgtc	cttctcaatg	acctgcacaa	cttcaatgaa	480
ttcctcttcc	gccgctgggg	acactggatg	gactgggtccc	tggcattcct	gctggtcac	540
tctctactgg	gcacatatgc	atccttgeta	ttggctctgg	ccctgctcct	gcggctttgt	600
agacagcccc	tgcatctgca	cagcctccac	aagggtgctg	tgctcctcat	tatgctgctt	660
gtggcggtg	gccttggtgg	actggacatc	caatggcagc	aggagaggca	tagcttgctg	720
gtgtcactgc	agactgcagg	tagctctgaa	ctccagcagt	caggccctaa	gaggaaagcg	780
gggaggggca	ctggagaaga	gccacctca	ccagctcttg	tccacaggcc	acagccccat	840
tccttcatat	tggagcagcc	gctggaattg	ccctcctggc	ctggcctgtg	gctgatacct	900
tctaccgtat	ccaccgaaga	gagcccaaga	ttctgctact	gctcctatct	tttggagtgt	960
tctgggtcat	ctacttggtg	cccctatgca	tctctcacc	ctgcatcatg	gaaccagag	1020
acttaccacc	caagcctggg	ctggtgggac	accgaggggc	ccccatgctg	gctcccagag	1080
acaccctgat	gtccttgctg	aagacagctg	aatgcggagc	tactgtgttt	gagactgatg	1140
tgatggtcag	ctccgatggg	gtccccttcc	tcatgcatga	tgagcacctc	agcaggacca	1200
cgaatgtagc	ctctgtattc	ccaaccgaa	tcacagccca	cagcagtg		1248

<210> 740
 <211> 185
 <212> Amino acid
 <213> Homo sapiens

<400> 740
 Phe Val Gly Arg Leu Leu Arg Leu Gly Glu Ala Leu Arg Leu Arg Pro
 1 5 10 15
 Asp Pro Ser Gly Gly Cys Arg Leu Gln Pro Ala Leu Val Gly Glu Thr
 20 25 30
 Glu Met Ser Glu Lys Glu Asn Asn Phe Pro Pro Leu Pro Lys Phe Ile
 35 40 45
 Pro Val Lys Pro Cys Phe Tyr Gln Asn Phe Ser Asp Glu Ile Pro Val
 50 55 60
 Glu His Gln Val Leu Val Lys Arg Ile Tyr Arg Leu Trp Met Phe Tyr
 65 70 75 80
 Cys Ala Thr Leu Gly Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile
 85 90 95
 Gly Gly Gly Ser Gly Thr Asn Phe Gly Leu Ala Phe Val Trp Leu Leu
 100 105 110
 Leu Phe Thr Pro Cys Gly Tyr Val Cys Trp Phe Arg Pro Val Tyr Lys
 115 120 125
 Ala Phe Arg Ala Asp Ser Ser Phe Asn Phe Met Ala Phe Phe Ile
 130 135 140
 Phe Arg Ser Pro Val Cys Pro Asp Arg His Pro Gly Asp Trp Leu Leu
 145 150 155 160
 Arg Leu Gly Arg Val Arg Leu Ala Val Gly Asn Trp Ile Leu Pro Val
 165 170 175
 Gln Pro Gly Arg Cys Arg Gly His Ala
 180 185

<210> 741
 <211> 177
 <212> Amino acid
 <213> Homo sapiens

<400> 741
 Phe Leu Gly Ala Gly Ala Asp Ile Phe Cys Ala Tyr Leu Arg Met Ser
 1 5 10 15
 Ser Lys Gln Ala Thr Ser Pro Phe Ala Cys Ala Ala Asp Gly Glu Asp
 20 25 30
 Ala Met Thr Gln Asp Leu Thr Ser Arg Glu Lys Glu Glu Gly Ser Asp
 35 40 45
 Gln His Val Ala Ser His Leu Pro Leu His Pro Ile Met His Asn Lys
 50 55 60
 Pro His Ser Glu Glu Leu Pro Thr Leu Val Ser Thr Ile Gln Gln Asp
 65 70 75 80
 Ala Asp Trp Asp Ser Val Leu Ser Ser Gln Gln Arg Met Glu Ser Glu
 85 90 95
 Asn Asn Lys Leu Cys Ser Leu Tyr Ser Phe Arg Asn Thr Ser Thr Ser
 100 105 110
 Pro His Lys Pro Asp Glu Gly Ser Arg Asp Arg Glu Ile Met Thr Ser
 115 120 125

Val Thr Phe Gly Thr Pro Glu Arg Arg Lys Gly Ser Leu Ala Asp Val
 130 135 140
 Val Asp Thr Leu Lys Gln Lys Lys Leu Glu Glu Met Thr Arg Thr Glu
 145 150 155 160
 Gln Glu Asp Ser Ser Cys Met Glu Lys Leu Leu Ser Lys Asp Trp Lys
 165 170 175
 Glu
 177

<210> 742
 <211> 434
 <212> Amino acid
 <213> Homo sapiens

<400> 742
 Glu Gly Tyr Leu Thr Gly Arg Pro Thr Arg Pro Val Ala Val Arg Gly
 1 5 10 15
 Lys Ser Thr Ala Asp Leu Arg Met Met Gly Arg Ser Pro Gly Phe Ala
 20 25 30
 Met Gln His Ile Val Gly Val Pro His Val Leu Val Arg Arg Gly Leu
 35 40 45
 Leu Gly Arg Asp Leu Phe Met Thr Arg Thr Leu Cys Ser Pro Gly Pro
 50 55 60
 Ser Gln Pro Gly Glu Lys Arg Pro Glu Glu Val Ala Leu Gly Leu His
 65 70 75 80
 His Arg Leu Pro Ala Leu Gly Arg Ala Leu Gly His Ser Ile Gln Gln
 85 90 95
 Arg Ala Thr Ser Thr Ala Lys Thr Trp Trp Asp Arg Tyr Glu Glu Phe
 100 105 110
 Val Gly Leu Asn Glu Val Arg Glu Ala Gln Gly Lys Val Thr Glu Ala
 115 120 125
 Glu Lys Val Phe Met Val Ala Arg Gly Leu Val Arg Glu Ala Arg Glu
 130 135 140
 Asp Leu Glu Val His Gln Ala Lys Leu Lys Glu Val Arg Asp Arg Leu
 145 150 155 160
 Asp Arg Val Ser Arg Glu Asp Ser Gln Tyr Leu Glu Leu Ala Thr Leu
 165 170 175
 Glu His Arg Met Leu Gln Glu Glu Lys Arg Leu Arg Thr Ala Tyr Leu
 180 185 190
 Arg Ala Glu Asp Ser Glu Arg Glu Lys Phe Ser Leu Phe Ser Ala Ala
 195 200 205
 Val Arg Glu Ser His Glu Lys Glu Arg Thr Arg Ala Glu Arg Thr Lys
 210 215 220
 Asn Trp Ser Leu Ile Gly Ser Val Leu Gly Ala Leu Ile Gly Val Ala
 225 230 235 240
 Gly Ser Thr Tyr Val Asn Arg Val Arg Leu Gln Glu Leu Lys Ala Leu
 245 250 255
 Leu Leu Glu Ala Gln Lys Gly Pro Val Ser Leu Gln Glu Ala Ile Arg
 260 265 270
 Glu Gln Ala Ser Ser Tyr Ser Arg Gln Gln Arg Asp Leu His Asn Leu
 275 280 285
 Met Val Asp Leu Arg Gly Leu Val His Ala Ala Gly Pro Gly Gln Asp
 290 295 300
 Ser Gly Ser Gln Ala Gly Ser Pro Pro Thr Arg Asp Arg Asp Val Asp
 305 310 315 320
 Val Leu Ser Ala Ala Leu Lys Glu Gln Leu Ser His Ser Arg Gln Val
 325 330 335
 His Ser Cys Leu Glu Gly Leu Arg Glu Gln Leu Asp Gly Leu Glu Lys
 340 345 350

Thr Cys Ser Gln Met Ala Gly Val Val Gln Leu Val Lys Ser Ala Ala
 355 360 365
 His Pro Gly Leu Val Glu Pro Ala Asp Gly Ala Met Pro Ser Phe Leu
 370 375 380
 Leu Glu Gln Gly Ser Met Ile Leu Ala Leu Ser Asp Thr Glu Gln Arg
 385 390 395 400
 Leu Glu Ala Gln Val Asn Arg Asn Thr Ile Tyr Ser Thr Leu Val Thr
 405 410 415
 Cys Val Thr Phe Val Ala Thr Leu Pro Val Leu Tyr Met Leu Phe Lys
 420 425 430
 Ala Ser
 434

<210> 743
 <211> 211
 <212> Amino acid
 <213> Homo sapiens

<400> 743
 Asn Leu Pro Pro Leu Thr Pro Gln Pro Gly Pro Arg Leu Ala Gly Ser
 1 5 10 15
 Gly Pro Ser His Trp Phe Ser Pro Leu Ser Leu Pro Val Ala Ser Lys
 20 25 30
 Ala Pro Gly Thr Met Ala Gln Ala Leu Gly Glu Asp Leu Val Gln Pro
 35 40 45
 Pro Glu Leu Gln Asp Asp Ser Ser Ser Leu Gly Ser Asp Ser Glu Leu
 50 55 60
 Ser Gly Pro Gly Pro Tyr Arg Gln Ala Asp Arg Tyr Gly Phe Ile Gly
 65 70 75 80
 Gly Ser Ser Ala Glu Pro Gly Pro Gly His Pro Pro Ala Asp Leu Ile
 85 90 95
 Arg Gln Arg Glu Met Lys Trp Val Glu Met Thr Ser His Trp Glu Lys
 100 105 110
 Thr Met Ser Arg Arg Tyr Lys Lys Val Lys Met Gln Cys Arg Lys Gly
 115 120 125
 Ile Pro Ser Ala Leu Arg Ala Arg Cys Trp Pro Leu Leu Cys Gly Ala
 130 135 140
 His Val Cys Gln Lys Asn Ser Pro Gly Thr Tyr Gln Glu Leu Ala Glu
 145 150 155 160
 Ala Pro Gly Asp Pro Gln Trp Met Glu Thr Ile Gly Arg Asp Leu His
 165 170 175
 Arg Gln Phe Pro Leu His Glu Met Phe Val Ser Pro Gln Gly His Gly
 180 185 190
 Gln Gln Gly Leu Leu Gln Val Leu Lys Ala Tyr Thr Leu Tyr Arg Pro
 195 200 205
 Glu Gln Gly
 210 211

<210> 744
 <211> 55
 <212> Amino acid
 <213> Homo sapiens

<400> 744

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Leu Arg Gly Met Ala Ala Ala Ala Ala Gly Pro Ala Ala Ser Gln Arg
 1           5           10           15
Phe Phe Gln Ser Phe Ser Asp Ala Leu Ile Asp Gln Asp Pro Gln Ala
          20           25           30
Ala Leu Glu Val Gly Glu Pro Phe Leu Leu Pro Pro Leu Pro Ala Asp
          35           40           45
Pro Pro Pro Ser Ser Thr Ala
          50           55

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<210> 745
 <211> 182
 <212> Amino acid
 <213> Homo sapiens

```

<400> 745
Trp Ala Cys Phe Arg Ser Ala His Cys Ser Arg His Leu Arg Asn Arg
 1           5           10           15
Ile Phe Met Tyr Leu Tyr Trp Asp Lys Thr Arg Ser Pro Val Cys Lys
          20           25           30
Gly Pro Ala Leu Arg Glu Glu Arg Pro Gln Pro Arg Leu Lys Leu Glu
          35           40           45
Asp Tyr Lys Asp Arg Leu Lys Ser Gly Glu His Leu Asn Pro Asp Gln
          50           55           60
Leu Glu Ala Val Glu Lys Tyr Glu Glu Val Leu His Asn Leu Glu Phe
          65           70           75           80
Ala Lys Glu Leu Gln Lys Thr Phe Ser Gly Leu Ser Leu Asp Leu Leu
          85           90           95
Lys Ala Gln Lys Lys Ala Gln Arg Arg Glu His Met Leu Lys Leu Glu
          100          105          110
Ala Glu Lys Lys Lys Leu Arg Thr Ile Leu Gln Val Gln Tyr Val Leu
          115          120          125
Gln Asn Leu Thr Gln Glu His Val Gln Lys Asp Phe Lys Gly Gly Leu
          130          135          140
Asn Gly Ala Val Tyr Leu Pro Ser Lys Glu Leu Asp Tyr Leu Ile Lys
          145          150          155          160
Phe Ser Lys Leu Thr Cys Pro Glu Arg Asn Glu Ser Leu Arg Gln Thr
          165          170          175
Leu Glu Gly Ser Thr Val
          180          182

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<210> 746
 <211> 136
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(136)
 <223> X = any amino acid or stop code

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<400> 746
Xaa Ala Gly Val Gln Met Lys Leu Glu Phe Leu Gln Arg Lys Phe Trp
 1           5           10           15
Ala Ala Thr Arg Gln Cys Ser Thr Val Asp Gly Pro Cys Thr Gln Ser

```

```

      20      25      30
Cys Glu Asp Ser Asp Leu Asp Cys Phe Val Ile Asp Asn Asn Gly Phe
      35      40      45
Ile Leu Ile Ser Lys Arg Ser Arg Glu Thr Gly Arg Phe Leu Gly Glu
      50      55      60
Val Asp Gly Ala Val Leu Thr Gln Leu Leu Ser Met Gly Val Phe Ser
      65      70      75      80
Gln Val Thr Met Tyr Asp Tyr Gln Ala Met Cys Lys Pro Ser Ser His
      85      90      95
His His Ser Ala Ala Gln Pro Leu Val Ser Pro Ile Ser Ala Phe Leu
      100      105      110
Thr Ala Thr Arg Trp Leu Leu Gln Glu Leu Val Leu Phe Leu Leu Glu
      115      120      125
Trp Ser Val Trp Gly Ser Xaa *
      130      135

```

<210> 747
 <211> 156
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 747
Cys Arg Gly Arg Leu Ala Gln Leu Glu Glu Ala Ala Val Ala Ala Thr
      1      5      10      15
Met Ser Ala Gly Asp Ala Val Cys Thr Gly Trp Leu Val Lys Ser Pro
      20      25      30
Pro Glu Arg Lys Leu Gln Arg Tyr Ala Trp Arg Lys Arg Trp Phe Val
      35      40      45
Leu Arg Arg Gly Arg Met Ser Gly Asn Pro Asp Val Leu Glu Tyr Tyr
      50      55      60
Arg Asn Lys His Ser Ser Lys Pro Ile Arg Val Ile Asp Leu Ser Glu
      65      70      75      80
Cys Ala Val Trp Lys His Val Gly Pro Ser Phe Val Arg Lys Glu Phe
      85      90      95
Gln Asn Asn Phe Val Phe Ile Val Lys Thr Thr Ser Arg Thr Phe Tyr
      100      105      110
Leu Val Ala Lys Thr Glu Gln Glu Met Gln Val Trp Val His Ser Ile
      115      120      125
Ser Gln Val Cys Asn Leu Gly His Leu Glu Asp Gly Ala Ala Asp Ser
      130      135      140
Met Glu Ser Leu Ser Tyr Thr Arg Ser Tyr Leu Gln
      145      150      155 156

```

<210> 748
 <211> 55
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 748
Ile Pro Ala Val Pro Leu Thr Ser Cys Val Thr Val Gly Ser Tyr Ser
      1      5      10      15
Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His
      20      25      30
Tyr Lys Ile Arg Thr Leu Asp Lys Arg Gly Phe Tyr Ile Ser Pro Arg

```

35 40 45
 Ser Thr Phe Ser Thr Leu Gln
 50 55

<210> 749
 <211> 381
 <212> Amino acid
 <213> Homo sapiens

<400> 749
 Lys Asp Ser Val Leu Asn Ile Ala Arg Gly Lys Lys Tyr Gly Glu Lys
 1 5 10 15
 Thr Lys Arg Val Ser Ser Arg Lys Lys Pro Ala Leu Lys Cys Thr Ser
 20 25 30
 Gln Lys Gln Pro Ala Leu Lys Ala Ile Cys Asp Lys Glu Asp Ser Val
 35 40 45
 Pro Asn Thr Ala Thr Glu Lys Lys Asp Glu Gln Ile Ser Gly Thr Val
 50 55 60
 Ser Ser Gln Lys Gln Pro Ala Leu Lys Ala Thr Ser Asp Lys Lys Asp
 65 70 75 80
 Ser Val Ser Asn Ile Pro Thr Glu Ile Lys Asp Gly Gln Gln Ser Gly
 85 90 95
 Thr Val Ser Ser Gln Lys Gln Pro Ala Trp Lys Ala Thr Ser Val Lys
 100 105 110
 Lys Asp Ser Val Ser Asn Ile Ala Thr Glu Ile Lys Asp Gly Gln Ile
 115 120 125
 Arg Gly Thr Val Ser Ser Gln Arg Gln Pro Ala Leu Lys Ala Thr Gly
 130 135 140
 Asp Glu Lys Asp Ser Val Ser Asn Ile Ala Arg Glu Ile Lys Asp Gly
 145 150 155 160
 Glu Lys Ser Gly Thr Val Ser Pro Gln Lys Gln Ser Ala Gln Lys Val
 165 170 175
 Ile Phe Lys Lys Lys Val Ser Leu Leu Asn Ile Ala Thr Arg Ile Thr
 180 185 190
 Gly Gly Trp Lys Ser Gly Thr Glu Tyr Pro Glu Asn Leu Pro Thr Leu
 195 200 205
 Lys Ala Thr Ile Glu Asn Lys Asn Ser Val Leu Asn Thr Ala Thr Lys
 210 215 220
 Met Lys Asp Val Gln Thr Ser Thr Pro Glu Gln Asp Leu Glu Met Ala
 225 230 235 240
 Ser Glu Gly Glu Gln Lys Arg Leu Glu Glu Tyr Glu Asn Asn Gln Pro
 245 250 255
 Gln Val Lys Asn Gln Ile His Ser Arg Asp Asp Leu Asp Asp Ile Ile
 260 265 270
 Gln Ser Ser Gln Thr Val Ser Glu Asp Gly Asp Ser Leu Cys Cys Asn
 275 280 285
 Cys Lys Asn Val Ile Leu Leu Ile Asp Gln His Glu Met Lys Cys Lys
 290 295 300
 Asp Cys Val His Leu Leu Lys Ile Lys Lys Thr Phe Cys Leu Cys Lys
 305 310 315 320
 Arg Leu Thr Glu Leu Lys Asp Asn His Cys Glu Gln Leu Arg Val Lys
 325 330 335
 Ile Arg Lys Leu Lys Asn Lys Ala Ser Val Leu Gln Lys Arg Leu Ser
 340 345 350
 Glu Lys Glu Glu Ile Lys Ser Gln Leu Lys His Glu Thr Leu Glu Leu
 355 360 365
 Glu Lys Glu Leu Cys Ser Leu Arg Phe Ala Ile Gln Gln
 370 375 380 381

<210> 750
 <211> 296
 <212> Amino acid
 <213> Homo sapiens

<400> 750
 Ser Pro Leu Arg Tyr Arg Ala Gly Gln Ser Gly Ser Thr Ile Ser Ser
 1 5 10 15
 Ser Ser Cys Ala Met Trp Arg Cys Gly Gly Arg Gln Gly Leu Cys Val
 20 25 30
 Leu Arg Arg Leu Ser Gly Gly His Ala His His Arg Ala Trp Arg Trp
 35 40 45
 Asn Ser Asn Arg Ala Cys Glu Arg Ala Leu Gln Tyr Lys Leu Gly Asp
 50 55 60
 Lys Ile His Gly Phe Thr Val Asn Gln Val Thr Ser Val Pro Glu Leu
 65 70 75 80
 Phe Leu Thr Ala Val Lys Leu Thr His Asp Asp Thr Gly Ala Arg Tyr
 85 90 95
 Leu His Leu Ala Arg Glu Asp Thr Asn Asn Leu Phe Ser Val Gln Phe
 100 105 110
 Arg Thr Thr Pro Met Asp Ser Thr Gly Val Pro His Ile Leu Glu His
 115 120 125
 Thr Val Leu Cys Gly Ser Gln Lys Tyr Pro Cys Arg Asp Pro Phe Phe
 130 135 140
 Lys Met Leu Asn Arg Ser Leu Ser Thr Phe Met Asn Ala Phe Thr Ala
 145 150 155 160
 Ser Asp Tyr Thr Leu Tyr Pro Phe Ser Thr Gln Asn Pro Lys Asp Phe
 165 170 175
 Gln Asn Leu Leu Ser Val Tyr Leu Asp Ala Thr Phe Phe Pro Cys Leu
 180 185 190
 Arg Glu Leu Asp Phe Trp Gln Glu Gly Trp Arg Leu Glu His Glu Asn
 195 200 205
 Pro Ser Asp Pro Gln Thr Pro Leu Val Phe Lys Gly Val Val Phe Asn
 210 215 220
 Glu Met Lys Gly Ala Phe Thr Asp Asn Glu Arg Ile Phe Ser Gln His
 225 230 235 240
 Leu Gln Asn Arg Leu Leu Pro Asp His Thr Tyr Ser Val Val Ser Gly
 245 250 255
 Gly Asp Pro Leu Cys Ile Pro Glu Leu Thr Trp Glu Gln Leu Lys Gln
 260 265 270
 Phe His Ala Thr His Tyr His Pro Ser Asn Ala Arg Phe Phe Thr Tyr
 275 280 285
 Gly Asn Phe Pro Leu Asp Gln His
 290 295 296

<210> 751
 <211> 163
 <212> Amino acid
 <213> Homo sapiens

<400> 751
 Arg Gly Ala Lys Ala Lys Ser Ala Val Leu Pro Pro Gly Pro Pro Cys
 1 5 10 15
 Ser Ser Ile Leu Ile Leu Ser Pro Pro Ala Pro Leu Thr Pro Arg Ser

```

      20      25      30
Pro Gly Thr Glu Ala Thr Arg Pro Thr Ala Met Ser Lys Ser Leu Lys
      35      40      45
Lys Lys Ser His Trp Thr Ser Lys Val His Glu Ser Val Ile Gly Arg
      50      55      60
Asn Pro Glu Gly Gln Leu Gly Phe Glu Leu Lys Gly Gly Ala Glu Asn
      65      70      75      80
Gly Gln Phe Pro Tyr Leu Gly Glu Val Lys Pro Gly Lys Val Ala Tyr
      85      90      95
Glu Ser Gly Ser Lys Leu Val Ser Glu Glu Leu Leu Leu Glu Val Asn
      100      105      110
Glu Thr Pro Val Ala Gly Leu Thr Ile Arg Asp Val Leu Ala Val Ile
      115      120      125
Lys His Cys Lys Asp Pro Leu Arg Leu Lys Cys Val Lys Gln Gly Glu
      130      135      140
Ser Ser Gly Leu Leu Ser Val Leu Pro Gly Gly Thr Ala Arg Gly
      145      150      155      160
Ala Gly Gln
      163

```

<210> 752
 <211> 99
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 752
Ser His Arg Pro Gln Pro Asp Ala Trp Arg Gln Gly Asn Ala Phe Gln
      1      5      10      15
Cys Val Gln Lys Glu Lys Met Gln Val Ser Ser Ala Glu Val Arg Ile
      20      25      30
Gly Pro Met Arg Leu Thr Gln Asp Pro Ile Gln Val Leu Leu Ile Phe
      35      40      45
Ala Lys Glu Asp Ser Gln Ser Asp Gly Phe Trp Trp Ala Cys Asp Arg
      50      55      60
Ala Gly Tyr Arg Cys Asn Ile Ala Arg Thr Pro Glu Ser Ala Leu Glu
      65      70      75      80
Cys Phe Leu Asp Lys His His Glu Ile Ile Val Ile Asp His Arg Gln
      85      90      95
Thr Gln Asn
      99

```

<210> 753
 <211> 193
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 753
Phe Arg Leu Ala Gly Cys Gly His Leu Leu Val Ser Leu Leu Gly Leu
      1      5      10      15
Leu Leu Leu Leu Ala Arg Ser Gly Thr Arg Ala Leu Val Cys Leu Pro
      20      25      30
Cys Asp Glu Ser Lys Cys Glu Glu Pro Arg Asn Cys Pro Gly Ser Ile
      35      40      45
Val Gln Gly Val Cys Gly Cys Cys Tyr Thr Cys Ala Ser Gln Arg Asn

```

```

      50              55              60
Glu Ser Cys Gly Gly Thr Phe Gly Ile Tyr Gly Thr Cys Asp Arg Gly
 65              70              75              80
Leu Arg Cys Val Ile Arg Pro Pro Leu Asn Gly Asp Ser Leu Thr Glu
      85              90              95
Tyr Glu Ala Gly Val Cys Glu Asp Glu Asn Trp Thr Asp Asp Gln Leu
      100              105              110
Leu Gly Phe Lys Pro Cys Asn Glu Asn Leu Ile Ala Gly Cys Asn Ile
      115              120              125
Ile Asn Gly Lys Cys Glu Cys Asn Thr Ile Arg Thr Cys Ser Asn Pro
      130              135              140
Phe Glu Phe Pro Ser Gln Asp Met Cys Leu Ser Ala Leu Lys Arg Ile
      145              150              155              160
Glu Glu Glu Lys Pro Asp Cys Ser Lys Ala Arg Cys Glu Val Gln Phe
      165              170              175
Ser Pro Arg Cys Pro Glu Asp Ser Val Leu Ile Glu Gly Tyr Ala Pro
      180              185              190
Pro
193

```

<210> 754
 <211> 73
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 754
Phe Arg Met Ala Ala Asn Val Gly Ser Met Phe Gln Tyr Trp Lys Arg
 1              5              10              15
Phe Asp Leu Gln Gln Leu Gln Arg Glu Leu Asp Ala Thr Ala Thr Val
      20              25              30
Leu Ala Asn Arg Gln Asp Glu Ser Glu Gln Ser Arg Lys Arg Leu Ile
      35              40              45
Glu Gln Ser Arg Glu Phe Lys Lys Asn Thr Pro Glu Val Arg Arg Val
      50              55              60
Thr Ile Val Phe Ala Leu Lys Gly Ser
 65              70              73

```

<210> 755
 <211> 83
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 755
Glu Thr Leu Ser Cys Arg Ile Met Asp His Pro Ser Arg Glu Lys Asp
 1              5              10              15
Glu Arg Gln Arg Thr Thr Lys Pro Met Ala Gln Arg Ser Ala His Cys
      20              25              30
Ser Arg Pro Ser Gly Ser Ser Ser Ser Gly Val Leu Met Val Gly
      35              40              45
Pro Asn Phe Arg Val Gly Lys Lys Ile Gly Cys Gly Asn Phe Gly Glu
      50              55              60
Leu Arg Leu Gly Glu Gly Leu Pro Gln Val Tyr Tyr Phe Gly Pro Cys
      65              70              75              80
Gly Lys Tyr

```


83

<210> 756
 <211> 100
 <212> Amino acid
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(100)
 <223> X = any amino acid or stop code

<400> 756
 Gly Cys Cys Lys Asp Xaa His Ser Gly Val Ile Gly Arg Ser Trp Ala
 1 5 10 15
 Met Leu Phe Ala Ser Gly Gly Phe Gln Val Lys Leu Tyr Asp Ile Glu
 20 25 30
 Gln Gln Gln Ile Arg Asn Ala Leu Glu Asn Ile Arg Trp Ala Ser Arg
 35 40 45
 Arg Ser Pro Glu Gly Met Glu Val Gly Leu Phe Leu Ser Val Gly Leu
 50 55 60
 Val Cys His Ile Leu Lys Ala Met Arg Ile Cys Asp Val Thr Phe Ser
 65 70 75 80
 Ser Asp Gly Tyr Cys Ser Ala Ser Glu Leu Val Lys Ala Arg Pro Thr
 85 90 95
 Val Ala Gly Met
 100

<210> 757
 <211> 130
 <212> Amino acid
 <213> Homo sapiens

<400> 757
 Asn Ser Arg Val Asp Asp Phe Val Ser Ala Arg Pro Lys Pro Arg Pro
 1 5 10 15
 Leu Pro Arg Ala Arg Gly Met Val Val Val Thr Gly Arg Glu Pro Asp
 20 25 30
 Ser Arg Arg Gln Asp Gly Ala Met Ser Ser Ser Asp Ala Glu Asp Asp
 35 40 45
 Phe Leu Glu Pro Ala Thr Pro Thr Ala Thr Gln Ala Gly His Ala Leu
 50 55 60
 Pro Pro Ala Ala Thr Gly Ser Phe Leu Arg Leu Phe Pro Leu Thr Ser
 65 70 75 80
 Glu Gly Leu Thr Ser Leu His Ala Cys Pro His Cys Gly Ala Thr Lys
 85 90 95
 Thr Pro Cys Trp Gln Pro Cys Ser Val Gly Gly Thr Thr Ser Pro Arg
 100 105 110
 Thr Pro Arg Ala Gly Thr Ser Ser Thr Glu Met Ala His Thr Leu Glu
 115 120 125
 Met Cys
 130

<210> 758
 <211> 121
 <212>Amino acid
 <213> Homo sapiens

<400> 758
 Arg Ala Leu Trp Val Gly Gly Cys Ser Gly Glu Ala Cys Gly Ile Gly
 1 5 10 15
 Met Ser Gly Leu Leu Thr Asp Pro Glu Gln Arg Ala Gln Glu Pro Arg
 20 25 30
 Tyr Pro Gly Phe Val Leu Gly Leu Asp Val Gly Ser Ser Val Ile Arg
 35 40 45
 Cys His Val Tyr Asp Arg Ala Ala Arg Val Cys Gly Ser Ser Val Gln
 50 55 60
 Lys Val Glu Asn Leu Tyr Pro Gln Ile Gly Trp Val Glu Ile Asp Pro
 65 70 75 80
 Asp Val Leu Trp Ile Gln Phe Val Ala Val Ile Lys Glu Ala Val Lys
 85 90 95
 Ala Ala Gly Ile Gln Met Asn Gln Ile Val Gly Leu Gly Ile Ser Thr
 100 105 110
 Gln Arg Ala Thr Phe Ile Thr Trp Asn
 115 120 121

<210> 759
 <211> 210
 <212>Amino acid
 <213> Homo sapiens

<400> 759
 Gly Leu Ala Ala Glu Gln Ser Met Gln Phe Val Lys Leu Trp Cys Gly
 1 5 10 15
 Cys Ser Gly Glu Phe Pro Thr Arg Leu Arg Arg Thr Pro Leu Thr
 20 25 30
 Glu Ala Met Glu Gly Gly Pro Ala Val Cys Cys Gln Asp Pro Arg Ala
 35 40 45
 Glu Leu Val Glu Arg Val Ala Ala Ile Asp Val Thr His Leu Glu Glu
 50 55 60
 Ala Asp Gly Gly Pro Glu Pro Thr Arg Asn Gly Val Asp Pro Pro Pro
 65 70 75 80
 Arg Ala Arg Ala Ala Ser Val Ile Pro Gly Ser Thr Ser Arg Leu Leu
 85 90 95
 Pro Ala Arg Pro Ser Leu Ser Ala Arg Lys Leu Ser Leu Gln Glu Arg
 100 105 110
 Pro Ala Gly Ser Tyr Leu Glu Ala Gln Ala Gly Pro Tyr Ala Thr Gly
 115 120 125
 Pro Ala Ser His Ile Ser Pro Arg Ala Trp Arg Arg Pro Thr Ile Glu
 130 135 140
 Ser His His Val Ala Ile Ser Asp Ala Glu Asp Cys Val Gln Leu Asn
 145 150 155 160
 Gln Tyr Lys Leu Gln Ser Glu Ile Gly Lys Gly Ala Tyr Gly Val Val
 165 170 175
 Arg Leu Ala Tyr Asn Glu Ser Glu Asp Arg His Tyr Ala Met Lys Val
 180 185 190
 Leu Ser Lys Lys Lys Leu Leu Lys Gln Tyr Gly Phe Pro Arg Arg Pro
 195 200 205

Pro Pro
210

<210> 760
<211> 172
<212> Amino acid
<213> Homo sapiens

<400> 760
Phe Val Tyr Gly Lys Pro Val Thr Leu Trp Pro Thr Ile Ser Ser Val
1 5 10 15
Val Pro Ser Thr Phe Leu Gly Leu Gly Asn Tyr Glu Val Glu Val Glu
20 25 30
Ala Glu Pro Asp Val Arg Gly Pro Glu Ile Val Thr Met Gly Glu Asn
35 40 45
Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly
50 55 60
Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val
65 70 75 80
Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile
85 90 95
Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly
100 105 110
Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys
115 120 125
Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp
130 135 140
Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly Gln Asn Ala Ala
145 150 155 160
Leu Gln Val Phe Thr Ala Ala Ser Arg Lys Thr Met
165 170 172

<210> 761
<211> 104
<212> Amino acid
<213> Homo sapiens

<400> 761
Ser Leu Ala Met Pro Phe Gly Cys Val Thr Leu Gly Asp Lys Lys Asn
1 5 10 15
Tyr Asn Gln Pro Ser Glu Val Thr Asp Arg Tyr Asp Leu Gly Gln Val
20 25 30
Ile Lys Thr Glu Glu Phe Cys Glu Ile Phe Arg Ala Lys Asp Lys Thr
35 40 45
Thr Gly Lys Leu His Thr Cys Lys Lys Phe Gln Lys Arg Asp Gly Arg
50 55 60
Lys Val Arg Lys Ala Ala Lys Asn Glu Ile Gly Ile Leu Lys Met Val
65 70 75 80
Lys His Pro Asn Ile Leu Gln Leu Val Asp Val Phe Val Thr Arg Lys
85 90 95
Glu Tyr Phe Ile Phe Leu Glu Leu
100 104

<210> 762
 <211> 249
 <212> Amino acid
 <213> Homo sapiens

<400> 762
 Gln Arg Arg Arg Phe Arg Ala Gly Leu Trp Gly Gly His Gly Leu Thr
 1 5 10 15
 Asp Gly Leu Arg Arg Asn Gly Gly Cys Gly Cys Ser Ala Arg Val Pro
 20 25 30
 Arg Val Gly Glu Arg Leu Arg Gly His Arg Cys Pro Asp Pro Leu Cys
 35 40 45
 Leu Leu Leu Asp Met Leu Phe Leu Ser Phe His Ala Gly Ser Trp Glu
 50 55 60
 Ser Trp Cys Cys Cys Cys Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg
 65 70 75 80
 Gly Gln His Trp Gln Leu Glu Met Ala Asp Thr Arg Ser Val His Glu
 85 90 95
 Thr Arg Phe Glu Ala Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn
 100 105 110
 Gly Ser Phe Gln Pro Thr Asn Glu Met Met Leu Lys Phe Tyr Ser Phe
 115 120 125
 Tyr Lys Gln Ala Thr Glu Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe
 130 135 140
 Trp Asp Pro Ile Gly Arg Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly
 145 150 155 160
 Asp Met Thr Lys Glu Glu Ala Met Ile Ala Tyr Val Glu Glu Met Lys
 165 170 175
 Lys Ile Ile Glu Thr Met Pro Met Thr Glu Lys Val Glu Glu Leu Leu
 180 185 190
 Arg Val Ile Gly Pro Phe Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly
 195 200 205
 Arg Ser Ser Asp Ile Thr Ser Asp Leu Gly Asn Val Leu Thr Ser Thr
 210 215 220
 Pro Asn Ala Lys Thr Val Asn Gly Lys Ala Glu Ser Ser Asp Ser Gly
 225 230 235 240
 Ala Glu Ser Glu Glu Glu Glu Ala Cys
 245 249

<210> 763
 <211> 184
 <212> Amino acid
 <213> Homo sapiens

<400> 763
 Ser Cys Phe Lys Gly Arg Thr Gly Gly Arg Ser Gly Ser Ser Gly Asp
 1 5 10 15
 Ser Ser Arg Trp Ala Arg Cys Gly Arg His Phe Ser Ala Ser Thr Glu
 20 25 30
 Glu Pro Pro Leu Ser Gln Pro Cys Ser Ala Leu Pro Arg Ser Gly Arg
 35 40 45
 Arg Gly Cys Ala Val Pro Ser Ser Val Thr Lys Met Leu Ser Phe Phe
 50 55 60
 Arg Arg Thr Leu Gly Arg Arg Ser Met Arg Lys His Ala Glu Lys Glu
 65 70 75 80

Arg Leu Arg Glu Ala Gln Arg Ala Ala Thr His Ile Pro Ala Ala Gly
 85 90 95
 Asp Ser Lys Ser Ile Ile Thr Cys Arg Val Ser Leu Leu Asp Gly Thr
 100 105 110
 Asp Val Ser Val Asp Leu Pro Lys Lys Ala Lys Gly Gln Glu Leu Phe
 115 120 125
 Asp Gln Ile Met Tyr His Leu Asp Leu Ile Glu Ser Asp Tyr Phe Gly
 130 135 140
 Leu Arg Phe Met Asp Ser Ala Gln Val Ala His Trp Leu Asp Gly Thr
 145 150 155 160
 Lys Ser Ile Lys Lys Gln Val Lys Ile Gly Ser Pro Tyr Cys Leu His
 165 170 175
 Leu Arg Val Lys Phe Tyr Ser Ser
 180 184

<210> 764
 <211> 138
 <212> Amino acid
 <213> Homo sapiens

<400> 764
 Glu Ser Arg Glu Arg Ser Gly Asn Arg Arg Gly Ala Glu Asp Arg Gly
 1 5 10 15
 Thr Cys Gly Leu Gln Ser Pro Ser Ala Met Leu Gly Ala Lys Pro His
 20 25 30
 Trp Leu Pro Gly Pro Leu His Ser Pro Gly Leu Pro Leu Val Leu Val
 35 40 45
 Leu Leu Ala Leu Gly Ala Gly Trp Ala Gln Glu Gly Ser Glu Pro Val
 50 55 60
 Leu Leu Glu Gly Glu Cys Leu Val Val Cys Glu Pro Gly Arg Ala Ala
 65 70 75 80
 Ala Gly Gly Pro Gly Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg
 85 90 95
 Val Ala Phe Ala Val Arg Ser His His His Glu Pro Ala Gly Glu
 100 105 110
 Thr Gly Asn Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val
 115 120 125
 Asn Glu Gly Gly Gly Phe Asp Arg Ala Ser
 130 135 138

<210> 765
 <211> 168
 <212> Amino acid
 <213> Homo sapiens

<400> 765
 Glu Asp Val Lys Ser Tyr Tyr Thr Val His Leu Pro Gln Leu Glu Asn
 1 5 10 15
 Ile Asn Ser Gly Glu Thr Arg Thr Ile Ser His Phe His Tyr Thr Thr
 20 25 30
 Trp Pro Asp Phe Gly Val Pro Gln Ser Pro Ala Ser Phe Leu Asn Phe
 35 40 45
 Leu Phe Lys Val Arg Glu Ser Gly Ser Leu Asn Pro Asp His Gly Pro
 50 55 60

Val Val Ile His Arg Ser Ala Gly Thr Gly Arg Ser Ser Thr Phe Ser
 65 70 75 80
 Val Val His Thr Cys Leu Val Leu Met Glu Lys Gly Asp Asp Ile Asn
 85 90 95
 Ile Lys Gln Val Leu Leu Asn Ile Arg Lys Phe Gln Met Gly Leu Ile
 100 105 110
 Gln Thr Pro Asp Gln Leu Arg Phe Ser Tyr Met Ala Ile Thr Glu Gly
 115 120 125
 Ala Lys Cys Val Lys Gly Asp Ser Ser Ile Gln Lys Arg Trp Lys Glu
 130 135 140
 Leu Ser Lys Glu Asp Leu Pro Pro Ala Phe Asp His Ser Pro Asn Lys
 145 150 155 160
 Ile Met Thr Glu Lys Tyr Asn Arg
 165 168

<210> 766

<211> 255

<212>Amino acid

<213> Homo sapiens

<400> 766

Leu Asn Arg Gln Arg Cys Gly Asp Gln Val Leu Val Pro Gly Thr Gly
 1 5 10 15
 Leu Ala Ala Ile Leu Arg Thr Leu Pro Met Phe His Asp Glu His
 20 25 30
 Ala Arg Ala Arg Gly Leu Ser Glu Asp Thr Leu Val Leu Pro Pro Ala
 35 40 45
 Ser Arg Asn Gln Arg Ile Leu Tyr Thr Val Leu Glu Cys Gln Pro Leu
 50 55 60
 Phe Asp Ser Ser Asp Met Thr Ile Ala Glu Trp Val Cys Leu Ala Gln
 65 70 75 80
 Thr Ile Lys Arg His Tyr Glu Gln Tyr His Gly Phe Val Val Ile His
 85 90 95
 Gly Thr Asp Thr Met Ala Phe Ala Ala Ser Met Leu Ser Phe Met Leu
 100 105 110
 Glu Asn Leu Gln Lys Thr Val Ile Leu Thr Gly Ala Gln Val Pro Ile
 115 120 125
 His Ala Leu Trp Ser Asp Gly Arg Glu Asn Leu Leu Gly Ala Leu Leu
 130 135 140
 Met Ala Gly Gln Tyr Val Ile Pro Glu Val Cys Leu Phe Phe Gln Asn
 145 150 155 160
 Gln Leu Phe Arg Gly Asn Arg Ala Thr Lys Val Asp Ala Arg Arg Phe
 165 170 175
 Ala Ala Phe Cys Ser Pro Asn Leu Leu Pro Leu Ala Thr Val Gly Ala
 180 185 190
 Asp Ile Thr Ile Asn Arg Glu Leu Val Arg Lys Val Asp Gly Lys Ala
 195 200 205
 Gly Leu Val Val His Ser Ser Met Glu Gln Asp Val Gly Leu Leu Arg
 210 215 220
 Leu Tyr Pro Gly Ile Pro Ala Ala Leu Val Arg Ala Phe Leu Gln Pro
 225 230 235 240
 Pro Leu Lys Gly Val Val Met Glu Thr Phe Gly Ser Gly Asn Gly
 245 250 255

<210> 767

<211> 260

<212>Amino acid

<213> Homo sapiens

<400> 767

```

Leu Phe Arg Leu Ala Pro Gly Phe Leu Arg Ser Leu Ala Arg Gln Gly
 1           5           10           15
Tyr His Gln Ile Trp Ala Phe Pro Phe Leu Pro Ser Gly Ala Thr Ala
          20           25           30
Thr Trp Pro Ala Ala Ser Arg Ser Arg Ser Leu Ala Ala Arg Ser Leu
          35           40           45
Pro Arg Ser Pro Ala Arg Pro Gly Pro Asn Asp Ala Leu Leu Gly Glu
 50           55           60
His Asp Phe Arg Gly Gln Gly Val Arg Ala Gln Arg Phe Arg Phe Ser
 65           70           75           80
Glu Glu Pro Gly Pro Gly Ala Asp Gly Ala Val Leu Glu Val His Val
          85           90           95
Pro Gln Ile Gly Ala Gly Val Ser Leu Pro Gly Ile Leu Ala Ala Lys
          100          105          110
Cys Gly Ala Glu Val Ile Leu Ser Asp Ser Ser Glu Leu Pro His Cys
          115          120          125
Leu Glu Val Cys Arg Gln Ser Cys Gln Met Asn Asn Leu Pro His Leu
          130          135          140
Gln Val Val Gly Leu Thr Trp Gly His Ile Ser Trp Asp Leu Leu Ala
          145          150          155          160
Leu Pro Pro Gln Asp Ile Ile Leu Ala Ser Asp Val Phe Phe Glu Pro
          165          170          175
Glu Asp Phe Glu Asp Ile Leu Ala Thr Ile Tyr Phe Leu Met His Lys
          180          185          190
Asn Pro Lys Val Gln Leu Trp Ser Thr Tyr Gln Val Arg Ser Ala Asp
          195          200          205
Trp Ser Leu Glu Ala Leu Leu Tyr Lys Trp Asp Met Lys Cys Val His
          210          215          220
Ile Pro Leu Glu Ser Phe Asp Ala Asp Lys Glu Asp Ile Ala Glu Ser
          225          230          235          240
Thr Leu Pro Gly Arg His Thr Val Glu Met Leu Val Ile Ser Phe Ala
          245          250          255
Lys Asp Ser Leu
          260

```

<210> 768

<211> 200

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(200)

<223> X = any amino acid or stop code

<400> 768

```

Ser Phe Ile Tyr Lys His Thr His Arg Ala Arg Phe Gly Pro Arg Ala
 1           5           10           15
Ile Val Ala Ser Pro Ala Leu Thr Ala Gly Pro His Val Ser Leu Thr
          20           25           30
Ala Ser Cys Arg Val Gly Met Trp Val Ser Cys Ser Pro Ser Pro Phe
          35           40           45
Leu His Pro Thr Asn Thr Leu Val Ala Val Leu Glu Arg Asp Thr Leu

```

```

      50              55              60
Gly Ile Arg Glu Val Arg Leu Phe Asn Ala Val Val Arg Trp Ser Glu
 65              70              75              80
Ala Glu Cys Gln Arg Gln Gln Leu Gln Val Thr Pro Glu Asn Arg Arg
      85              90              95
Lys Val Leu Gly Lys Ala Leu Gly Leu Ile Arg Phe Pro Leu Met Thr
      100              105              110
Ile Glu Glu Phe Ala Ala Gly Asn Arg Ala Arg Ala Gln Gly Leu Val
      115              120              125
Trp Glu Gly Ser Gly Thr Gln Val Gly Ile Trp Cys Thr Glu Asp Ser
      130              135              140
Ala Pro Glu Phe Thr Ala Glu Ser Leu Ala Asp Ala Trp His Ile Gln
      145              150              155              160
Ile Gly Arg Asn Leu Ala Cys Glu Asp Ala Ser Thr Trp Ala Ile Cys
      165              170              175
Xaa Pro Arg Pro Gly Ser Val Pro Thr Val His Thr Ala Arg Pro Arg
      180              185              190
Leu Ser Cys Leu Ser Ser Cys Phe
      195              200

```

<210> 769

<211> 33

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(33)

<223> X = any amino acid or stop code

<400> 769

```

Met Ala Ser Thr Gln Asp Ala Glu Leu Ala Val Ser Arg Xaa Arg Ala
 1              5              10              15
Ile Ala Leu Xaa Pro Gly Xaa Gln Ser Xaa Xaa Pro Ser Gln Lys Lys
      20              25              30
Lys
33

```

<210> 770

<211> 599

<212>Amino acid

<213> Homo sapiens

<400> 770

```

Leu Leu Lys Ser Cys Gly Val Leu Leu Ser Gly Val Cys Ile Pro Cys
 1              5              10              15
Glu Gly Lys Gly Pro Thr Val Leu Val Ile Gln Thr Ala Val Pro Gln
      20              25              30
Asp Arg Pro Thr Lys Ser Ser Met Arg Ser Ala Ala Lys Pro Trp Asn
      35              40              45
Pro Ala Ile Arg Ala Gly Gly His Gly Pro Asp Arg Val Arg Pro Leu
      50              55              60
Pro Ala Ala Ser Ser Gly Met Lys Ser Ser Lys Ser Ser Thr Ser Leu
      65              70              75              80

```


Ala Phe Glu Ser Arg Leu Ser Arg Leu Lys Arg Ala Ser Ser Glu Asp
 85 90 95
 Thr Leu Asn Lys Pro Gly Ser Thr Ala Ala Ser Gly Val Val Arg Leu
 100 105 110
 Lys Lys Thr Ala Thr Ala Gly Ala Ile Ser Glu Leu Thr Glu Ser Arg
 115 120 125
 Leu Arg Ser Gly Thr Gly Ala Phe Thr Thr Thr Lys Arg Thr Gly Ile
 130 135 140
 Pro Ala Pro Arg Glu Phe Ser Val Thr Val Ser Arg Glu Arg Ser Val
 145 150 155 160
 Pro Arg Gly Pro Ser Asn Pro Arg Lys Ser Val Ser Ser Pro Thr Ser
 165 170 175
 Ser Asn Thr Pro Thr Pro Thr Lys His Leu Arg Thr Pro Ser Thr Lys
 180 185 190
 Pro Lys Gln Glu Asn Glu Gly Gly Glu Lys Val Arg Leu Ser Pro Lys
 195 200 205
 Phe Arg Glu Leu Leu Ala Glu Ala Lys Ala Lys Asp Ser Glu Ile Asn
 210 215 220
 Arg Leu Arg Ser Glu Leu Lys Lys Tyr Lys Glu Lys Arg Thr Leu Asn
 225 230 235 240
 Ala Glu Gly Thr Asp Ala Leu Gly Pro Asn Val Asp Gly Thr Ser Val
 245 250 255
 Ser Pro Gly Asp Thr Glu Pro Met Ile Arg Ala Leu Glu Glu Lys Asn
 260 265 270
 Lys Asn Phe Gln Lys Glu Leu Ser Asp Leu Glu Glu Glu Asn Arg Val
 275 280 285
 Leu Lys Glu Lys Leu Ile Tyr Leu Glu His Ser Pro Asn Ser Glu Gly
 290 295 300
 Ala Ala Ser His Thr Gly Asp Ser Ser Cys Pro Thr Ser Ile Thr Gln
 305 310 315 320
 Glu Ser Ser Phe Gly Ser Pro Thr Gly Asn Gln Leu Ser Ser Asp Ile
 325 330 335
 Asp Glu Tyr Lys Lys Asn Ile His Gly Asn Ala Leu Arg Thr Ser Gly
 340 345 350
 Ser Ser Ser Ser Asp Val Thr Lys Ala Ser Leu Ser Pro Asp Ala Ser
 355 360 365
 Asp Phe Glu His Ile Thr Ala Glu Thr Pro Ser Arg Pro Leu Ser Ser
 370 375 380
 Thr Ser Asn Pro Phe Lys Ser Ser Lys Cys Ser Thr Ala Gly Ser Ser
 385 390 395 400
 Pro Asn Ser Val Ser Glu Leu Ser Leu Ala Ser Leu Thr Glu Lys Ile
 405 410 415
 Gln Lys Met Glu Glu Asn His His Ser Thr Ala Glu Glu Leu Gln Ala
 420 425 430
 Thr Leu Gln Glu Leu Ser Asp Gln Gln Gln Met Val Gln Glu Leu Thr
 435 440 445
 Ala Glu Asn Glu Lys Leu Val Asp Glu Lys Thr Ile Leu Glu Thr Ser
 450 455 460
 Phe His Gln His Arg Glu Arg Ala Glu Gln Leu Ser Gln Glu Asn Glu
 465 470 475 480
 Lys Leu Met Asn Leu Leu Gln Glu Arg Val Lys Asn Glu Glu Pro Thr
 485 490 495
 Thr Gln Glu Gly Lys Ile Ile Glu Leu Glu Gln Lys Cys Thr Gly Ile
 500 505 510
 Leu Glu Gln Gly Arg Phe Glu Arg Glu Lys Leu Leu Asn Ile Gln Gln
 515 520 525
 Gln Leu Thr Cys Ser Leu Arg Lys Val Glu Glu Glu Asn Gln Gly Ala
 530 535 540
 Leu Glu Met Ile Lys Arg Leu Lys Glu Glu Asn Glu Lys Leu Asn Glu
 545 550 555 560
 Phe Leu Glu Leu Glu Arg His Asn Asn Asn Met Met Ala Lys Thr Leu
 565 570 575
 Glu Glu Cys Arg Val Thr Leu Glu Gly Leu Lys Met Glu Asn Gly Ser
 580 585 590

Leu Lys Ser His Leu Gln Gly
595 599

<210> 771
<211> 103
<212> Amino acid
<213> Homo sapiens

<400> 771
Ser Gln Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn
1 5 10 15
Phe Cys Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile
20 25 30
Lys Ala Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu
35 40 45
Thr Asp Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly
50 55 60
Tyr Val Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu
65 70 75 80
Leu Thr Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val
85 90 95
Phe Asp Asn Gln Phe Gly Leu
100 103

<210> 772
<211> 218
<212> Amino acid
<213> Homo sapiens

<400> 772
Pro Phe Lys Lys Met Thr Asp Leu Leu Arg Ser Val Val Thr Val Ile
1 5 10 15
Asp Val Phe Tyr Lys Tyr Thr Lys Gln Asp Gly Glu Cys Gly Thr Leu
20 25 30
Ser Lys Gly Glu Leu Lys Glu Leu Glu Lys Glu Leu His Pro Val
35 40 45
Leu Lys Asn Pro Asp Asp Pro Asp Thr Val Asp Val Ile Met His Met
50 55 60
Leu Asp Arg Asp His Asp Arg Arg Leu Asp Phe Thr Glu Phe Leu Leu
65 70 75 80
Met Ile Phe Lys Leu Thr Met Ala Cys Asn Lys Val Leu Ser Lys Glu
85 90 95
Tyr Cys Lys Ala Ser Gly Ser Lys Lys His Arg Arg Gly His Arg His
100 105 110
Gln Glu Glu Glu Ser Glu Thr Glu Glu Asp Glu Glu Asp Thr Pro Gly
115 120 125
His Lys Ser Gly Tyr Arg His Ser Ser Trp Ser Glu Gly Glu Glu His
130 135 140
Gly Tyr Ser Ser Gly His Ser Arg Gly Thr Val Lys Cys Arg His Gly
145 150 155 160
Ser Asn Ser Arg Arg Leu Gly Arg Gln Gly Asn Leu Ser Ser Ser Gly
165 170 175
Asn Gln Glu Gly Ser Gln Lys Arg Tyr His Arg Ser Ser Cys Gly His
180 185 190

Ser Trp Ser Gly Gly Lys Asp Arg His Gly Ser Ser Ser Val Glu Leu
 195 200 205
 Arg Glu Arg Ile Asn Lys Ser His Ile Lys
 210 215 218

<210> 773
 <211> 130
 <212> Amino acid
 <213> Homo sapiens

<400> 773
 Val Pro Lys Ile Ser Gly Pro Asp His Ile Asp Phe Ile Pro Trp Asp
 1 5 10 15
 Gln Leu Phe Met Ala Ser Ser Ser Ser Val Thr Glu Phe Leu Val Leu
 20 25 30
 Gly Phe Ser Ser Leu Gly Glu Leu Gln Leu Val Leu Phe Ala Val Phe
 35 40 45
 Leu Cys Leu Tyr Leu Ile Ile Leu Ser Gly Asn Ile Ile Ile Ile Ser
 50 55 60
 Val Ile His Leu Asp His Ser Leu His Thr Pro Met Tyr Phe Phe Leu
 65 70 75 80
 Gly Ile Leu Ser Ile Ser Glu Ile Phe Tyr Thr Thr Val Ile Leu Pro
 85 90 95
 Lys Met Leu Ile Asn Leu Phe Ser Val Phe Arg Thr Leu Ser Phe Val
 100 105 110
 Ser Cys Ala Thr Gln Met Phe Tyr Glu Ile Val Gly Pro Gly Thr Gln
 115 120 125
 Glu Arg
 130

<210> 774
 <211> 204
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(204)
 <223> X = any amino acid or stop code

<400> 774
 Asp His Ser Thr Glu Thr Pro Gly Ile Pro Ala Ala Glu Pro Val Ser
 1 5 10 15
 His Gly Thr Gly Lys Leu Glu Arg Ala Pro Thr Leu Pro Ala Gly Ala
 20 25 30
 Glu Leu Pro Ala Pro Ala Ala Val Pro Cys Pro Thr Leu Xaa Val Cys
 35 40 45
 Leu Tyr Pro Gln Leu Leu Gly Leu Ser Val Ala Thr Met Val Thr Leu
 50 55 60
 Thr Tyr Phe Gly Ala His Phe Ala Val Ile Arg Arg Ala Ser Leu Glu
 65 70 75 80
 Lys Asn Pro Tyr Gln Ala Val His Gln Trp Gly Thr Gln Gln Arg Leu
 85 90 95
 Ile Gln His Pro Glu Ser Gly Ser Glu Gly Gln Ser Leu Leu Gly Pro

```

      100              105              110
Leu Arg Ala Phe Ser Ala Gly Leu Ser Leu Val Gly Leu Leu Thr Leu
      115              120              125
Gly Ala Val Leu Ser Ala Ala Thr Val Arg Glu Ala Gln Gly Leu
      130              135              140
Met Ala Gly Gly Phe Leu Cys Phe Ser Leu Ala Phe Cys Ala Gln Val
      145              150              155              160
Gln Val Val Phe Trp Arg Leu His Ser Pro Thr Gln Val Glu Asp Ala
      165              170              175
Met Leu Asp Thr Tyr Asp Leu Val Tyr Glu Gln Ala Met Lys Gly Thr
      180              185              190
Ser His Val Arg Arg Gln Glu Leu Ala Ala Ile Gln
      195              200              204

```

<210> 775
 <211> 121
 <212> Amino acid
 <213> Homo sapiens

```

<400> 775
Gln Pro Gly Tyr Ser Glu Tyr Asp Lys Asn Arg Gly Gln Gly Met Leu
  1              5              10              15
Leu Asn Met Met Cys Gly Arg Gln Leu Ser Ala Ile Ser Leu Cys Leu
      20              25              30
Ala Val Thr Phe Ala Pro Leu Phe Asn Ala Gln Ala Asp Glu Pro Glu
      35              40              45
Val Ile Pro Gly Asp Ser Pro Val Ala Val Ser Glu Gln Gly Glu Ala
      50              55              60
Leu Pro Gln Ala Gln Ala Thr Ala Ile Met Ala Gly Ile Gln Pro Leu
      65              70              75              80
Pro Glu Gly Ala Ala Glu Lys Ala Arg Thr Gln Ile Glu Ser Gln Leu
      85              90              95
Pro Ala Gly Tyr Lys Pro Val Tyr Leu Asn Gln Leu Gln Leu Leu Tyr
      100              105              110
Ala Ala Arg Gly Ile Ser Cys Ser Val
      115              120 121

```

<210> 776
 <211> 142
 <212> Amino acid
 <213> Homo sapiens

```

<400> 776
Arg Thr Arg Ala Ala Asp Val Tyr Val Phe Ser Leu Thr Gly Lys Ser
  1              5              10              15
Arg Asn Val Ser Ser Thr Val Arg Arg Ser Ala Val Gly Gly Met
      20              25              30
Ser Ala Leu Ala Leu Phe Asp Leu Leu Lys Pro Asn Tyr Ala Leu Ala
      35              40              45
Thr Gln Val Glu Phe Thr Asp Pro Glu Ile Val Ala Glu Tyr Ile Thr
      50              55              60
Tyr Pro Ser Pro Asn Gly His Gly Glu Val Arg Gly Tyr Leu Val Lys
      65              70              75              80
Pro Ala Lys Met Ser Gly Lys Thr Pro Ala Val Val Val Val His Glu

```

				85					90				95				
Asn	Arg	Gly	Leu	Asn	Pro	Tyr	Ile	Glu	Asp	Val	Ala	Arg	Arg	Val	Ala		
			100					105					110				
Lys	Ala	Gly	Tyr	Ile	Ala	Leu	Ala	Pro	Asp	Gly	Leu	Ser	Ser	Val	Gly		
		115					120					125					
Gly	Tyr	Pro	Gly	Asn	Asp	Ile	Lys	Val	Val	Ser	Ala	Ala	Ala				
	130					135					140		142				

<210> 777

<211> 150

<212>Amino acid

<213> Homo sapiens

<400> 777

Val	Lys	Gln	Arg	His	Gly	Asn	Ser	Leu	Leu	Thr	Thr	Glu	Thr	Lys	Cys		
1				5					10					15			
Ile	Ser	Cys	Arg	Leu	Gly	Val	Pro	Leu	Ser	Pro	Gln	Arg	Arg	Phe	Gln		
			20					25					30				
Ala	Ile	Arg	Ile	Glu	Glu	Val	Lys	Leu	Arg	Trp	Phe	Ala	Phe	Leu	Ile		
		35					40				45						
Val	Leu	Leu	Ala	Gly	Cys	Ser	Ser	Lys	His	Asp	Tyr	Thr	Asn	Pro	Pro		
	50					55					60						
Trp	Asn	Ala	Lys	Val	Pro	Val	Gln	Arg	Ala	Met	Gln	Trp	Met	Pro	Ile		
	65				70					75					80		
Ser	Gln	Lys	Ala	Gly	Ala	Ala	Trp	Gly	Val	Asp	Pro	Gln	Leu	Ile	Thr		
				85					90					95			
Ala	Ile	Ile	Ala	Ile	Glu	Ser	Gly	Gly	Asn	Pro	Asn	Ala	Val	Ser	Lys		
			100					105					110				
Ser	Asn	Ala	Ile	Gly	Leu	Met	Gln	Leu	Lys	Ala	Ser	Thr	Ser	Gly	Arg		
	115					120						125					
Asp	Val	Tyr	Arg	Arg	Met	Gly	Trp	Ser	Gly	Glu	Pro	Thr	Thr	Ser	Glu		
	130					135					140						
Leu	Lys	Asn	Ser	Ser	Arg												
145					150												

<210> 778

<211> 296

<212>Amino acid

<213> Homo sapiens

<400> 778

His	Ala	Ala	Gly	Ile	Arg	His	Glu	Ala	Lys	Pro	Lys	Arg	Ser	Phe	Tyr		
1				5					10					15			
Ala	Ala	Arg	Asp	Leu	Tyr	Lys	Tyr	Arg	His	Gln	Tyr	Pro	Asn	Phe	Lys		
			20					25					30				
Asp	Ile	Arg	Tyr	Gln	Asn	Asp	Leu	Ser	Asn	Leu	Arg	Phe	Tyr	Lys	Asn		
	35					40					45						
Lys	Ile	Pro	Phe	Lys	Pro	Asp	Gly	Val	Tyr	Ile	Glu	Glu	Val	Leu	Ser		
	50					55					60						
Lys	Trp	Lys	Gly	Asp	Tyr	Glu	Lys	Leu	Glu	His	Asn	His	Thr	Tyr	Ile		
	65				70				75						80		
Gln	Trp	Leu	Phe	Pro	Leu	Arg	Glu	Gln	Gly	Leu	Asn	Phe	Tyr	Ala	Lys		
				85					90					95			
Glu	Leu	Thr	Thr	Tyr	Glu	Ile	Glu	Glu	Phe	Lys	Lys	Thr	Lys	Glu	Ala		

```

      100      105      110
Ile Arg Arg Phe Leu Leu Ala Tyr Lys Met Met Leu Glu Phe Phe Gly
      115      120      125
Ile Lys Leu Thr Asp Lys Thr Gly Asn Val Ala Arg Ala Val Asn Trp
      130      135      140
Gln Glu Arg Phe Gln His Leu Asn Glu Ser Gln His Asn Tyr Leu Arg
      145      150      155
Ile Thr Arg Ile Leu Lys Ser Leu Gly Glu Leu Gly Tyr Glu Ser Phe
      165      170      175
Lys Ser Pro Leu Val Lys Phe Ile Leu His Glu Ala Leu Val Glu Asn
      180      185      190
Thr Ile Pro Asn Ile Lys Gln Ser Ala Leu Glu Tyr Phe Val Tyr Thr
      195      200      205
Ile Arg Asp Arg Arg Glu Arg Arg Lys Leu Leu Arg Phe Ala Gln Lys
      210      215      220
His Tyr Thr Pro Ser Glu Asn Phe Ile Trp Gly Pro Pro Arg Lys Glu
      225      230      235
Gln Ser Glu Gly Ser Lys Ala Gln Lys Met Ser Ser Pro Leu Ala Ser
      245      250      255
Ser His Asn Ser Gln Thr Ser Met His Lys Lys Ala Lys Asp Ser Lys
      260      265      270
Asn Ser Ser Ser Ala Val His Leu Asn Ser Lys Thr Ala Glu Asp Lys
      275      280      285
Lys Val Ala Pro Lys Glu Pro Val
      290      295 296

```

<210> 779
 <211> 90
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 779
Glu Leu Gln Val Phe Gln Pro Ile Gly Gly Met Ser Asp Ser Gly Ser
  1      5      10      15
Gln Leu Gly Ser Met Gly Ser Leu Thr Met Lys Ser Gln Leu Gln Ile
      20      25      30
Thr Val Ile Ser Ala Lys Leu Lys Glu Asn Lys Lys Asn Trp Phe Gly
      35      40      45
Pro Ser Pro Tyr Val Glu Val Thr Val Asp Gly Gln Ser Lys Lys Thr
      50      55      60
Glu Lys Cys Asn Asn Thr Asn Ser Pro Lys Trp Lys Gln Pro Leu Thr
      65      70      75      80
Val Ile Val Thr Pro Val Ser Lys Leu His
      85      90

```

<210> 780
 <211> 88
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 780
Ile Glu Thr Leu Ser Phe Val Ile Arg Asn Trp Asn Thr His Ala Met
  1      5      10      15
Ser Lys Pro Ile Val Met Glu Arg Gly Val Lys Tyr Arg Asp Ala Asp

```

```

      20      25      30
Lys Met Ala Leu Ile Pro Val Lys Asn Val Ala Thr Glu Arg Glu Ala
      35      40      45
Leu Leu Arg Lys Pro Glu Trp Met Lys Ile Lys Leu Pro Ala Asp Ser
      50      55      60
Thr Arg Ile Gln Gly Ile Lys Ala Ala Met Arg Lys Asn Gly Leu His
      65      70      75      80
Ser Val Cys Glu Glu Ala Ser Cys
      85      88

```

<210> 781
 <211> 35
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 781
Pro Arg Met Val Leu Gly Lys Pro Gln Thr Asp Pro Thr Leu Glu Trp
  1      5      10      15
Phe Leu Ser His Cys His Ile His Lys Tyr Pro Ser Lys Ser Thr Leu
      20      25      30
Ile Pro Gln
      35

```

<210> 782
 <211> 145
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 782
Gly Leu Arg Ile Ser Val Gln Glu Arg Ile Lys Ala Cys Phe Thr Glu
  1      5      10      15
Ser Ile Gln Thr Gln Ile Ala Ala Ala Glu Ala Leu Pro Asp Ala Ile
      20      25      30
Ser Arg Ala Ala Met Thr Leu Val Gln Ser Leu Leu Asn Gly Asn Lys
      35      40      45
Ile Leu Cys Cys Gly Asn Gly Thr Ser Ala Ala Asn Ala Gln His Phe
      50      55      60
Ala Ala Ser Met Ile Asn Arg Phe Glu Thr Glu Arg Pro Ser Leu Pro
      65      70      75      80
Ala Ile Ala Leu Asn Thr Asp Asn Val Val Leu Thr Ala Ile Ala Asn
      85      90      95
Asp Arg Leu His Asp Glu Val Tyr Ala Lys Gln Val Arg Ala Leu Gly
      100      105      110
His Ala Gly Asp Val Leu Leu Ala Ile Ser Thr Arg Gly Asn Ser Arg
      115      120      125
Asp Ile Val Lys Ala Val Glu Ala Ala Val Thr Arg Asp Thr Thr Ile
      130      135      140
Val
145

```

<210> 783
 <211> 102
 <212> Amino acid

<213> Homo sapiens

<400> 783

```

Lys Gln Thr Gln His Ala Pro Gly Met Met Lys Lys Tyr Leu Ala Leu
 1              5              10              15
Ala Leu Ile Ala Pro Leu Leu Ile Ser Cys Ser Thr Thr Lys Lys Gly
      20              25              30
Asp Thr Tyr Asn Glu Ala Trp Val Lys Asp Thr Asn Gly Phe Asp Ile
      35              40              45
Leu Met Gly Gln Phe Ala His Asn Ile Glu Asn Ile Trp Gly Phe Lys
      50              55              60
Glu Val Val Ile Ala Gly Pro Lys Asp Tyr Val Lys Tyr Thr Asp Gln
      65              70              75              80
Tyr Gln Thr Arg Ser His Ile Asn Phe Asp Asp Gly Thr Ile Thr Ile
      85              90              95
Glu Pro Ile Pro Gly Thr
      100              102

```

<210> 784

<211> 78

<212>Amino acid

<213> Homo sapiens

<400> 784

```

Thr Asp Arg Thr Ala Leu Asn Pro Gly Gln Glu Ser Ala Met Asn Arg
 1              5              10              15
Leu Phe Ser Gly Arg Ser Asp Met Pro Phe Ala Leu Leu Leu Leu Ala
      20              25              30
Pro Ser Leu Leu Leu Gly Gly Leu Val Ala Trp Pro Met Val Ser
      35              40              45
Asn Ile Glu Ile Ser Phe Leu Arg Leu Pro Leu Asn Pro Asn Ile Glu
      50              55              60
Ser Thr Phe Val Gly Val Ser Asn Tyr Val Arg Ile Leu Ser
      65              70              75              78

```

<210> 785

<211> 148

<212>Amino acid

<213> Homo sapiens

<400> 785

```

Lys Glu Leu Val Asp Glu Lys Ser Glu Arg Gly Arg Ala Met Asp Pro
 1              5              10              15
Val Ser Gln Leu Ala Ser Ala Gly Thr Phe Arg Val Leu Lys Glu Pro
      20              25              30
Leu Ala Phe Leu Arg Ala Leu Glu Leu Leu Phe Ala Ile Phe Ala Phe
      35              40              45
Ala Thr Cys Gly Gly Tyr Ser Gly Gly Leu Arg Leu Ser Val Asp Cys
      50              55              60
Val Asn Lys Thr Glu Ser Asn Leu Ser Ile Asp Ile Ala Phe Ala Tyr

```


65					70					75				80	
Pro	Phe	Arg	Leu	His	Gln	Val	Thr	Phe	Glu	Val	Pro	Thr	Cys	Glu	Gly
				85					90					95	
Lys	Glu	Arg	Gln	Lys	Leu	Ala	Leu	Ile	Gly	Asp	Ser	Ser	Ser	Ser	Ala
			100					105					110		
Glu	Phe	Phe	Val	Thr	Val	Ala	Val	Phe	Ala	Phe	Leu	Tyr	Ser	Leu	Ala
		115					120					125			
Ala	Thr	Gly	Arg	Tyr	Ile	Phe	Phe	His	Asn	Lys	Asn	Arg	Glu	Asn	Asn
	130					135						140			
Arg	Gly	Pro	Leu												
145			148												

<210> 786
 <211> 246
 <212> Amino acid
 <213> Homo sapiens

Leu	Gly	Thr	Val	Ser	Tyr	Gly	Ala	Asp	Thr	Met	Asp	Glu	Ile	Gln	Ser
1				5					10					15	
His	Val	Arg	Asp	Ser	Tyr	Ser	Gln	Met	Gln	Ser	Gln	Ala	Gly	Gly	Asn
			20					25					30		
Asn	Thr	Gly	Ser	Thr	Pro	Leu	Arg	Lys	Ala	Gln	Ser	Ser	Ala	Pro	Lys
		35					40					45			
Val	Arg	Lys	Ser	Val	Ser	Ser	Arg	Ile	His	Glu	Ala	Val	Lys	Ala	Ile
	50					55				60					
Val	Leu	Cys	His	Asn	Val	Thr	Pro	Val	Tyr	Glu	Ser	Arg	Ala	Gly	Val
	65				70					75					80
Thr	Glu	Glu	Thr	Glu	Phe	Ala	Glu	Ala	Asp	Gln	Asp	Phe	Ser	Asp	Glu
				85					90					95	
Asn	Arg	Thr	Tyr	Gln	Ala	Ser	Ser	Pro	Asp	Glu	Val	Ala	Leu	Val	Gln
		100					105						110		
Trp	Thr	Glu	Ser	Val	Gly	Leu	Thr	Leu	Val	Ser	Arg	Asp	Leu	Thr	Ser
		115				120						125			
Met	Gln	Leu	Lys	Thr	Pro	Ser	Gly	Gln	Val	Leu	Ser	Phe	Cys	Ile	Leu
	130					135					140				
Gln	Leu	Phe	Pro	Phe	Thr	Ser	Glu	Ser	Lys	Arg	Met	Gly	Val	Ile	Val
	145				150					155				160	
Arg	Asp	Glu	Ser	Thr	Ala	Glu	Ile	Thr	Phe	Tyr	Met	Lys	Gly	Ala	Asp
				165					170					175	
Val	Ala	Met	Ser	Pro	Ile	Val	Gln	Tyr	Asn	Asp	Trp	Leu	Glu	Glu	Glu
		180					185						190		
Cys	Gly	Asn	Met	Ala	Arg	Glu	Gly	Leu	Arg	Thr	Leu	Val	Val	Ala	Lys
		195					200					205			
Lys	Ala	Leu	Thr	Glu	Glu	Gln	Tyr	Gln	Asp	Phe	Glu	Val	Ser	Arg	Leu
	210					215					220				
Pro	Gly	Ile	Pro	Ser	Ser	Tyr	Asp	Gly	Ala	Phe	Leu	Thr	Leu	Lys	Leu
	225				230					235					240
Val	Leu	Pro	Val	Phe	Val										
				245	246										

<210> 787
 <211> 176
 <212> Amino acid
 <213> Homo sapiens

<400> 787

Glu Gly Pro His Arg Arg Leu Phe Gln Met Val Lys Ala Leu Gln Glu
 1 5 10 15
 Ala Pro Glu Asp Pro Asn Gln Ile Leu Ile Gly Tyr Ser Arg Gly Leu
 20 25 30
 Val Val Ile Trp Asp Leu Gln Gly Ser Arg Val Leu Tyr His Phe Leu
 35 40 45
 Ser Ser Gln Gln Leu Glu Asn Ile Trp Trp Gln Arg Asp Gly Arg Leu
 50 55 60
 Leu Val Ser Cys His Ser Asp Gly Ser Tyr Cys Gln Trp Pro Val Ser
 65 70 75 80
 Ser Glu Ala Gln Gln Pro Glu Pro Leu Arg Ser Leu Val Pro Tyr Gly
 85 90 95
 Pro Phe Pro Cys Lys Ala Ile Thr Arg Ile Leu Trp Leu Thr Thr Arg
 100 105 110
 Gln Gly Leu Pro Phe Thr Ile Phe Gln Gly Gly Met Pro Arg Ala Ser
 115 120 125
 Tyr Gly Asp Arg His Cys Ile Ser Val Ile His Asp Gly Gln Gln Thr
 130 135 140
 Ala Phe Asp Phe Thr Ser Arg Val Ile Gly Phe Thr Val Leu Thr Glu
 145 150 155 160
 Ala Asp Pro Ala Ala Ser Arg Arg Ala Ser Gly Val Gly Ala Gln Gly
 165 170 175 176

<210> 788

<211> 180

<212> Amino acid

<213> Homo sapiens

<400> 788

Lys Gln Gly Leu Glu Val Arg Asp Leu His Phe Lys Glu Ile Thr Ser
 1 5 10 15
 Gly Arg Ala Leu Leu Arg Val Ala Cys Lys Arg Pro Ser Met Val Pro
 20 25 30
 Gly Gly Gln Leu Gln Arg Ala Gly Ala Gly Ala Gln Ala Arg Ile Thr
 35 40 45
 Gly Leu Ser Pro Ala Leu Trp Gly Ala Arg Val His Gly Trp Ile Pro
 50 55 60
 Glu Leu Pro Ala Gly Leu Pro Pro Gly Ala Cys Leu Trp Pro Leu Ile
 65 70 75 80
 Pro Ala Cys Pro Ser Arg His Trp Gly Trp Val Ser Ala Pro Val Lys
 85 90 95
 Gly Trp Ala Gln Ala Ile Leu Gly Leu Ala Leu Cys Leu Arg Gly Glu
 100 105 110
 His Arg Gly Leu Gly Ala Gly Val Ser Lys Val Arg Ser Leu Lys Met
 115 120 125
 Asp Arg Lys Val Trp Thr Glu Thr Leu Ile Glu Val Gly Met Pro Leu
 130 135 140
 Leu Ala Thr Asp Thr Trp Gly Leu Pro His Ser Thr Ala Val Trp Val
 145 150 155 160
 Ser Gln Pro Pro Pro Tyr Leu Ser Asp His Ser Thr Leu Glu Leu Glu
 165 170 175
 Arg Asp Pro Leu
 180

<210> 789
 <211> 145
 <212>Amino acid
 <213> Homo sapiens

<400> 789
 Leu Ser Cys Asn Ser Glu Gln Ala Leu Leu Ser Leu Val Pro Val Gln
 1 5 10 15
 Arg Glu Leu Leu Arg Arg Arg Tyr Gln Ser Ser Pro Ala Lys Pro Asp
 20 25 30
 Ser Ser Phe Tyr Lys Gly Leu Gly Thr Cys Pro Ser Gln Leu Arg Leu
 35 40 45
 Ser Glu Pro Pro Thr Pro Arg His Leu Ser Val Ala Ser Val Ser
 50 55 60
 His His Met Phe Pro Ser His Arg Ser Leu Cys Pro His Leu Pro Asp
 65 70 75 80
 Phe Phe Ala Ala Pro Phe Pro Ser Asp Asn Leu Pro Tyr Thr Leu Gln
 85 90 95
 Ser Pro Phe Pro Ser Pro Pro Pro Ala Thr Pro Ser Asp His Ala Leu
 100 105 110
 Ile Leu His His Asp Leu Asn Gly Gly Pro Asp Asp Pro Leu Gln Gln
 115 120 125
 Thr Gly Gln Leu Phe Gly Gly Leu Val Arg Asp Ile Arg Arg Arg Tyr
 130 135 140
 Pro
 145

<210> 790
 <211> 65
 <212>Amino acid
 <213> Homo sapiens

<400> 790
 Ser Pro Ser Ser Lys Leu Val Gly Met Trp Trp Ala Gly Arg Ala Gly
 1 5 10 15
 Ser Ser Arg Thr Thr Ser Val Ser Leu Leu Cys Leu Pro Ser Ala Pro
 20 25 30
 Phe Gly Ala Ser Asn Leu Leu Val Asn Pro Leu Glu Pro Gln Asn Ala
 35 40 45
 Asp Lys Ile Lys Ile Lys Ile Ala Asp Leu Gly Asn Ala Cys Trp Val
 50 55 60
 Val
 65

<210> 791
 <211> 144
 <212>Amino acid
 <213> Homo sapiens

<400> 791

```

Arg Val Asp Pro Arg Val Arg Ala Pro Arg Cys Gly Asp Lys Ile Lys
 1           5           10           15
Asn His Met Tyr Lys Cys Asp Cys Gly Ser Leu Lys Asp Cys Ala Ser
 20           25           30
Asp Arg Cys Cys Glu Thr Ser Cys Thr Leu Ser Leu Gly Ser Val Cys
 35           40           45
Asn Thr Gly Leu Cys Cys His Lys Cys Lys Tyr Ala Ala Pro Gly Val
 50           55           60
Val Cys Arg Asp Leu Gly Gly Ile Cys Asp Leu Pro Glu Tyr Cys Asp
 65           70           75           80
Gly Lys Lys Glu Glu Cys Pro Asn Asp Ile Tyr Ile Gln Asp Gly Thr
 85           90           95
Pro Cys Ser Ala Val Ser Val Cys Ile Arg Gly Asn Cys Ser Asp Arg
 100          105          110
Asp Met Gln Cys Gln Ala Leu Phe Gly Tyr Gln Val Lys Asp Gly Ser
 115          120          125
Pro Ala Cys Tyr Arg Lys Leu Asn Arg Ile Gly Asn Arg Phe Gly Thr
 130          135          140          144

```

<210> 792

<211> 242

<212> Amino acid

<213> Homo sapiens

<400> 792

```

Pro Gly Arg Pro Thr Arg Pro Asp Ala Ser Leu Ala Gln Asp Pro Arg
 1           5           10           15
Thr Thr Met Phe Arg Ile Pro Glu Phe Lys Trp Ser Pro Met His Gln
 20           25           30
Arg Leu Leu Thr Asp Leu Leu Phe Ala Leu Glu Thr Asp Val His Val
 35           40           45
Trp Arg Ser His Ser Thr Lys Ser Val Met Asp Phe Val Asn Ser Asn
 50           55           60
Glu Asn Ile Ile Phe Val His Asn Thr Ile His Leu Ile Ser Gln Met
 65           70           75           80
Val Asp Asn Ile Ile Ile Ala Cys Gly Gly Ile Leu Pro Leu Leu Ser
 85           90           95
Ala Ala Thr Ser Pro Thr Gly Ser Lys Thr Glu Leu Glu Asn Ile Glu
 100          105          110
Val Thr Gln Gly Met Ser Ala Glu Thr Ala Val Thr Phe Leu Ser Arg
 115          120          125
Leu Met Ala Met Val Asp Val Leu Val Phe Ala Ser Ser Leu Asn Phe
 130          135          140
Ser Glu Ile Glu Ala Glu Lys Asn Met Ser Ser Gly Gly Leu Met Arg
 145          150          155          160
Gln Cys Leu Lys Leu Val Cys Cys Val Ala Val Arg Asn Cys Leu Glu
 165          170          175
Cys Arg Gln Arg Gln Arg Asp Arg Gly Asn Lys Ser Ser His Gly Ser
 180          185          190
Ser Lys Pro Gln Glu Val Pro Gln Ser Val Thr Ala Thr Ala Ala Ser
 195          200          205
Lys Thr Pro Leu Glu Asn Val Pro Gly Asn Leu Ser Pro Ile Lys Asp
 210          215          220
Pro Asp Arg Leu Leu Gln Asp Val Asp Ile Asn Arg Leu Arg Ala Val
 225          230          235          240
Val Phe

```

242

<210> 793
 <211> 412
 <212> Amino acid
 <213> Homo sapiens

<400> 793
 Asn Ser Ser Gly Val Lys Leu Leu Gln Ala Leu Gly Leu Ser Pro Gly
 1 5 10 15
 Asn Gly Lys Asp His Ser Ile Leu His Ser Arg Asn Asp Leu Glu Glu
 20 25 30
 Ala Phe Ile His Phe Met Gly Lys Gly Ala Ala Ala Glu Arg Phe Phe
 35 40 45
 Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln Val Ala Ser Glu Phe
 50 55 60
 Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala Ala Leu Ile Gly Gln
 65 70 75 80
 Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu Leu Cys Gly Pro Val
 85 90 95
 Gly Pro Lys Leu His Glu Leu Leu Asp Asp Asn Val Phe Val Pro Pro
 100 105 110
 Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu Ile Leu Glu Tyr Gln
 115 120 125
 Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro His Ala Asn Arg Phe
 130 135 140
 Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met Asn Met Leu Glu Val
 145 150 155 160
 Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp Leu Gly Gly Leu Ser
 165 170 175
 Gly Leu His Met Met Glu Gly Gln Ser Lys Glu Leu Gln Arg Lys Arg
 180 185 190
 Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile Pro Thr Gly Ile Pro
 195 200 205
 Val His Leu Glu Leu Gly Ser Met Thr Asn Arg Glu Leu Met Ser Ser
 210 215 220
 Ile Val Leu Gln Gln Val Phe Pro Ala Val Thr Ser Leu Gly Leu Asn
 225 230 235 240
 Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala Ser Gly Pro His Ser
 245 250 255
 Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val Gly Met Val Ser Asp
 260 265 270
 Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg Ser Lys Ser Arg Ala
 275 280 285
 Ser Asp Leu Thr Arg Ile His Phe His Thr Leu Val Tyr His Ile Leu
 290 295 300
 Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu Ala Ala Val Ala Ala
 305 310 315 320
 Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala Thr Glu Thr Ile Asp
 325 330 335
 Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu Phe Met Thr Ser His
 340 345 350
 Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro Asn Lys Pro Val Val
 355 360 365
 Glu Trp His Arg Glu Gly Ile Ser Phe His Phe Thr Pro Val Leu Val
 370 375 380
 Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly Asp Ala Ile Ser Ala
 385 390 395 400
 Glu Gly Leu Phe Tyr Ser Glu Val His Pro His Tyr

405

410

412

<210> 794

<211> 83

<212>Amino acid

<213> Homo sapiens

<400> 794

```

Asp Asp Ser Ser Gly Trp Gly Leu Glu Gln Leu Val Val Arg Trp Ser
 1          5          10          15
Leu Ala Leu Trp Pro Arg Leu Glu Cys Ser Gly Met Ile Ser Ala His
          20          25          30
Cys Asn Leu Cys Leu Leu Gly Ser Ser Asp Ser Pro Ala Ser Ala Pro
          35          40          45
Arg Val Ala Gly Ile Thr Asp Val Cys His His Ala Trp Leu Val Phe
          50          55          60
Val Phe Leu Val Val Met Gly Phe Pro His Val Gly His Val Gly Leu
          65          70          75          80
Glu Leu Leu
          83

```

<210> 795

<211> 391

<212>Amino acid

<213> Homo sapiens

<400> 795

```

Leu Gly Glu Val Leu Lys Cys Gln Gln Gly Val Ser Ser Leu Ala Phe
 1          5          10          15
Ala Leu Ala Phe Leu Gln Arg Met Asp Met Lys Pro Leu Val Val Leu
          20          25          30
Gly Leu Pro Ala Pro Thr Ala Pro Ser Gly Cys Leu Ser Phe Trp Glu
          35          40          45
Ala Lys Ala Gln Leu Ala Lys Ser Cys Lys Val Leu Val Asp Ala Leu
          50          55          60
Arg His Asn Ala Ala Ala Val Pro Phe Phe Gly Gly Gly Ser Val
          65          70          75          80
Leu Arg Ala Ala Glu Pro Ala Pro His Ala Ser Tyr Gly Gly Ile Val
          85          90          95
Ser Val Glu Thr Asp Leu Leu Gln Trp Cys Leu Glu Ser Gly Ser Ile
          100          105          110
Pro Ile Leu Cys Pro Ile Gly Glu Thr Ala Ala Arg Arg Ser Val Leu
          115          120          125
Leu Asp Ser Leu Glu Val Thr Ala Ser Leu Ala Lys Ala Leu Arg Pro
          130          135          140
Thr Lys Ile Ile Phe Leu Asn Asn Thr Gly Gly Leu Arg Asp Ser Ser
          145          150          155          160
His Lys Val Leu Ser Asn Val Asn Leu Pro Ala Asp Leu Asp Leu Val
          165          170          175
Cys Asn Ala Glu Trp Val Ser Thr Lys Glu Arg Gln Gln Met Arg Leu
          180          185          190
Ile Val Asp Val Leu Ser Arg Leu Pro His His Ser Ser Ala Val Ile
          195          200          205
Thr Ala Ala Ser Thr Leu Leu Thr Glu Leu Phe Ser Asn Lys Gly Ser

```

```

      210              215              220
Gly Thr Leu Phe Lys Asn Ala Glu Arg Met Leu Arg Val Arg Ser Leu
225              230              235              240
Asp Lys Leu Asp Gln Gly Arg Leu Val Asp Leu Val Asn Ala Ser Phe
      245              250              255
Gly Lys Lys Leu Arg Asp Asp Tyr Leu Ala Ser Leu Arg Pro Arg Leu
      260              265              270
His Ser Ile Tyr Val Ser Glu Gly Tyr Asn Ala Ala Ala Ile Leu Thr
      275              280              285
Met Glu Pro Val Leu Gly Gly Thr Pro Tyr Leu Asp Lys Phe Val Val
      290              295              300
Ser Ser Ser Arg Gln Gly Gln Gly Ser Gly Gln Met Leu Trp Glu Cys
305              310              315              320
Leu Arg Arg Asp Leu Gln Thr Leu Phe Trp Arg Ser Arg Val Thr Asn
      325              330              335
Pro Ile Asn Pro Trp Tyr Phe Lys His Ser Asp Gly Ser Phe Ser Asn
      340              345              350
Lys Gln Trp Ile Phe Phe Trp Phe Gly Leu Ala Asp Ile Arg Asp Ser
      355              360              365
Tyr Glu Leu Val Asn His Ala Lys Gly Leu Pro Asp Ser Phe His Lys
      370              375              380
Pro Ala Ser Asp Pro Gly Ser
385              390 391

```

<210> 796

<211> 127

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(127)

<223> X = any amino acid or stop code

<400> 796

```

Tyr His Ala Pro Ala Leu Gln Pro Gly Gln Gln Ser Lys Thr Leu Ser
  1              5              10              15
Gln Glu Lys Lys Asn Phe Phe Arg Pro Gly Ala Val Ala His Thr Cys
      20              25              30
Asn Pro Ser Thr Leu Gly Gly Arg Gly Gly Arg Ile Thr Arg Ser Gly
      35              40              45
Asp Arg Asp His Pro Gly Xaa His Gly Glu Thr Pro Ser Leu Leu Lys
      50              55              60
Ile Gln Lys Lys Leu Ala Gly Arg Asp Gly Gly Arg Leu Xaa Ser Gln
      65              70              75              80
Leu Leu Gly Arg Leu Arg Gln Glu Asn Gly Val Asn Pro Gly Gly Gly
      85              90              95
Gly Cys Ser Glu Pro Arg Leu Arg His Cys Thr Pro Ala Trp Xaa Gln
      100              105              110
Ser Glu Thr Ile Ser Arg Lys Lys Arg Lys Lys Glu Arg Lys Tyr
      115              120              125              127

```

<210> 797

<211> 159

<212>Amino acid

<213> Homo sapiens

<400> 797

```

Phe Arg Pro Ile Gly Ile Ile Arg Gln Ala Leu Cys Ser Ala Asp Gly
 1           5           10           15
His Gln Arg Arg Ile Leu Thr Leu Arg Leu Gly Leu Leu Val Ile Pro
      20           25           30
Phe Leu Pro Ala Ser Asn Leu Phe Phe Arg Val Gly Phe Val Val Pro
      35           40           45
Ser Val Gly Cys Cys Val Met Leu Leu Phe Gly Phe Gly Ala Leu Arg
      50           55           60
Lys His Thr Glu Lys Lys Lys Leu Ile Ala Ala Val Val Leu Gly Ile
      65           70           75           80
Leu Leu Ser Asn Asp Ala Glu Arg Leu Arg Cys Ala Val Arg Gly Gly
      85           90           95
Glu Trp Arg Ser Glu Glu Ala Val Phe Arg Gly Ala Val Ser Val Cys
      100          105          110
Pro Leu Ser Ala Glu Val Arg Cys Asn Ile Gly Arg Asn Leu Ala Ala
      115          120          125
Lys Gly Asn Gln Thr Gly Ala Ile Arg Tyr His Arg Glu Ala Val Ser
      130          135          140
Leu Asn Pro Lys Thr Lys Ser Ser Thr Arg Glu Phe Arg Pro Cys
      145          150          155          159

```

<210> 798

<211> 236

<212> Amino acid

<213> Homo sapiens

<400> 798

```

Lys Ile Ala Asp Phe Gly Phe Ser Asn Leu Phe Thr Pro Gly Gln Leu
 1           5           10           15
Leu Lys Thr Trp Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe
      20           25           30
Glu Gly Lys Glu Tyr Asp Gly Pro Lys Val Asp Ile Trp Ser Leu Gly
      35           40           45
Val Val Leu Tyr Val Leu Val Cys Gly Ala Leu Pro Phe Asp Gly Ser
      50           55           60
Thr Leu Gln Asn Leu Arg Ala Arg Val Leu Ser Gly Lys Phe Arg Ile
      65           70           75           80
Pro Phe Phe Met Ser Thr Glu Cys Glu His Leu Ile Arg His Met Leu
      85           90           95
Val Leu Asp Pro Asn Lys Arg Leu Ser Met Glu Gln Ile Cys Lys His
      100          105          110
Lys Trp Met Lys Leu Gly Asp Ala Asp Pro Asn Phe Asp Arg Leu Ile
      115          120          125
Ala Glu Cys Gln Gln Leu Lys Glu Glu Arg Gln Val Asp Pro Leu Asn
      130          135          140
Glu Asp Val Leu Leu Ala Met Glu Asp Met Gly Leu Asp Lys Glu Gln
      145          150          155          160
Thr Leu Gln Ser Leu Arg Ser Asp Ala Tyr Asp His Tyr Ser Ala Ile
      165          170          175
Tyr Ser Leu Leu Cys Asp Arg His Lys Arg His Lys Thr Leu Arg Leu
      180          185          190
Gly Ala Leu Pro Ser Met Pro Arg Ala Leu Gly Leu Ser Ser Thr Ser
      195          200          205
Gln Tyr Pro Ala Glu Gln Ala Gly Thr Ala Met Asn Ile Ser Val Pro
      210          215          220

```


Gln Val Gln Leu Ile Asn Pro Glu Asn Gln Ile Val
 225 230 235 236

<210> 799
 <211> 114
 <212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(114)
 <223> X = any amino acid or stop code

<400> 799
 Ala Arg Glu Phe Leu Gly His Arg Ala Ser Ile Thr Trp Ser Xaa Ala
 1 5 10 15
 Arg Val His His Arg Phe Pro Lys Ala Glu Val Ala Xaa Pro Ser Leu
 20 25 30
 Leu Arg Thr Asp Leu Thr Glu Asp Arg Thr Lys Cys Cys His Gly Asp
 35 40 45
 Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Val Glu Asp Ile Trp
 50 55 60
 Glu Asn Gln Asp Ser Ile Ser Thr Ile Leu Ile Glu Cys Cys Glu Lys
 65 70 75 80
 Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu
 85 90 95
 Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys
 100 105 110
 Asp Val
 114

<210> 800
 <211> 328
 <212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(328)
 <223> X = any amino acid or stop code

<400> 800
 Val Pro Pro Lys Met Lys Arg Gly Thr Ser Leu His Ser Arg Arg Gly
 1 5 10 15
 Lys Pro Glu Ala Pro Lys Gly Ser Pro Gln Ile Asn Arg Lys Ser Gly
 20 25 30
 Gln Glu Met Thr Ala Val Met Gln Ser Gly Arg Pro Arg Ser Ser Ser
 35 40 45
 Thr Thr Asp Ala Pro Thr Gly Ser Ala Met Met Glu Ile Ala Cys Ala
 50 55 60
 Ala Ala Ala Ala Ala Cys Leu Pro Gly Glu Glu Gly Thr Ala
 65 70 75 80
 Glu Arg Ile Glu Arg Leu Glu Val Ser Ser Leu Ala Gln Thr Ser Ser
 85 90 95

Ala Val Ala Ser Ser Thr Asp Gly Ser Ile His Thr Asp Ser Val Asp
 100 105 110
 Gly Thr Pro Asp Pro Gln Arg Thr Lys Ala Ala Ile Ala His Leu Gln
 115 120 125
 Gln Lys Ile Leu Lys Leu Thr Glu Gln Ile Lys Ile Ala Gln Thr Ala
 130 135 140
 Arg Arg Asn Arg Arg Pro Gly Ser Xaa Lys Asp Cys Thr Pro Xaa Lys
 145 150 155 160
 Cys Leu Arg Lys Ser Asp Glu Ala Leu Asn Arg Val Leu Gln Gln Ile
 165 170 175
 Arg Val Pro Pro Lys Met Lys Arg Gly Thr Ser Leu His Ser Arg Arg
 180 185 190
 Gly Lys Pro Glu Ala Pro Lys Gly Ser Pro Gln Ile Asn Arg Lys Ser
 195 200 205
 Gly Gln Glu Met Thr Ala Val Met Gln Ser Gly Arg Pro Arg Ser Ser
 210 215 220
 Ser Thr Thr Asp Ala Pro Thr Gly Ser Ala Met Met Glu Ile Ala Cys
 225 230 235 240
 Ala Ala Ala Ala Ala Ala Ala Cys Leu Pro Gly Glu Glu Gly Thr
 245 250 255
 Ala Glu Arg Ile Glu Arg Leu Glu Val Ser Ser Leu Ala Gln Thr Ser
 260 265 270
 Ser Ala Val Ala Ser Ser Thr Asp Gly Ser Ile His Thr Asp Ser Val
 275 280 285
 Asp Gly Thr Pro Asp Pro Gln Arg Thr Lys Ala Ala Ile Ala His Leu
 290 295 300
 Gln Gln Lys Ile Leu Lys Leu Thr Glu Gln Ile Lys Ile Ala Gln Thr
 305 310 315 320
 Ala Arg Arg Asn Arg Arg Pro Gly
 325 328

<210> 801
 <211> 356
 <212> Amino acid
 <213> Homo sapiens

<400> 801
 Met Gln Thr Ile Glu Arg Leu Val Lys Glu Arg Asp Asp Leu Met Ser
 1 5 10 15
 Ala Leu Val Ser Val Arg Ser Ser Leu Ala Asp Thr Gln Gln Arg Glu
 20 25 30
 Ala Ser Ala Tyr Glu Gln Val Lys Gln Val Leu Gln Ile Ser Glu Glu
 35 40 45
 Ala Asn Phe Glu Lys Thr Lys Ala Leu Ile Gln Cys Asp Gln Leu Arg
 50 55 60
 Lys Glu Leu Glu Arg Gln Ala Glu Arg Leu Glu Lys Glu Leu Ala Ser
 65 70 75 80
 Gln Gln Glu Lys Arg Ala Ile Glu Lys Asp Met Met Lys Lys Glu Ile
 85 90 95
 Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu Ser Gln
 100 105 110
 Asn Ile Ala Gln Leu Glu Ala Gln Val Glu Lys Val Thr Lys Glu Lys
 115 120 125
 Ile Ser Ala Ile Asn Gln Leu Glu Glu Ile Gln Ser Gln Leu Ala Ser
 130 135 140
 Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr Gln Leu
 145 150 155 160
 Asn Lys Thr Asn Met Glu Lys Asp Glu Ala Glu Lys Glu His Arg Glu
 165 170 175

Phe Arg Ala Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln Glu Ile
 180 185 190
 Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu Glu Gln
 195 200 205
 Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg Leu Thr
 210 215 220
 Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Gln Glu
 225 230 235 240
 Lys Asp Ser Ile Gln Gln Ser Phe Ser Lys Glu Ala Lys Ala Gln Ala
 245 250 255
 Leu Gln Ala Gln Gln Arg Glu Gln Glu Leu Thr Gln Lys Ile Gln Gln
 260 265 270
 Met Glu Ala Gln His Asp Lys Thr Glu Asn Glu Gln Tyr Leu Leu Leu
 275 280 285
 Thr Ser Gln Asn Thr Phe Leu Thr Lys Leu Lys Glu Glu Cys Cys Thr
 290 295 300
 Leu Ala Lys Lys Leu Glu Gln Ile Ser Gln Lys Thr Arg Ser Glu Ile
 305 310 315 320
 Ala Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu Gly Lys
 325 330 335
 Leu Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His Gly
 340 345 350
 Arg Ser Thr *
 355

<210> 802

<211> 210

<212> Amino acid

<213> Homo sapiens

<400> 802

Ser Tyr Pro Val Trp Trp Asn Ser Pro Leu Thr Ala Glu Val Pro Pro
 1 5 10 15
 Glu Leu Leu Ala Ala Ala Gly Phe Phe His Thr Gly His Gln Asp Lys
 20 25 30
 Val Arg Cys Phe Phe Cys Tyr Gly Gly Leu Gln Ser Trp Lys Arg Gly
 35 40 45
 Asp Asp Pro Trp Thr Glu His Ala Lys Trp Phe Pro Ser Cys Gln Phe
 50 55 60
 Leu Leu Arg Ser Lys Gly Arg Asp Phe Val His Ser Val Gln Glu Thr
 65 70 75 80
 His Ser Gln Leu Leu Gly Ser Trp Asp Pro Trp Glu Glu Pro Glu Asp
 85 90 95
 Ala Ala Pro Val Ala Pro Ser Val Pro Ala Ser Gly Tyr Pro Glu Leu
 100 105 110
 Pro Thr Pro Arg Arg Glu Val Gln Ser Glu Ser Ala Gln Glu Pro Gly
 115 120 125
 Gly Val Ser Pro Ala Glu Ala Gln Arg Ala Trp Trp Val Leu Glu Pro
 130 135 140
 Pro Gly Ala Arg Asp Val Glu Ala Gln Leu Arg Arg Leu Gln Glu Glu
 145 150 155 160
 Arg Thr Cys Lys Val Cys Leu Asp Arg Ala Val Ser Ile Val Phe Val
 165 170 175
 Pro Cys Gly His Leu Val Cys Ala Glu Cys Ala Pro Gly Leu Gln Leu
 180 185 190
 Cys Pro Ile Cys Arg Ser Pro Cys Gly Pro Leu Arg Pro Cys Leu Trp
 195 200 205
 Val Pro
 210

<210> 803
 <211> 130
 <212> Amino acid
 <213> Homo sapiens

<400> 803
 Met Cys Ser Tyr Arg Glu Lys Lys Ala Glu Pro Gln Glu Leu Leu Gln
 1 5 10 15
 Leu Asp Gly Tyr Thr Val Asp Tyr Thr Asp Pro Gln Pro Gly Leu Glu
 20 25 30
 Gly Gly Arg Ala Phe Phe Asn Ala Val Lys Glu Gly Asp Thr Val Ile
 35 40 45
 Phe Ala Ser Asp Asp Glu Gln Asp Arg Ile Leu Trp Val Gln Ala Met
 50 55 60
 Tyr Arg Ala Thr Gly Gln Ser His Lys Pro Val Pro Pro Thr Gln Val
 65 70 75 80
 Gln Lys Leu Asn Ala Lys Gly Gly Asn Val Pro Gln Leu Asp Ala Pro
 85 90 95
 Ile Ser Gln Phe Tyr Ala Asp Arg Ala Gln Lys His Gly Met Asp Glu
 100 105 110
 Phe Ile Ser Ser Asn Pro Cys Asn Phe Asp His Ala Ser Leu Phe Glu
 115 120 125
 Met *
 129

<210> 804
 <211> 458
 <212> Amino acid
 <213> Homo sapiens

<400> 804
 Lys Gln Leu Ile Val Leu Gly Asn Lys Val Asp Leu Leu Pro Gln Asp
 1 5 10 15
 Ala Pro Gly Tyr Arg Gln Arg Leu Arg Glu Arg Leu Trp Glu Asp Cys
 20 25 30
 Ala Arg Ala Gly Leu Leu Leu Ala Pro Gly His Gln Gly Pro Gln Arg
 35 40 45
 Pro Val Lys Asp Glu Pro Gln Asp Gly Glu Asn Pro Asn Pro Pro Asn
 50 55 60
 Trp Ser Arg Thr Val Val Arg Asp Val Arg Leu Ile Ser Ala Lys Thr
 65 70 75 80
 Gly Tyr Gly Val Glu Glu Leu Ile Ser Ala Leu Gln Arg Ser Trp Arg
 85 90 95
 Tyr Arg Gly Asp Val Tyr Leu Val Gly Ala Thr Asn Ala Gly Lys Ser
 100 105 110
 Thr Leu Phe Asn Thr Leu Leu Glu Ser Asp Tyr Cys Thr Ala Lys Gly
 115 120 125
 Ser Glu Ala Ile Asp Arg Ala Thr Ile Ser Pro Trp Pro Gly Thr Thr
 130 135 140
 Leu Asn Leu Leu Lys Phe Pro Ile Cys Asn Pro Thr Pro Tyr Arg Met
 145 150 155 160
 Phe Lys Arg His Gln Arg Leu Lys Lys Asp Ser Thr Gln Ala Glu Glu
 165 170 175

Asp Leu Ser Glu Gln Glu Gln Asn Gln Leu Asn Val Leu Lys Lys His
 180 185 190
 Gly Tyr Val Val Gly Arg Val Gly Arg Thr Phe Leu Tyr Ser Glu Glu
 195 200 205
 Gln Lys Asp Asn Ile Pro Phe Glu Phe Asp Ala Asp Ser Leu Ala Phe
 210 215 220
 Asp Met Glu Asn Asp Pro Val Met Gly Thr His Lys Ser Thr Lys Gln
 225 230 235 240
 Val Glu Leu Thr Ala Gln Asp Val Lys Asp Ala His Trp Phe Tyr Asp
 245 250 255
 Thr Pro Gly Ile Thr Lys Glu Asn Cys Ile Leu Asn Leu Leu Thr Glu
 260 265 270
 Lys Glu Val Asn Ile Val Leu Pro Thr Gln Ser Ile Val Pro Arg Thr
 275 280 285
 Phe Val Leu Lys Pro Gly Met Val Leu Phe Leu Gly Ala Ile Gly Arg
 290 295 300
 Ile Asp Phe Leu Gln Gly Asn Gln Ser Ala Trp Phe Thr Val Val Ala
 305 310 315 320
 Ser Asn Ile Leu Pro Val His Ile Thr Ser Leu Asp Arg Ala Asp Ala
 325 330 335
 Leu Tyr Gln Lys His Ala Gly His Thr Leu Leu Gln Ile Pro Met Gly
 340 345 350
 Gly Lys Glu Arg Met Ala Gly Phe Pro Pro Leu Val Ala Glu Asp Ile
 355 360 365
 Met Leu Lys Glu Gly Leu Gly Ala Ser Glu Ala Val Ala Asp Ile Lys
 370 375 380
 Phe Ser Ser Ala Gly Trp Val Ser Val Thr Pro Asn Phe Lys Asp Arg
 385 390 395 400
 Leu His Leu Arg Gly Tyr Thr Pro Glu Gly Thr Val Leu Thr Val Arg
 405 410 415
 Pro Pro Leu Leu Pro Tyr Ile Val Asn Ile Lys Gly Gln Arg Ile Lys
 420 425 430
 Lys Ser Val Ala Tyr Lys Thr Lys Lys Pro Pro Ser Leu Met Tyr Asn
 435 440 445
 Val Arg Lys Lys Lys Gly Lys Ile Asn Val
 450 455 458

<210> 805

<211> 290

<212> Amino acid

<213> Homo sapiens

<400> 805

Ser Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val Glu Cys Leu
 1 5 10 15
 Arg Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr
 20 25 30
 Met Leu Val Ser Arg Asn Phe Ser Ala Ala Lys Ser Leu Leu Asn Lys
 35 40 45
 Lys Ser Asp Gly Gly Val Lys Pro Gln Ser Asn Asn Lys Asn Ser Leu
 50 55 60
 Val Ser Pro Ala Gln Glu Pro Ala Pro Leu Gln Thr Ala Met Glu Pro
 65 70 75 80
 Gln Thr Thr Val Val His Asn Ala Thr Asp Gly Ile Lys Gly Ser Thr
 85 90 95
 Glu Ser Cys Asn Thr Thr Thr Glu Asp Glu Asp Leu Lys Ala Ala Pro
 100 105 110
 Leu Arg Thr Gly Asn Gly Ser Ser Val Pro Glu Gly Arg Ser Ser Arg
 115 120 125

Asp Arg Thr Ala Pro Ser Ala Gly Met Gln Pro Gln Pro Ser Leu Cys
 130 135 140
 Ser Ser Ala Met Arg Lys Gln Glu Ile Ile Lys Ile Thr Glu Gln Leu
 145 150 155 160
 Ile Glu Ala Ile Asn Asn Gly Asp Phe Glu Ala Tyr Thr Lys Ile Cys
 165 170 175
 Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu Gly Asn Leu Val
 180 185 190
 Glu Gly Met Asp Phe His Lys Phe Tyr Phe Glu Asn Leu Leu Ser Lys
 195 200 205
 Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn Pro His Val His Val
 210 215 220
 Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr Gln Tyr
 225 230 235 240
 Ile Asp Gly Gln Gly Arg Pro Ser Asn Pro Ala Lys Ser Glu Glu Thr
 245 250 255
 Arg Val Trp His Arg Arg Asp Gly Lys Trp Leu Asn Val His Tyr His
 260 265 270
 Cys Ser Gly Ala Pro Cys Pro His Arg Cys Ser Glu Leu Ser His Arg
 275 280 285
 Gly Phe
 290

<210> 806

<211> 570

<212> Amino acid

<213> Homo sapiens

<400> 806

Leu Pro Lys Asn Val Val Phe Val Leu Asp Ser Ser Ala Ser Met Val
 1 5 10 15
 Gly Thr Lys Leu Arg Gln Thr Lys Asp Ala Leu Phe Thr Ile Leu His
 20 25 30
 Asp Leu Arg Pro Gln Asp Arg Phe Ser Ile Ile Gly Phe Ser Asn Arg
 35 40 45
 Ile Lys Val Trp Lys Asp His Leu Ile Ser Val Thr Pro Asp Ser Ile
 50 55 60
 Arg Asp Gly Lys Val Tyr Ile His His Met Ser Pro Thr Gly Gly Thr
 65 70 75 80
 Asp Ile Asn Gly Ala Leu Gln Arg Ala Ile Arg Leu Leu Asn Lys Tyr
 85 90 95
 Val Ala His Ser Gly Ile Gly Asp Arg Arg Val Ser Leu Ile Val Phe
 100 105 110
 Leu Thr Asp Gly Lys Pro Thr Val Gly Glu Thr His Thr Leu Lys Ile
 115 120 125
 Leu Asn Asn Thr Arg Glu Ala Ala Arg Gly Gln Val Cys Ile Phe Thr
 130 135 140
 Ile Gly Ile Gly Asn Asp Val Asp Phe Arg Leu Leu Glu Lys Leu Ser
 145 150 155 160
 Leu Glu Asn Cys Gly Leu Thr Arg Arg Val His Glu Glu Glu Asp Ala
 165 170 175
 Gly Ser Gln Leu Ile Gly Phe Tyr Asp Glu Ile Arg Thr Pro Leu Leu
 180 185 190
 Ser Asp Ile Arg Ile Asp Tyr Pro Pro Ser Ser Val Val Gln Ala Thr
 195 200 205
 Lys Thr Leu Phe Pro Asn Tyr Phe Asn Gly Ser Glu Ile Ile Ile Ala
 210 215 220
 Gly Lys Leu Val Asp Arg Lys Leu Asp His Leu His Val Glu Val Thr
 225 230 235 240

Ala Ser Asn Ser Lys Lys Phe Ile Ile Leu Lys Thr Asp Val Pro Val
 245 250 255
 Arg Pro Gln Lys Ala Gly Lys Asp Val Thr Gly Ser Pro Arg Pro Gly
 260 265 270
 Gly Asp Gly Glu Gly Asp Thr Asn His Ile Glu Arg Leu Trp Ser Tyr
 275 280 285
 Leu Thr Thr Lys Glu Leu Leu Ser Ser Trp Leu Gln Ser Asp Asp Glu
 290 295 300
 Pro Glu Lys Glu Arg Leu Arg Gln Arg Ala Gln Ala Leu Ala Val Ser
 305 310 315 320
 Tyr Arg Phe Leu Thr Pro Phe Thr Ser Met Lys Leu Arg Gly Pro Val
 325 330 335
 Pro Arg Met Asp Gly Leu Glu Glu Ala His Gly Met Ser Ala Ala Met
 340 345 350
 Gly Pro Glu Pro Val Val Gln Ser Val Arg Gly Ala Gly Thr Gln Pro
 355 360 365
 Gly Pro Leu Leu Lys Lys Pro Tyr Gln Pro Arg Ile Lys Ile Ser Lys
 370 375 380
 Thr Ser Val Asp Gly Asp Pro His Phe Val Val Asp Phe Pro Leu Ser
 385 390 395 400
 Arg Leu Thr Val Cys Phe Asn Ile Asp Gly Gln Pro Gly Asp Ile Leu
 405 410 415
 Arg Leu Val Ser Asp His Arg Asp Ser Gly Val Thr Val Asn Gly Glu
 420 425 430
 Leu Ile Gly Ala Pro Ala Pro Pro Asn Gly His Lys Lys Gln Arg Thr
 435 440 445
 Tyr Leu Arg Thr Ile Thr Ile Leu Ile Asn Lys Pro Glu Arg Ser Tyr
 450 455 460
 Leu Glu Ile Thr Pro Ser Arg Val Ile Leu Asp Gly Gly Asp Arg Leu
 465 470 475 480
 Val Leu Pro Cys Asn Gln Ser Val Val Val Gly Ser Trp Gly Leu Glu
 485 490 495
 Val Ser Val Ser Ala Asn Ala Asn Val Thr Val Thr Ile Gln Gly Ser
 500 505 510
 Ile Ala Phe Val Ile Leu Ile His Leu Tyr Lys Lys Pro Ala Pro Phe
 515 520 525
 Gln Arg His His Leu Gly Phe Tyr Ile Ala Asn Ser Glu Gly Leu Ser
 530 535 540
 Ser Asn Cys Arg Val Phe Cys Glu Ser Gly Ile Leu Ile Gln Glu Leu
 545 550 555 560
 Thr Gln Gln Ser Val Ala Val Ala Gly Arg
 565 570

<210> 807

<211> 279

<212> Amino acid

<213> Homo sapiens

<400> 807

Phe Phe Leu Glu Gln Val Ser Gln Tyr Thr Phe Ala Met Cys Ser Tyr
 1 5 10 15
 Arg Glu Lys Lys Ser Glu Pro Gln Glu Leu Met Gln Leu Glu Gly Tyr
 20 25 30
 Thr Val Asp Tyr Thr Asp Pro His Pro Gly Leu Gln Gly Gly Cys Met
 35 40 45
 Phe Phe Asn Ala Val Lys Glu Gly Asp Thr Val Ile Phe Ala Ser Asp
 50 55 60
 Asp Glu Gln Asp Arg Ile Leu Trp Val Gln Ala Met Tyr Arg Ala Thr
 65 70 75 80

Gly Gln Ser Tyr Lys Pro Val Pro Ala Ile Gln Thr Gln Lys Leu Asn
 85 90 95
 Pro Lys Gly Gly Thr Leu His Ala Asp Ala Gln Leu Tyr Ala Asp Arg
 100 105 110
 Phe Gln Lys His Gly Met Asp Glu Phe Ile Ser Ala Asn Pro Cys Lys
 115 120 125
 Leu Asp His Ala Phe Leu Phe Arg Ile Leu Gln Arg Gln Thr Leu Asp
 130 135 140
 His Arg Leu Asn Asp Ser Tyr Ser Cys Leu Gly Trp Phe Ser Pro Gly
 145 150 155 160
 Gln Val Phe Val Leu Asp Glu Tyr Cys Ala Arg Tyr Gly Val Arg Gly
 165 170 175
 Cys His Arg His Leu Cys Tyr Leu Ala Glu Leu Met Glu His Ser Glu
 180 185 190
 Asn Gly Ala Val Ile Asp Pro Thr Leu Leu His Tyr Ser Phe Ala Phe
 195 200 205
 Cys Ala Ser His Val His Gly Asn Arg Pro Asp Gly Ile Gly Thr Val
 210 215 220
 Ser Val Glu Glu Lys Glu Arg Phe Glu Glu Ile Lys Glu Arg Leu Ser
 225 230 235 240
 Ser Leu Leu Glu Asn Gln Ile Ser His Phe Arg Tyr Cys Phe Pro Phe
 245 250 255
 Gly Arg Pro Glu Gly Ala Leu Lys Ala Thr Leu Ser Leu Leu Glu Arg
 260 265 270
 Val Leu Met Lys Asp Ile Ala
 275 279

<210> 808

<211> 251

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(251)

<223> X = any amino acid or stop code

<400> 808

Asp Gly Leu Leu His Glu Val Leu Asn Gly Leu Leu Asp Arg Pro Asp
 1 5 10 15
 Trp Glu Glu Ala Val Lys Met Pro Val Gly Ile Leu Pro Cys Gly Ser
 20 25 30
 Gly Asn Ala Leu Ala Gly Ala Val Asn Gln His Gly Gly Phe Glu Pro
 35 40 45
 Ala Leu Gly Leu Asp Leu Leu Leu Asn Cys Ser Leu Leu Leu Cys Arg
 50 55 60
 Gly Gly Gly His Pro Leu Asp Leu Leu Ser Val Thr Leu Ala Ser Gly
 65 70 75 80
 Ser Arg Cys Phe Ser Phe Leu Ser Val Ala Trp Gly Phe Val Ser Asp
 85 90 95
 Val Asp Ile Gln Ser Glu Arg Phe Arg Ala Leu Gly Ser Ala Arg Phe
 100 105 110
 Thr Leu Gly Thr Val Leu Gly Leu Ala Thr Leu His Thr Tyr Arg Gly
 115 120 125
 Arg Leu Ser Tyr Leu Pro Ala Thr Val Glu Pro Ala Ser Pro Thr Pro
 130 135 140
 Ala His Ser Leu Pro Arg Ala Lys Ser Glu Leu Thr Leu Thr Pro Asp
 145 150 155 160
 Pro Ala Pro Pro Met Ala His Ser Pro Leu His Arg Ser Val Ser Asp


```

                165                170                175
Leu Pro Leu Pro Leu Pro Gln Pro Ala Leu Ala Ser Pro Gly Ser Pro
                180                185                190
Glu Pro Leu Pro Ile Leu Ser Leu Asn Gly Gly Gly Pro Glu Leu Ala
                195                200                205
Gly Asp Trp Gly Gly Ala Gly Asp Ala Pro Leu Ser Pro Asp Pro Gln
                210                215                220
Leu Ser Ser Pro Pro Gly Ser Pro Lys Ala Ala Leu His Ser Pro Val
225                230                235                240
Xaa Lys Lys Ala Pro Val Ile Pro Pro Asp Met
                245                250 251

```

<210> 809
 <211> 174
 <212>Amino acid
 <213> Homo sapiens

```

    <400> 809
Lys Gly Val Pro Thr Leu Leu Met Ala Ala Gly Ser Phe Tyr Asp Ile
 1                5                10                15
Leu Ala Ile Thr Gly Phe Asn Thr Cys Leu Gly Ile Ala Phe Ser Thr
                20                25                30
Gly Ser Thr Val Phe Asn Val Leu Arg Gly Val Leu Glu Val Val Ile
                35                40                45
Gly Val Ala Thr Gly Ser Val Leu Gly Phe Phe Ile Gln Tyr Phe Pro
 50                55                60
Ser Arg Asp Gln Asp Lys Leu Val Cys Lys Arg Thr Phe Leu Val Leu
 65                70                75                80
Gly Leu Ser Val Leu Ala Val Phe Ser Ser Val His Phe Gly Phe Pro
                85                90                95
Gly Ser Gly Gly Leu Cys Thr Leu Val Met Ala Phe Leu Ala Gly Met
                100                105                110
Gly Trp Thr Ser Glu Lys Ala Glu Val Glu Lys Ile Ile Ala Val Ala
                115                120                125
Trp Asp Ile Phe Gln Pro Leu Leu Phe Gly Leu Ile Gly Ala Glu Val
 130                135                140
Ser Ile Ser Ser Leu Arg Pro Glu Thr Val Gly Leu Cys Val Ala Thr
 145                150                155                160
Val Gly Ile Ala Val Leu Ile Arg Ile Phe Asp Tyr Ile Phe
                165                170                174

```

<210> 810
 <211> 104
 <212>Amino acid
 <213> Homo sapiens

```

    <400> 810
Leu Leu Lys Glu Val Val Val Gln Ala Ser Pro Val Cys Lys Thr Cys
 1                5                10                15
Cys Ser Gln Leu Val Arg Thr Pro Val Thr Phe Thr Glu Val Gln Asn
                20                25                30
Val Cys Arg Cys Ser Ala Gly Tyr Leu Ile Ser Val Cys Ser Tyr Thr
                35                40                45
Ser Ser Asp His Asn Gln Cys Tyr Ala Gly Thr Ala Ser Leu Ala Leu

```

```

      50              55              60
Leu Trp Ile Gly Gly Ile Leu Lys Gly Cys Leu Leu Trp Lys Gln Phe
  65              70              75              80
Arg Trp Thr Glu Arg Ser His Trp Asn Phe Gly Tyr Trp Ala Leu Trp
      85              90              95
Ser Pro Gly Asn Gly Asn Gly Cys
      100              104

```

<210> 811
 <211> 77
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 811
Ile Cys Thr Ser Thr Tyr Leu Gln Ile Phe Pro Gly Lys Pro Ser Cys
  1              5              10              15
Phe Met Cys Lys Gly Arg Leu Met Cys Ile Tyr Phe Ile Leu Trp Tyr
      20              25              30
Leu Gly His Tyr Thr Ser Leu His Trp Asn Trp Cys Arg Tyr Ile Ser
      35              40              45
Asp Pro Asn Val Asp Ala Cys Pro Asp Pro Arg Asn Ala Glu Val Ser
      50              55              60
Met Thr His Thr Val Pro Ala Leu Met Glu Leu Ile Asp
      65              70              75              77

```

<210> 812
 <211> 194
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 812
Leu Glu Ser Leu Pro Gly Phe Lys Glu Ile Val Ser Arg Gly Val Lys
  1              5              10              15
Val Asp Tyr Leu Thr Pro Asp Phe Pro Ser Leu Ser Tyr Pro Asn Tyr
      20              25              30
Tyr Thr Leu Met Thr Gly Arg His Cys Glu Val His Gln Met Ile Gly
      35              40              45
Asn Tyr Met Trp Asp Pro Thr Asn Lys Ser Phe Asp Ile Gly Val
      50              55              60
Asn Lys Asp Ser Leu Met Pro Leu Trp Trp Asn Gly Ser Glu Pro Leu
      65              70              75              80
Trp Val Thr Leu Thr Lys Ala Lys Arg Lys Val Tyr Met Tyr Tyr Trp
      85              90              95
Pro Gly Cys Glu Val Glu Ile Leu Gly Val Arg Pro Thr Tyr Cys Leu
      100              105              110
Glu Tyr Lys Asn Val Pro Thr Asp Ile Asn Phe Ala Asn Ala Val Ser
      115              120              125
Asp Ala Leu Asp Ser Phe Lys Ser Gly Arg Ala Asp Leu Ala Ala Ile
      130              135              140
Tyr His Glu Arg Ile Asp Val Glu Gly His His Tyr Gly Pro Ala Ser
      145              150              155              160
Pro Gln Arg Lys Asp Ala Leu Lys Ala Val Asp Thr Val Leu Lys Tyr
      165              170              175
Met Thr Lys Trp Ile Gln Glu Arg Gly Leu Gln Asp Arg Leu Asn Val

```

Ile Ile 180 185 190
194

<210> 813
<211> 116
<212> Amino acid
<213> Homo sapiens

<220> .
<221> misc_feature
<222> (1)...(116)
<223> X = any amino acid or stop code

<400> 813
Ala Arg Asp Phe His Pro Lys Gln Thr Leu Asp Phe Leu Arg Ser Asp
1 5 10 15
Met Ala Asn Ser Lys Ile Thr Glu Glu Val Lys Arg Ser Ile Ala Gln
20 25 30
Gln Tyr Leu Asp Leu Thr Val Ala Leu Glu Gln Val Asp Pro Asp Ala
35 40 45
Glu Val Asp Ala Ala Pro Ser Thr Thr Ser Ser Cys Gly His Xaa Asp
50 55 60
Ser His Ala Gly Ser Xaa Arg Val Leu Ser Leu Leu Gly Asp Xaa Gly
65 70 75 80
Pro Ala Xaa Thr Gly Ala Asn Ser Met Ala Gly Lys Leu Leu Leu Val
85 90 95
Ala Trp Leu Gly Phe Pro Asp Pro Phe Trp Gly Lys Glu Leu Ser Asp
100 105 110
Pro Ala Phe Lys
115 116

<210> 814
<211> 121
<212> Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(121)
<223> X = any amino acid or stop code

<400> 814
Lys Gln Ser Gly Asp Val Thr Cys Asn Cys Thr Asp Gly Arg Leu Ala
1 5 10 15
Pro Ser Cys Leu Thr Cys Val Gly His Cys Ile Phe Gly Gly Tyr Cys
20 25 30
Thr Met Asn Ser Lys Met Met Pro Glu Cys Gln Ser Pro Pro His Met
35 40 45
Thr Gly Pro Arg Cys Glu Glu His Val Phe Ser Gln His Gln Pro Gly
50 55 60
His Ile Thr Ser Ile Leu Ile Pro Met Leu Xaa Leu Leu Leu Val
65 70 75 80
Leu Val Ala Gly Val Ile Phe Cys His Lys Arg Arg Val Gln Gly Ala

```

      85      90      95
Lys Gly Phe Gln His Gln Arg Met Thr Asn Gly Ala Met Asn Ala Gln
      100      105      110
Ile Ala Asn Pro Thr Tyr Lys Met Tyr
      115      120 121

```

```

<210> 815
<211> 86
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(86)
<223> X = any amino acid or stop code

```

```

<400> 815
Thr Val Glu Asn Ala Gly Arg Trp Leu Xaa Glu Glu Ala Glu Ile Gln
 1      5      10      15
Ala Glu Leu Glu Arg Leu Glu Arg Val Arg Asn Leu His Ile Arg Glu
      20      25      30
Leu Lys Arg Ile Asn Asn Glu Asp Asn Ser Gln Phe Lys Asp His Pro
      35      40      45
Thr Leu Asn Glu Arg Tyr Leu Leu His Leu Leu Gly Arg Gly Gly
      50      55      60
Phe Ser Glu Val Tyr Lys Val Met Tyr Gly Leu Phe Trp Phe Phe Tyr
      65      70      75      80
Thr Asn Val Ala Arg Ile
      85 86

```

```

<210> 816
<211> 130
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(130)
<223> X = any amino acid or stop code

```

```

<400> 816
Met Cys Glu Glu Phe Leu Val Met Gly Lys Gly Cys Ser Cys Val Phe
 1      5      10      15
Xaa Ile Leu Leu Ser Asn Pro Gln Met Trp Trp Leu Asn Asp Ser Asn
      20      25      30
Pro Glu Thr Asp Asn Arg Gln Glu Ser Pro Ser Gln Glu Asn Ile Asp
      35      40      45
Arg Val Ser Asp Met Ala Phe Val Pro Ser Ala Trp Thr Ala Ser Gly
      50      55      60
Gly Val Ala Trp Gly Asn Leu Gly Glu Ser Gly Ser Arg Thr Gly Gly
      65      70      75      80
Val Arg Ala Glu Thr Leu Ala Pro Arg Leu Gln Val Xaa Pro Ala His
      85      90      95
Leu Arg Gly His Pro Arg Ser Asn Arg Gly Gln Gly Arg Pro Pro Trp

```

```

          100          105          110
Lys Ala Gly Lys Leu Gly Lys Cys Gln Glu Val Leu Phe Arg Phe Ala
      115          120          125
Ala Phe
    130

```

```

<210> 817
<211> 119
<212> Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(119)
<223> X = any amino acid or stop code

```

```

<400> 817
Phe Arg Ala Met Phe Leu Ala Val Gln His Asp Cys Arg Pro Met Asp
 1          5          10          15
Lys Ser Ala Gly Ser Gly His Lys Ser Glu Glu Lys Arg Glu Lys Met
      20          25          30
Lys Arg Thr Leu Leu Lys Asp Trp Lys Thr Arg Leu Ser Tyr Phe Leu
      35          40          45
Gln Asn Ser Ser Thr Pro Gly Lys Pro Lys Thr Gly Lys Lys Ser Lys
      50          55          60
Gln Gln Ala Phe Ile Lys Xaa Val Glu Asn Pro Glu Leu Ala Asn Ile
      65          70          75          80
Asn Ser Xaa Leu Leu Asn Xaa Lys Gly Glu Leu Xaa Xaa Ala Xaa Ala
      85          90          95
Asn Ile Gln Asn Leu Ser Cys Arg Pro Ser Pro Glu Glu Ala Gln Leu
      100          105          110
Trp Ser Glu Ala Phe Asp Glu
      115          119

```

```

<210> 818
<211> 131
<212> Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(131)
<223> X = any amino acid or stop code

```

```

<400> 818
Gly Phe Phe Asn Phe Ser Ser Pro Lys Leu Lys Gly Trp Lys Ile Asn
 1          5          10          15
Ser Ser Leu Val Leu Glu Ile Arg Lys Asn Ile Leu Arg Phe Leu Asp
      20          25          30
Ala Glu Arg Asp Val Ser Val Val Lys Ser Ser Phe Pro Ser Lys Asp
      35          40          45
Ala Arg His Ser Ser Val His Arg Xaa Phe Thr Gln Leu His Trp Gly
      50          55          60
Pro Pro Ser His Thr Pro Ala Arg Pro Xaa Arg Gly Phe Phe Asn Phe

```

```

65              70              75              80
Ser Ser Pro Lys Leu Lys Gly Trp Lys Ile Asn Ser Ser Leu Val Leu
              85              90              95
Glu Ile Arg Lys Asn Ile Leu Arg Phe Leu Asp Ala Glu Arg Asp Val
              100              105              110
Ser Val Val Lys Ser Ser Phe Pro Ser Lys Asp Ala Arg His Ser Ser
              115              120              125
Val His Arg
              130 131

```

```

<210> 819
<211> 85
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(85)
<223> X = any amino acid or stop code

```

```

<400> 819
Arg Ile Asp Asp Gln Gln Glu Leu Lys Arg Val Thr Xaa Tyr Ser Gln
 1              5              10              15
Lys Glu Tyr Thr Lys Lys Lys Leu His Lys Lys Cys Asn Ile Ile Gln
              20              25              30
Ala Asp Ile Lys Pro Asp Asn Ile Leu Asp Asn Glu Ser Ile Thr Ile
              35              40              45
Leu Lys Leu Ser Asp Phe Gly Ser Ala Ser His Val Ala Asp Asn Asp
              50              55              60
Ile Thr Pro Ser Ser Ser Gln Thr Thr Ser Ala Ala Ser Ser Pro Pro
              65              70              75              80
Arg Thr Leu Arg Arg
              85

```

```

<210> 820
<211> 44
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(44)
<223> X = any amino acid or stop code

```

```

<400> 820
Ser Ser Lys Pro Trp Asp Xaa Ser Leu Ala Pro Lys His Ser Gly Xaa
 1              5              10              15
Thr Lys Asn Met Asp Cys Tyr Cys Ile Ile Pro Thr Cys Ile Gly Arg
              20              25              30
Glu Arg Cys Tyr Gly Thr Cys Ile Gly Asp Thr Val
              35              40              44

```

```

<210> 821

```

<211> 105
 <212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(105)
 <223> X = any amino acid or stop code

<400> 821
 Asn Ser Ser Lys Lys Leu Val Met Glu His Gln Trp Lys Lys Tyr Leu
 1 5 10 15
 Arg Arg Asn Tyr Gln Arg Met Leu Asn Arg Leu Ile Thr Leu Ile Gly
 20 25 30
 Ser Cys Gly Val Leu Xaa Leu Ile Ser Thr Ile Pro Thr Ser Arg Leu
 35 40 45
 Lys Phe Leu Lys Glu Thr Gly His Gly Thr Pro Met Glu Glu Ile Pro
 50 55 60
 Glu Glu Glu Leu Ser Glu Asp Val Glu Gln Ile Asp His Ala Asp Arg
 65 70 75 80
 Glu Leu Arg Arg Gly Gln Asn Leu Arg Cys Lys Gly Ile His Arg Leu
 85 90 95
 Pro Thr His Ile Gln Val Gly Gln Asn
 100 105

<210> 822
 <211> 172
 <212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(172)
 <223> X = any amino acid or stop code

<400> 822
 Lys Trp Met Leu Leu His Ser Phe Lys Ile Phe Cys Leu Ser Leu Tyr
 1 5 10 15
 Pro Gln Leu Xaa Cys Pro Phe Glu Phe Ser His Ser Ala Thr Ile
 20 25 30
 Phe His Glu Leu Val Tyr Lys Gln Thr Lys Ile Ile Ser Ser Asn Gln
 35 40 45
 Glu Leu Ile Tyr Glu Gly Arg Arg Leu Val Leu Glu Pro Gly Arg Leu
 50 55 60
 Ala Gln His Phe Pro Lys Thr Thr Glu Glu Asn Pro Ile Phe Val Val
 65 70 75 80
 Ser Arg Glu Pro Leu Asn Thr Ile Gly Leu Ile Tyr Glu Lys Ile Ser
 85 90 95
 Leu Pro Lys Val His Pro Arg Tyr Asp Leu Asp Gly Asp Ala Ser Met
 100 105 110
 Ala Lys Ala Ile Thr Gly Val Val Cys Tyr Ala Cys Arg Ile Ala Ser
 115 120 125
 Thr Leu Leu Leu Tyr Gln Glu Leu Met Arg Lys Gly Ile Arg Trp Leu
 130 135 140
 Ile Glu Leu Ile Lys Asp Asp Tyr Asn Glu Thr Val His Lys Lys Thr

```
<210> 823
<211> 104
<212> Amino acid
<213> Homo sapiens

<220> .
<221> misc_feature
<222> (1)...(104)
<223> X = any amino acid or stop code
```

```
<210> 824
<211> 99
<212> Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(99)
<223> X = any amino acid or stop code
```

454

99

<210> 825
 <211> 111
 <212>Amino acid
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(111)
 <223> X = any amino acid or stop code

<400> 825
 Pro Val Pro Leu Pro His Pro Ile Leu Glu Val Cys Pro Gly Gln Xaa
 1 5 10 15
 Glu Pro Gln Ser Ala Ile Ser Leu Thr Ala Phe Gln Val Gln Ala Gly
 20 25 30
 Ala Ser Arg Ala Ser Pro Gly Pro Pro Ala Pro Ser Ser Ser Lys Pro
 35 40 45
 Gly Arg Lys Ala Lys Val Ala Ser Pro Cys Pro Asp Arg Pro Ala Pro
 50 55 60
 Pro Pro Thr Xaa Pro Arg Pro Ala Ala Ala Pro Gly Ser Glu Ser Ser
 65 70 75 80
 Pro Arg Pro Pro Arg Pro Arg Thr Gly Arg Arg Gln Gln Arg Ala His
 85 90 95
 Ala Arg Arg Ala Ala Ala Arg Thr Ala Pro Trp Arg Pro Ser Cys
 100 105 110 111

<210> 826
 <211> 95
 <212>Amino acid
 <213> Homo sapiens

<400> 826
 His Glu Gly Arg Arg Arg Gly Trp Ala Ser Ala Ser Gln Arg Phe Leu
 1 5 10 15
 Arg Asn Trp Ala Phe Leu Thr Pro Ser Lys Val Arg Arg Leu Lys Gly
 20 25 30
 Gln Lys Ala Phe Gly Lys Leu Pro Ser His Ser Asp Thr Ser Leu Thr
 35 40 45
 Ser Asp Leu Gly Phe His His Arg Phe Asn Pro Asn Ala Ser Ser Ser
 50 55 60
 Phe Lys Pro Ser Gly Thr Lys Phe Ala Ile Gln Tyr Gly Thr Gly Arg
 65 70 75 80
 Val Asp Gly Ile Leu Ser Glu Asp Lys Leu Thr Val Ser Gly Leu
 85 90 95

<210> 827
 <211> 33
 <212>Amino acid
 <213> Homo sapiens

<220>

<221> misc_feature
 <222> (1)...(33)
 <223> X = any amino acid or stop code

<400> 827

Gly	Arg	Asn	Ile	Met	His	Tyr	Pro	Asn	Gly	His	Ala	Ile	Cys	Ile	Ala
1				5					10				15		
Asn	Gly	His	Cys	Ile	Ile	Leu	Xaa	Asn	Ser	His	Asn	Ile	Lys	Val	Trp
			20					25					30		
Val															
33															

<210> 828
 <211> 178
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(178)
 <223> X = any amino acid or stop code

<400> 828

Ile	Asn	Leu	Gly	Asn	Thr	Cys	Tyr	Met	Asn	Ser	Val	Ile	Xaa	Ala	Leu
1				5					10					15	
Phe	Met	Ala	Thr	Asp	Phe	Arg	Arg	Gln	Val	Leu	Ser	Leu	Asn	Leu	Asn
			20					25					30		
Gly	Cys	Asn	Ser	Leu	Met	Lys	Lys	Leu	Gln	His	Leu	Phe	Ala	Phe	Leu
		35				40						45			
Ala	His	Thr	Gln	Arg	Glu	Ala	Tyr	Ala	Pro	Arg	Ile	Phe	Phe	Glu	Ala
	50					55					60				
Ser	Arg	Pro	Pro	Trp	Phe	Thr	Pro	Arg	Ser	Gln	Gln	Asp	Cys	Ser	Glu
	65				70					75				80	
Tyr	Leu	Arg	Phe	Leu	Leu	Asp	Arg	Leu	His	Glu	Glu	Glu	Lys	Ile	Leu
			85					90						95	
Lys	Val	Gln	Ala	Ser	His	Lys	Pro	Ser	Glu	Ile	Leu	Glu	Cys	Ser	Glu
		100						105					110		
Thr	Ser	Leu	Gln	Glu	Val	Ala	Ser	Lys	Ala	Ala	Val	Leu	Thr	Glu	Thr
		115						120					125		
Pro	Arg	Thr	Ser	Asp	Gly	Glu	Lys	Thr	Leu	Ile	Glu	Lys	Met	Phe	Gly
	130				135						140				
Gly	Lys	Leu	Arg	Thr	His	Ile	Arg	Cys	Leu	Asn	Cys	Thr	Ser	Thr	Ser
	145				150					155				160	
Gln	Lys	Val	Glu	Ala	Phe	Thr	Asp	Leu	Ser	Leu	Ala	Phe	Trp	Pro	Ser
				165					170					175	
Ser	Ser														
178															

<210> 829
 <211> 43
 <212> Amino acid
 <213> Homo sapiens

<220>

<221> misc_feature
 <222> (1)...(43)
 <223> X = any amino acid or stop code

<400> 829
 Ala Arg Asp Asp Pro Arg Val Arg Leu Ser Leu Ser Pro Asn Phe Phe
 1 5 10 15
 Xaa Leu Ala Ser Lys Leu Gly Lys Gln Trp Thr Pro Leu Ile Ile Leu
 20 25 30
 Ala Asn Ser Leu Ser Gly Thr Asn Met Gly Glu
 35 40 43

<210> 830
 <211> 259
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(259)
 <223> X = any amino acid or stop code

<400> 830
 Met His Arg Ile Lys Leu Asn Asp Arg Met Thr Phe Pro Glu Glu Leu
 1 5 10 15
 Asp Met Ser Thr Phe Ile Asp Val Glu Asp Glu Lys Ser Pro Gln Thr
 20 25 30
 Glu Ser Cys Thr Asp Ser Gly Ala Glu Asn Glu Gly Ser Cys His Ser
 35 40 45
 Asp Gln Met Ser Asn Asp Phe Ser Asn Asp Asp Gly Val Asp Glu Gly
 50 55 60
 Ile Cys Leu Glu Thr Asn Ser Gly Thr Glu Lys Ile Ser Lys Ser Gly
 65 70 75 80
 Leu Glu Lys Asn Ser Leu Ile Tyr Glu Leu Phe Ser Val Met Val His
 85 90 95
 Ser Gly Ser Ala Ala Gly Gly His Tyr Tyr Ala Cys Ile Lys Ser Phe
 100 105 110
 Ser Asp Glu Gln Trp Tyr Ser Phe Asn Asp Gln His Val Ser Arg Ile
 115 120 125
 Thr Gln Glu Asp Ile Lys Lys Thr His Gly Gly Ser Ser Gly Ser Arg
 130 135 140
 Gly Tyr Tyr Ser Ser Ala Phe Ala Ser Ser Thr Asn Ala Tyr Met Leu
 145 150 155 160
 Ile Tyr Arg Leu Lys Asp Pro Ala Arg Asn Ala Lys Phe Leu Glu Val
 165 170 175
 Asp Glu Tyr Pro Glu His Ile Lys Asn Leu Val Gln Lys Glu Arg Glu
 180 185 190
 Leu Glu Glu Gln Glu Lys Arg Gln Arg Glu Ile Glu Arg Asn Thr Cys
 195 200 205
 Lys Ile Lys Leu Phe Cys Leu His Pro Thr Lys Gln Val Met Met Glu
 210 215 220
 Asp Xaa Ile Glu Val His Lys Asp Lys Thr Leu Lys Glu Ala Val Glu
 225 230 235 240
 Met Ala Tyr Lys Met Met Asp Leu Glu Glu Val Ile Pro Leu Asp Cys
 245 250 255

Cys Arg Leu
259

<210> 831
<211> 200
<212> Amino acid
<213> Homo sapiens

<400> 831
Ser Val Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met
1 5 10 15
Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala
20 25 30
Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu Gly
35 40 45
Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg Leu Thr Lys
50 55 60
Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu Leu Leu Gly
65 70 75 80
Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu Arg Ala Ser
85 90 95
Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu Gln Leu Gln Ala Glu
100 105 110
Ala Thr Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln Lys Val Leu
115 120 125
Arg Asp Ser Val Gln Arg Leu Glu Val Gln Leu Arg Ser Ala Trp Leu
130 135 140
Gly Pro Ala Tyr Arg Glu Phe Glu Val Leu Lys Ala His Ala Asp Lys
145 150 155 160
Gln Ser His Ile Leu Trp Ala Leu Thr Gly His Val Gln Arg Gln Arg
165 170 175
Arg Glu Met Val Ala Gln Gln His Arg Leu Arg Gln Ile Gln Glu Arg
180 185 190
Leu His Thr Ala Ala Leu Pro Ala
195 200

<210> 832
<211> 225
<212> Amino acid
<213> Homo sapiens

<400> 832
Ile Thr Ser Val Asp Pro Arg Val Arg Gly Asn Ala Ser Thr Gly Tyr
1 5 10 15
Gly Lys Ile Trp Leu Asp Asp Val Ser Cys Asp Gly Asp Glu Ser Asp
20 25 30
Leu Trp Ser Cys Arg Asn Ser Gly Trp Gly Asn Asn Asp Cys Ser His
35 40 45
Ser Glu Asp Val Gly Val Ile Cys Ser Asp Ala Ser Asp Met Glu Leu
50 55 60
Arg Leu Val Gly Gly Ser Ser Arg Cys Ala Gly Lys Val Glu Val Asn
65 70 75 80
Val Gln Gly Ala Val Gly Ile Leu Cys Ala Asn Gly Trp Gly Met Asn
85 90 95

```

Ile Ala Glu Val Val Cys Arg Gln Leu Glu Cys Gly Ser Ala Ile Arg
      100                      105                      110
Val Ser Arg Glu Pro His Phe Thr Glu Arg Thr Leu His Ile Leu Met
      115                      120                      125
Ser Asn Ser Gly Cys Ala Gly Gly Glu Ala Ser Leu Trp Asp Cys Ile
      130                      135                      140
Arg Trp Glu Trp Lys Gln Thr Ala Cys His Leu Asn Met Glu Ala Ser
      145                      150                      155                      160
Leu Ile Cys Ser Ala His Arg Gln Pro Arg Leu Val Gly Ala Asp Met
      165                      170                      175
Pro Cys Ser Gly Arg Val Glu Val Lys His Ala His Thr Trp Arg Ser
      180                      185                      190
Val Cys Asp Ser Asp Phe Ser Leu His Ala Ala Asn Val Leu Cys Arg
      195                      200                      205
Glu Leu Asn Cys Gly Asp Ala Ile Ser Leu Ser Val Gly Asp His Phe
      210                      215                      220
Gly
      225

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```

<210> 833
<211> 206
<212>Amino acid
<213> Homo sapiens

```

```

<400> 833
Ser Asn Tyr Pro Ser Ser Arg Phe Arg Val Ala Gly Ile Thr Gly Val
  1      5      10      15
Lys Leu Gly Met Arg Ser Ile Pro Ile Ala Thr Ala Cys Thr Ile Tyr
      20      25      30
His Lys Phe Phe Cys Glu Thr Asn Leu Asp Ala Tyr Asp Pro Tyr Leu
      35      40      45
Ile Ala Met Ser Ser Ile Tyr Leu Ala Gly Lys Val Glu Glu Gln His
      50      55      60
Leu Arg Thr Arg Asp Ile Ile Asn Val Ser Asn Arg Tyr Phe Asn Pro
      65      70      75      80
Ser Gly Glu Pro Leu Glu Leu Asp Ser Arg Phe Trp Glu Leu Arg Asp
      85      90      95
Ser Ile Val Gln Cys Glu Leu Leu Met Leu Arg Val Leu Arg Phe Gln
      100     105     110
Val Ser Phe Gln His Pro His Lys Tyr Leu Leu His Tyr Leu Val Ser
      115     120     125
Leu Gln Asn Trp Leu Asn Arg His Ser Trp Gln Arg Thr Pro Val Ala
      130     135     140
Val Thr Ala Trp Ala Leu Leu Arg Asp Ser Tyr His Gly Ala Leu Cys
      145     150     155     160
Leu Arg Phe Gln Ala Gln His Ile Ala Val Ala Val Leu Tyr Leu Ala
      165     170     175
Leu Gln Val Tyr Gly Val Glu Val Pro Ala Glu Val Glu Ala Asp Glu
      180     185     190
Ala Val Gly Trp Gln Ile Tyr Ala Met Asp Thr Glu Ile Pro
      195     200     205 206

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```

<210> 834
<211> 86
<212>Amino acid
<213> Homo sapiens

```

<400> 834

```

Arg Gly Ser Arg His Ala Val His Gly Trp Ala Phe Gly Leu Leu Phe
 1           5           10           15
Ile Asn Lys Glu Ser Val Val Met Ala Tyr Leu Phe Thr Thr Phe Asn
      20           25           30
Ala Phe Gln Gly Val Phe Ile Phe Val Phe His Cys Ala Leu Gln Lys
      35           40           45
Lys Val Arg Ser Arg Arg Gly Pro Gly Ser Gln Pro Pro Leu Glu Thr
      50           55           60
Phe Pro Gly Tyr Pro Gly Glu Gly Gly Glu Gly Gly Gly Asp Ser Gly
      65           70           75           80
Ala Pro Ser Ser Pro Gln
              85 86

```

<210> 835

<211> 110

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(110)

<223> X = any amino acid or stop code

<400> 835

```

Ala Arg Lys Asp Asp Leu Pro Pro Asn Met Arg Phe His Glu Glu Lys
 1           5           10           15
Arg Leu Asp Phe Glu Trp Thr Leu Lys Ala Gly Xaa Glu Lys Gly Xaa
      20           25           30
Pro Ser Lys Xaa Asn Lys Gly Trp Glu Gly Gln Glu Xaa Xaa Thr
      35           40           45
Val Arg Asp Xaa Gly Ile Ser Xaa Xaa Val Lys Pro Gln His Leu Ser
      50           55           60
Xaa Ala Leu Gln Met Ala Leu Lys Arg Val Tyr Thr Leu Leu Ser Ser
      65           70           75           80
Trp Asn Cys Leu Glu Asp Phe Asp Gln Ile Phe Trp Gly Gln Lys Ser
              85           90           95
Ala Leu Ala Gly Gln Trp Phe Pro Glu Val Ser Ile Ile Pro
      100           105           110

```

<210> 836

<211> 70

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(70)

<223> X = any amino acid or stop code

<400> 836

Gly Lys Gln Gln Arg Glu Thr Leu Arg Arg Pro Ser Pro Thr Ile Ser
 1 5 10 15
 Val Gln Arg Ala Gly Ser Pro Glu His Ser Ser Ala Ser His Xaa His
 20 25 30
 Ser Pro Cys Pro Ala Pro Gly Gln Arg Val Leu Pro Thr Ala Leu Cys
 35 40 45
 Thr Leu Met Thr Ser Lys His Phe His Gly Cys Pro Leu Ala Gly Gln
 50 55 60
 Gly Arg Ala Val Thr Leu
 65 70

<210> 837
 <211> 473
 <212> Amino acid
 <213> Homo sapiens

<400> 837
 Gly Val Cys Gly Leu Pro Arg Phe Cys Gly Ser Ile Ile Leu Cys His
 1 5 10 15
 Tyr Glu Met Ser Ser Leu Gly Ala Ser Phe Val Gln Ile Lys Phe Asp
 20 25 30
 Asp Leu Gln Phe Phe Glu Asn Cys Gly Gly Gly Ser Phe Gly Ser Val
 35 40 45
 Tyr Arg Ala Lys Trp Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys
 50 55 60
 Leu Leu Lys Ile Glu Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His
 65 70 75 80
 Arg Asn Ile Ile Gln Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr
 85 90 95
 Gly Ile Val Thr Glu Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile
 100 105 110
 Asn Ser Asn Arg Ser Glu Glu Met Asp Met Asp His Ile Met Thr Trp
 115 120 125
 Ala Thr Asp Val Ala Lys Gly Met His Tyr Leu His Met Glu Ala Pro
 130 135 140
 Val Lys Val Ile His Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala
 145 150 155 160
 Ala Asp Gly Val Leu Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His
 165 170 175
 Asn His Thr Thr His Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala
 180 185 190
 Pro Glu Val Ile Gln Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr
 195 200 205
 Ser Tyr Gly Val Val Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe
 210 215 220
 Lys Gly Leu Glu Gly Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn
 225 230 235 240
 Glu Arg Leu Thr Ile Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu
 245 250 255
 Leu His Gln Cys Trp Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys
 260 265 270
 Gln Ile Ile Ser Ile Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro
 275 280 285
 Asp Lys Cys Asn Ser Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu
 290 295 300
 Ile Glu Ala Thr Leu Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser
 305 310 315 320
 Phe Lys Glu Gln Glu Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp
 325 330 335

Glu Gln Lys Leu Thr Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu
 340 345 350
 Ala Ala Arg Met Ser Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu
 355 360 365
 Ser Asn Ser Ala Glu Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly
 370 375 380
 Glu Gly His Gly Met Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly
 385 390 395 400
 Phe Gly Asp Ile Phe Ser Met Asn Lys Ala Gly Ala Val Met His Ser
 405 410 415
 Gly Met Gln Ile Asn Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr
 420 425 430
 Ser Lys Arg Arg Gly Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp
 435 440 445
 Phe Asp Leu Ser Glu Gly Asp Asp Asp Asp Asp Asp Gly Glu Glu
 450 455 460
 Glu Tyr Asn Asp Met Asp Asn Ser Glu
 465 470 473

<210> 838
 <211> 48
 <212> Amino acid
 <213> Homo sapiens

<400> 838
 Met Leu Trp Glu Thr Gly Cys Ser Ala Ala Cys Arg Val Thr Val Ser
 1 5 10 15
 Pro Thr Val Thr Phe Ala Thr Phe Ser Thr Arg Gly Ile Asp Ala Met
 20 25 30
 Arg Pro Gly Pro Ser Phe Leu Trp Arg Gln Gln Leu Ser Gln Gly *
 35 40 45 47

<210> 839
 <211> 116
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(116)
 <223> X = any amino acid or stop code

<400> 839
 Pro Thr Leu Gly Asp Gln Pro Asp Leu His Ser Ile Thr Arg Ala Ser
 1 5 10 15
 Arg Pro Lys Leu Cys Thr Arg Lys Asn Cys Asn Pro Leu Thr Ile Thr
 20 25 30
 Val His Asp Pro Asn Ser Thr Gln Xaa Tyr Tyr Gly Met Ser Trp Glu
 35 40 45
 Leu Arg Phe Tyr Ile Pro Gly Phe Asp Val Gly Thr Met Phe Thr Ile
 50 55 60
 Gln Lys Ile Leu Val Ser Trp Ser Pro Pro Lys Pro Ile Gly Pro Leu
 65 70 75 80
 Thr Asp Leu Gly Asp Pro Met Phe Gln Lys Pro Pro Asn Lys Val Asp


```
<210> 840
<211> 138
<212> Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(138)
<223> X = any amino acid or stop code
```

```
<210> 841
<211> 82
<212> Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(82)
<223> X = any amino acid or stop code
```

463

50 55 60
 Cys Ala His Arg Pro Arg Leu Lys Val Ile Lys Glu Gly Gly Trp Leu
 65 70 75 80
 Gly Gly
 82

<210> 842

<211> 58

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(58)

<223> X = any amino acid or stop code

<400> 842

Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg Gln Leu Thr Ala Gly Thr
 1 5 10 15
 Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile Arg Asn Pro Asp His Ser
 20 25 30
 Arg Ala Leu Ser Glu Xaa His Leu Ser Ser Leu Pro His Leu Ile Trp
 35 40 45
 Ile Gln Val Phe Leu Ala Leu Gln Pro Ser
 50 55 58

<210> 843

<211> 230

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(230)

<223> X = any amino acid or stop code

<400> 843

Ala Thr Tyr Ile Val Asp Phe Gly Phe Ser Thr Thr Phe Arg Glu Gly
 1 5 10 15
 Gln Met Leu Thr Ala Phe Cys Gly Met Tyr Pro Tyr Val Ala Pro Glu
 20 25 30
 Arg Ser Leu Gly Gln Ala Cys Gln Xaa Pro Ala Arg Asp Ile Gln Ser
 35 40 45
 Leu Ser Val Ile Leu Tyr Phe Arg Asn Thr Val Gly Arg Arg Ala Arg
 50 55 60
 Thr Leu Pro Phe Tyr Ser Ala Glu Ala Ser Lys Leu Gln Glu Lys Ile
 65 70 75 80
 Leu Thr Gly Arg Tyr His Ala Pro Pro Leu Leu Ala Leu Gln Leu Asp
 85 90 95
 Ser Leu Ile Lys Leu Leu Met Leu Asn Ala Arg Lys Cys Pro Ser Leu
 100 105 110
 Xaa Leu Met Lys Asn Pro Trp Val Lys Ser Ser Gln Lys Met Pro Leu
 115 120 125
 Ile Pro Tyr Glu Glu Pro Leu Arg Gly Pro Pro Gln Thr Ile Gln Leu

```

      130              135              140
Met Val Ala Met Gly Phe Gln Ala Lys Asn Ile Ser Val Ala Ile Ile
145              150              155              160
Glu Arg Lys Phe Asn Tyr Pro Met Ala Thr Tyr Leu Ile Leu Glu His
      165              170              175
Thr Lys Gln Glu Arg Lys Cys Ser Thr Ile Arg Glu Leu Ser Leu Pro
      180              185              190
Pro Gly Val Pro Thr Ser Pro Ser Pro Ser Thr Glu Leu Ser Thr Phe
      195              200              205
Pro Leu Ser Leu Met Arg Ala His Arg Glu Pro Ala Phe Asn Val Gln
      210              215              220
Pro Pro Glu Glu Ser Gln
225              230

```

```

<210> 844
<211> 258
<212> Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(258)
<223> X = any amino acid or stop code

```

```

      <400> 844
Ala Lys Gln Glu Leu Ala Lys Leu Met Arg Ile Glu Asp Pro Ser Leu
 1              5              10              15
Leu Asn Ser Arg Val Leu Leu His His Ala Lys Ala Gly Thr Ile Ile
      20              25              30
Ala Arg Gln Gly Asp Gln Asp Val Ser Leu His Phe Val Leu Trp Gly
      35              40              45
Cys Leu His Val Tyr Gln Arg Met Ile Asp Lys Ala Glu Asp Val Cys
      50              55              60
Leu Phe Val Ala Gln Pro Gly Glu Leu Val Gly Gln Leu Ala Val Leu
      65              70              75              80
Thr Gly Glu Pro Leu Ile Phe Thr Leu Arg Ala Gln Arg Asp Cys Thr
      85              90              95
Phe Leu Arg Ile Ser Lys Ser Asp Phe Tyr Glu Ile Met Arg Ala Gln
      100              105              110
Pro Ser Val Val Leu Ser Ala Ala His Thr Val Ala Ala Arg Met Ser
      115              120              125
Pro Phe Val Arg Gln Met Asp Phe Ala Ile Asp Trp Thr Ala Val Glu
      130              135              140
Ala Gly Arg Ala Leu Tyr Arg Cys Ser Ser His Arg Ala Ala Gln Ala
145              150              155              160
Arg Pro Arg Gly Gly Asp Leu Gly Val Val Arg Pro Cys Xaa Pro Pro
      165              170              175
Arg Pro Leu Arg Gln Gly Asp Arg Ser Asp Cys Thr Tyr Ile Val Leu
      180              185              190
Asn Gly Arg Leu Arg Ser Val Ile Gln Arg Gly Ser Gly Lys Lys Glu
      195              200              205
Leu Val Gly Glu Tyr Gly Arg Gly Asp Leu Ile Gly Val Val Ser Ala
      210              215              220
Thr Pro Thr His Xaa Pro Leu Ala Phe Ser Arg Pro Val Pro Arg Gln
225              230              235              240
Leu Thr Arg Ile Ile Pro Gly Asn Pro Gly Ser Gly Glu Val Phe Pro
      245              250              255
Gly Ala
258

```

<210> 845
 <211> 235
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(235)
 <223> X = any amino acid or stop code

<400> 845
 His Ala Ser Gly Trp Thr Pro Gly Thr Thr Gln Thr Leu Gly Gln Gly
 1 5 10 15
 Thr Ala Trp Asp Thr Val Ala Ser Thr Pro Gly Thr Ser Glu Thr Thr
 20 25 30
 Ala Ser Ala Glu Gly Arg Arg Thr Pro Gly Ala Thr Arg Pro Ala Ala
 35 40 45
 Pro Gly Thr Gly Ser Trp Ala Glu Gly Ser Val Lys Ala Pro Ala Pro
 50 55 60
 Ile Pro Glu Ser Pro Pro Ser Lys Ser Arg Ser Met Ser Asn Thr Thr
 65 70 75 80
 Glu Gly Val Trp Glu Gly Thr Arg Ser Ser Val Thr Asn Arg Ala Arg
 85 90 95
 Ala Ser Lys Asp Arg Arg Glu Met Thr Thr Thr Lys Ala Asp Arg Pro
 100 105 110
 Arg Glu Asp Ile Glu Gly Val Arg Ile Ala Leu Asp Ala Ala Lys Lys
 115 120 125
 Val Leu Gly Thr Ile Gly Pro Pro Ala Leu Val Ser Glu Thr Leu Ala
 130 135 140
 Trp Glu Ile Leu Pro Gln Ala Thr Pro Val Ser Lys Gln Gln Ser Gln
 145 150 155 160
 Gly Ser Ile Gly Glu Thr Thr Pro Ala Ala Gly Met Trp Thr Leu Gly
 165 170 175
 Thr Pro Ala Ala Asp Val Trp Ile Leu Gly Thr Pro Ala Ala Asp Val
 180 185 190
 Trp Thr Ser Met Glu Ala Ala Ser Gly Glu Gly Ser Ala Ala Gly Asp
 195 200 205
 Leu Asp Ala Ala Thr Gly Asp Arg Gly Pro Gln Ala Thr Leu Ser Gln
 210 215 220
 Thr Pro Ala Val Xaa Pro Trp Gly Pro Pro Gly
 225 230 235

<210> 846
 <211> 134
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(134)
 <223> X = any amino acid or stop code

<400> 846

```

Ala Gly Thr Ser Gly Thr Gly Asp Thr Gly Pro Gly Asn Thr Ala Val
 1           5           10           15
Ser Gly Thr Pro Val Val Ser Pro Gly Ala Thr Pro Gly Ala Pro Gly
          20           25           30
Ser Ser Thr Pro Gly Glu Ala Asp Ile Gly Asn Thr Ser Phe Gly Lys
          35           40           45
Ser Gly Thr Pro Thr Val Ser Ala Ala Ser Thr Thr Ser Ser Pro Val
          50           55           60
Ser Lys His Thr Asp Ala Ala Ser Ala Thr Ala Val Thr Ile Ser Gly
          65           70           75           80
Ser Lys Pro Gly Thr Pro Gly Thr Pro Gly Gly Ala Thr Ser Gly Gly
          85           90           95
Lys Ile Thr Pro Gly Ile Ala Xaa Pro Thr Leu Asp Gln Lys Ser Pro
          100          105          110
Cys Phe Ser Gly Tyr Gly Gly Tyr Phe Pro Val Asn Pro His Gln Asn
          115          120          125
Pro Cys Ala Asp Ser Leu
          130          134

```

```

<210> 847
<211> 188
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(188)
<223> X = any amino acid or stop code

```

```

<400> 847
Arg Ala His Arg Cys Cys Leu Pro Leu Pro Ser Leu Ser Cys Glu Ile
 1           5           10           15
Gln Ile Gly Phe Ser Xaa Ser Ser Ile Phe Pro Gly Gln Xaa Ala Cys
          20           25           30
Pro Cys Ser Cys Cys Arg Ser Cys Arg Arg Asn Trp Pro Gln Ser Pro
          35           40           45
Arg Cys Pro His His Pro Pro Ala Pro Cys Ser Leu Leu Leu Ser Ser
          50           55           60
Cys Leu Pro Pro Pro Leu Ser Cys Ser Trp Arg Gly Thr Ser Gly Lys
          65           70           75           80
Pro Pro Ser Gln Ser Pro Ala Ala Ser Arg Ser Met Arg Pro Arg Cys
          85           90           95
Ser Pro Arg Thr Ser Ser Leu Arg Gly Ala Ser Cys Arg Gly Pro Gly
          100          105          110
Gly Ser Ala Pro Ala Ala Ala Ser Gly Pro Arg Cys Arg Gly Cys Ser
          115          120          125
Arg Ser Pro Arg Arg Cys Ser Arg Ser Gly Cys Ala Ala Ala Ser Pro
          130          135          140
Pro Arg Ser Gln Arg Arg Ser Pro Pro Leu Ser Pro Pro Pro Phe Pro
          145          150          155          160
Thr Ser Gly Thr Leu Leu Leu Lys Thr Ser Arg Phe Gly Ser Ala Thr
          165          170          175
Arg Glu Xaa Ser Ser Pro Arg Pro Arg Pro Arg Pro
          180          185          188

```

```

<210> 848
<211> 328
<212>Amino acid

```

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(328)

<223> X = any amino acid or stop code

<400> 848

```

Asp Asp Val Pro Pro Pro Ala Pro Asp Leu Tyr Asp Val Pro Pro Gly
 1          5          10          15
Leu Arg Arg Pro Gly Pro Gly Thr Leu Tyr Asp Val Pro Arg Glu Arg
 20          25          30
Val Leu Pro Pro Glu Val Ala Asp Gly Gly Val Val Asp Ser Gly Val
 35          40          45
Tyr Ala Val Pro Pro Pro Ala Glu Arg Glu Ala Pro Ala Glu Gly Lys
 50          55          60
Arg Leu Ser Ala Ser Ser Thr Gly Ser Thr Arg Ser Ser Gln Ser Ala
 65          70          75          80
Ser Ser Leu Glu Val Ala Gly Pro Gly Arg Glu Pro Leu Glu Leu Glu
 85          90          95
Val Ala Val Glu Ala Leu Ala Arg Leu Gln Gln Gly Val Ser Ala Thr
100          105          110
Val Ala His Leu Leu Asp Leu Ala Gly Ser Ala Gly Ala Thr Gly Ser
115          120          125
Trp Arg Ser Pro Ser Glu Pro Gln Glu Pro Leu Val Gln Asp Leu Gln
130          135          140
Ala Ala Val Ala Ala Val Gln Ser Ala Val His Glu Leu Leu Glu Phe
145          150          155          160
Ala Arg Ser Ala Val Gly Asn Ala Ala His Thr Ser Asp Arg Ala Leu
165          170          175
His Ala Lys Leu Ser Arg Gln Leu Gln Lys Met Glu Asp Val His Gln
180          185          190
Thr Leu Val Ala His Gly Gln Ala Leu Asp Ala Gly Arg Gly Gly Ser
195          200          205
Gly Ala Thr Leu Glu Asp Leu Asp Arg Leu Val Ala Cys Ser Arg Ala
210          215          220
Val Pro Glu Asp Ala Lys Gln Leu Ala Ser Phe Leu His Gly Asn Ala
225          230          235          240
Ser Leu Leu Phe Arg Arg Thr Lys Ala Thr Ala Pro Gly Pro Glu Gly
245          250          255
Gly Gly Thr Leu His Pro Asn Pro Thr Asp Lys Thr Ser Ser Ile Gln
260          265          270
Ser Arg Pro Leu Pro Ser Pro Pro Lys Phe Thr Ser Gln Asp Ser Pro
275          280          285
Asp Gly Gln Tyr Glu Asn Ser Glu Gly Gly Trp Met Glu Asp Tyr Asp
290          295          300
Tyr Val His Leu Thr Gly Gly Arg Arg Ser Phe Xaa Lys Thr Gln Lys
305          310          315          320
Glu Leu Leu Gly Lys Arg Ala Ala
325          328

```

<210> 849

<211> 98

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(98)

<223> X = any amino acid or stop code

<400> 849

```

Met Ala Thr Asp Glu Glu Asn Val Tyr Gly Leu Glu Glu Asn Ala Gln
 1          5          10          15
Ser Arg Gln Glu Ser Thr Arg Arg Leu Ile Leu Val Gly Arg Thr Gly
          20          25          30
Ala Gly Lys Ser Ala Thr Gly Asn Ser Ile Leu Gly Gln Arg Arg Phe
          35          40          45
Phe Ser Arg Leu Gly Ala Thr Ser Val Thr Arg Ala Cys Thr Thr Gly
          50          55          60
Ser Arg Arg Trp Asp Lys Cys His Val Glu Val Val Asp Thr Pro Asp
65          70          75          80
Ile Phe Ser Ser Gln Val Ser Lys Thr Asp Pro Gly Cys Glu Glu Arg
          85          90          95
Xaa *
97

```

<210> 850

<211> 94

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(94)

<223> X = any amino acid or stop code

<400> 850

```

Thr Leu Gly Leu Arg Ser Leu Thr Lys Glu Gly Gly Gly Gly Gly Asp
 1          5          10          15
Val Ala Ala Phe Glu Val Gly Thr Gly Ala Ala Ala Ser Arg Ala Leu
          20          25          30
Gly Gln Cys Gly Gln Leu Gln Lys Leu Ile Val Ile Phe Ile Gly Ser
          35          40          45
Leu Cys Gly Leu Cys Thr Lys Cys Ala Val Ser Asn Asp Leu Thr Gln
          50          55          60
Gln Glu Ile Gln Thr Pro Glu Ile Gln Gln Arg Asn Ala Xaa Cys Asp
65          70          75          80
Ser Arg Val Thr Phe Thr Asn Glu Gly Gly Arg Trp Trp Gly
          85          90          94

```

<210> 851

<211> 50

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(50)

<223> X = any amino acid or stop code

<400> 851

Phe Phe Phe Leu Val Glu Thr Arg Phe His His Ile Gly Gln Ala Gly
 1 5 10 15
 Leu Glu Leu Leu Thr Leu Ser Ile Lys Xaa Ser Ala Arg Leu Gly Leu
 20 25 30
 Pro Lys Cys Trp Asp Asp Arg Arg Glu Pro Pro Tyr Leu Ala Gly Phe
 35 40 45
 Met Ile
 50

<210> 852

<211> 143

<212>Amino acid

<213> Homo sapiens

<400> 852

Arg Arg Ser Pro Pro Pro Ala Pro Pro Pro Leu Pro Ser Pro Leu Ser
 1 5 10 15
 Pro Pro Pro Arg Ala Pro Val Ser Pro Ala Ser Thr Met Pro Ile Leu
 20 25 30
 Leu Phe Leu Ile Asp Thr Ser Ala Ser Met Asn Gln Arg Ser His Leu
 35 40 45
 Gly Thr Thr Tyr Leu Asp Thr Ala Lys Gly Ala Val Glu Thr Phe Met
 50 55 60
 Lys Leu Arg Ala Arg Asp Pro Ala Ser Arg Gly Asp Arg Tyr Met Leu
 65 70 75 80
 Val Thr Phe Glu Glu Pro Pro Tyr Ala Ile Lys Ala Gly Trp Lys Glu
 85 90 95
 Asn His Ala Thr Phe Met Asn Glu Leu Lys Asn Leu Gln Ala Glu Gly
 100 105 110
 Leu Thr Thr Leu Gly Gln Ser Leu Arg Thr Ala Phe Asp Leu Leu Asn
 115 120 125
 Leu Asn Arg Leu Val Thr Gly Ile Asp Asn Tyr Gly Gln Val Gly
 130 135 140 143

<210> 853

<211> 154

<212>Amino acid

<213> Homo sapiens

<400> 853

Asn Cys Arg Thr Tyr Val Phe Cys Phe Val Leu Val Phe Arg Leu Leu
 1 5 10 15
 Phe Leu His Gly Ser Pro Leu Ser Pro Ser Leu Leu Ser Arg Ala Gly
 20 25 30
 Leu Leu Cys Gly Ser Ala Glu Asn Pro Thr Pro Phe Leu Cys Gly Ile
 35 40 45
 Thr Met Ala Ala Gly Val Ser Leu Leu Ala Leu Val Val Arg Val Ile
 50 55 60
 Leu Ser Thr Ala Ile Leu Cys Pro Ser Gly Ala Ser Arg Arg Gln Arg
 65 70 75 80
 Ser Ser Glu Val Glu Trp Gly Thr Asp Ser Gly Val Tyr Arg Leu Tyr


```

      85      90      95
Cys Trp Arg Val Gly Phe Leu Gly Pro Gly Gly Glu Leu Arg Leu Gly
      100      105      110
Leu Ser Glu Ala Arg Gly Gly Arg Val Trp Gly Arg Gly Glu Lys Arg
      115      120      125
Cys Arg Val Trp Ala Val Arg Ser Leu Arg Lys Gly Phe Gly Ser Val
      130      135      140
Ala Ala Leu Arg Arg Gly Ile Trp Ala Gly
145      150      154

```

```

<210> 854
<211> 90
<212> Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(90)
<223> X = any amino acid or stop code

```

```

<400> 854
Val Thr Pro Thr Pro Pro Gln Tyr Tyr Thr Cys Ser Cys Val Leu Gly
 1      5      10      15
Phe Ile Ala Cys Ser Ile Phe Leu Gln Met Ser Leu Lys Pro Lys Val
      20      25      30
Met Leu Leu Thr Val Ala Leu Val Ala Cys Leu Val Leu Phe Asn Leu
      35      40      45
Ser Gln Cys Trp Gln Arg Asp Cys Cys Ser Gln Gly Leu Gly Asn Leu
      50      55      60
Thr Glu Pro Ser Gly Thr Asn Arg Xaa Gly Pro Ala Ala Val Ser Trp
      65      70      75      80
Ala Ser Leu Pro Ala Pro Ser Ser Cys Arg
      85      90

```

```

<210> 855
<211> 61
<212> Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(61)
<223> X = any amino acid or stop code

```

```

<400> 855
Gly Lys Ala Gly Gly Ala Ala Gly Leu Phe Ala Lys Gln Val Gln Lys
 1      5      10      15
Lys Phe Ser Arg Ala Gln Glu Lys Xaa Thr Arg Arg Phe Gly Lys Thr
      20      25      30
Cys Gln Pro Glu Glu Arg Ala Arg Glu Glu Arg Gln Glu Gly Pro Glu
      35      40      45
Ile Glu Phe Gly Phe Ser Phe Phe Ser Leu Ser Leu Tyr
      50      55      60      61

```

<210> 856
 <211> 779
 <212> Amino acid
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(779)
 <223> X = any amino acid or stop code

<400> 856
 Pro Lys Arg Leu Phe Leu Phe Gln Asp Val Asn Thr Leu Gln Gly Gly
 1 5 10 15
 Gly Gln Pro Val Val Thr Pro Ser Val Gln Pro Ser Leu Gln Pro Ala
 20 25 30
 His Pro Ala Leu Pro Gln Met Thr Ser Gln Ala Pro Gln Pro Ser Val
 35 40 45
 Thr Gly Leu Gln Ala Pro Ser Ala Ala Leu Met Gln Val Ser Ser Leu
 50 55 60
 Asp Ser His Ser Ala Val Ser Gly Asn Ala Gln Ser Phe Gln Pro Tyr
 65 70 75 80
 Ala Gly Met Gln Ala Tyr Ala Tyr Pro Gln Ala Ser Ala Val Thr Ser
 85 90 95
 Gln Leu Gln Pro Val Arg Pro Leu Tyr Pro Ala Pro Leu Ser Gln Pro
 100 105 110
 Pro His Phe Gln Gly Ser Gly Asp Met Ala Ser Phe Leu Met Thr Glu
 115 120 125
 Ala Arg Gln His Asn Thr Glu Ile Arg Met Ala Val Ser Lys Val Ala
 130 135 140
 Asp Lys Met Asp His Leu Met Thr Lys Val Glu Glu Leu Gln Lys His
 145 150 155 160
 Ser Ala Gly Asn Ser Met Leu Ile Pro Ser Met Ser Val Thr Met Glu
 165 170 175
 Thr Ser Met Ile Met Ser Asn Ile Gln Arg Ile Ile Gln Glu Asn Glu
 180 185 190
 Arg Leu Lys Gln Glu Ile Leu Glu Lys Ser Asn Arg Ile Glu Glu Gln
 195 200 205
 Asn Asp Lys Ile Ser Glu Leu Ile Glu Arg Asn Gln Arg Tyr Val Glu
 210 215 220
 Gln Ser Asn Leu Met Met Glu Lys Arg Asn Asn Ser Leu Gln Thr Ala
 225 230 235 240
 Thr Glu Asn Thr Gln Ala Arg Val Leu His Ala Glu Gln Glu Lys Ala
 245 250 255
 Lys Val Thr Glu Glu Leu Ala Ala Thr Ala Gln Val Ser His Leu
 260 265 270
 Gln Leu Lys Met Thr Ala His Gln Lys Lys Glu Thr Glu Leu Gln Met
 275 280 285
 Gln Leu Thr Glu Ser Leu Lys Glu Thr Asp Leu Leu Arg Gly Gln Leu
 290 295 300
 Thr Lys Val Gln Ala Lys Leu Ser Glu Leu Gln Glu Thr Ser Glu Gln
 305 310 315 320
 Ala Gln Ser Lys Phe Lys Ser Glu Lys Gln Asn Arg Lys Gln Leu Glu
 325 330 335
 Leu Lys Val Thr Ser Leu Glu Glu Glu Leu Thr Asp Leu Arg Val Glu
 340 345 350
 Lys Glu Ser Leu Glu Lys Asn Leu Ser Glu Arg Lys Lys Lys Ser Ala
 355 360 365
 Gln Glu Arg Ser Gln Ala Glu Glu Glu Ile Asp Glu Ile Arg Lys Ser
 370 375 380

```

Tyr Gln Glu Glu Leu Asp Lys Leu Arg Gln Leu Leu Lys Lys Thr Arg
385                      390                      395                      400
Val Ser Thr Asp Gln Ala Ala Ala Glu Gln Leu Ser Leu Val Gln Ala
                      405                      410                      415
Glu Leu Gln Thr Gln Trp Glu Ala Lys Cys Glu His Leu Leu Ala Ser
                      420                      425                      430
Ala Lys Asp Glu His Leu Gln Gln Tyr Gln Glu Val Cys Ala Gln Arg
                      435                      440                      445
Asp Ala Tyr Gln Gln Lys Leu Val Gln Leu Gln Glu Lys Ser Val Cys
                      450                      455                      460
Phe Ala Cys Leu Ala Leu Gln Ala Gln Ile Thr Ala Leu Thr Lys Gln
465                      470                      475                      480
Asn Glu Gln His Ile Lys Glu Leu Glu Lys Asn Lys Ser Gln Met Ser
                      485                      490                      495
Gly Val Glu Ala Ala Ala Ser Asp Pro Ser Glu Lys Val Lys Lys Ile
                      500                      505                      510
Met Asn Gln Val Phe Gln Ser Leu Arg Arg Glu Phe Glu Leu Glu Glu
                      515                      520                      525
Ser Tyr Asn Gly Arg Thr Ile Leu Gly Thr Ile Met Asn Thr Ile Lys
                      530                      535                      540
Met Val Thr Leu Gln Leu Leu Asn Gln Gln Glu Gln Glu Lys Glu Glu
545                      550                      555                      560
Ser Ser Ser Glu Glu Glu Glu Glu Lys Ala Glu Glu Arg Pro Arg Arg
                      565                      570                      575
Pro Ser Gln Glu Gln Ser Ala Ser Ala Ser Ser Gly Gln Pro Gln Ala
                      580                      585                      590
Pro Leu Asn Arg Glu Arg Pro Glu Ser Pro Met Val Pro Ser Glu Gln
                      595                      600                      605
Val Val Glu Glu Ala Val Pro Leu Pro Pro Gln Ala Leu Thr Thr Ser
                      610                      615                      620
Gln Asp Gly His Arg Arg Lys Gly Asp Ser Glu Ala Glu Ala Leu Ser
625                      630                      635                      640
Glu Ile Lys Asp Gly Ser Leu Pro Pro Glu Leu Ser Cys Ile Pro Ser
                      645                      650                      655
His Arg Val Leu Gly Pro Pro Thr Ser Ile Pro Pro Glu Pro Leu Gly
                      660                      665                      670
Pro Val Ser Met Asp Ser Glu Cys Glu Glu Ser Leu Ala Ala Ser Pro
                      675                      680                      685
Met Ala Ala Lys Pro Asp Asn Pro Ser Gly Lys Val Cys Val Gln Gly
                      690                      695                      700
Lys Xaa Ala Pro Asp Gly Pro Thr Tyr Lys Glu Ser Ser Thr Arg Leu
705                      710                      715                      720
Phe Pro Gly Phe Gln Asp Pro Glu Glu Gly Asp Pro Leu Ala Leu Gly
                      725                      730                      735
Leu Glu Ser Pro Gly Glu Pro Gln Pro Pro Gln Leu Gln Gly Lys Val
                      740                      745                      750
Asp Val His Xaa Val Pro Pro Val Pro His Lys Gly Ala Phe Gln Glu
                      755                      760                      765
Gln Glu Gly Arg Phe Pro Gln Phe Cys Arg Glu
770                      775                      779

```

<210> 857

<211> 510

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (510)

<223> X = any amino acid or stop code

<400> 857

Ser	Glu	Thr	Ala	Gln	Gln	Ile	Ile	Asp	Arg	Leu	Arg	Val	Lys	Leu	Ala	1	5	10	15
Lys	Glu	Pro	Gly	Ala	Asn	Leu	Phe	Leu	Met	Ala	Val	Gln	Asp	Ile	Arg	20	25	30	
Val	Gly	Gly	Arg	Gln	Ser	Asn	Ala	Ser	Tyr	Gln	Tyr	Thr	Leu	Leu	Ser	35	40	45	
Asp	Asp	Leu	Ala	Ala	Leu	Arg	Glu	Trp	Glu	Pro	Lys	Ile	Arg	Lys	Lys	50	55	60	
Leu	Ala	Thr	Leu	Pro	Glu	Leu	Ala	Asp	Val	Asn	Ser	Asp	Gln	Gln	Asp	65	70	75	80
Asn	Gly	Ala	Glu	Met	Asn	Leu	Val	Tyr	Asp	Arg	Asp	Thr	Met	Ala	Arg	85	90	95	
Leu	Gly	Ile	Asp	Val	Gln	Ala	Ala	Asn	Ser	Leu	Leu	Asn	Asn	Ala	Phe	100	105	110	
Gly	Gln	Arg	Gln	Ile	Ser	Thr	Ile	Tyr	Gln	Pro	Met	Asn	Gln	Tyr	Lys	115	120	125	
Val	Val	Met	Glu	Val	Asp	Pro	Arg	Tyr	Thr	Gln	Asp	Ile	Ser	Ala	Leu	130	135	140	
Glu	Lys	Met	Phe	Val	Ile	Asn	Asn	Glu	Gly	Lys	Ala	Ile	Pro	Leu	Ser	145	150	155	160
Tyr	Phe	Ala	Lys	Trp	Gln	Pro	Ala	Asn	Ala	Pro	Leu	Ser	Val	Asn	His	165	170	175	
Gln	Gly	Leu	Ser	Ala	Ala	Leu	Thr	Ile	Ser	Phe	Asn	Leu	Pro	Thr	Gly	180	185	190	
Lys	Ser	Leu	Ser	Asp	Ala	Ser	Ala	Ile	Asp	Arg	Ala	Met	Ser	Gln		195	200	205	
Leu	Gly	Val	Pro	Ser	Thr	Val	Arg	Gly	Ser	Phe	Ala	Gly	Pro	Ala	Gln	210	215	220	
Val	Phe	Gln	Glu	Thr	Met	Asn	Ser	Gln	Val	Ile	Leu	Ile	Ile	Ala	Ala	225	230	235	240
Ile	Ala	Thr	Val	Tyr	Ile	Val	Leu	Gly	Ile	Pro	Tyr	Glu	Arg	Tyr	Val	245	250	255	
His	Pro	Pro	Thr	Ile	Leu	Leu	Xaa	Arg	Pro	Gly	Ala	Asn	Leu	Phe	Leu	260	265	270	
Met	Ala	Val	Gln	Asp	Ile	Arg	Val	Gly	Gly	Arg	Gln	Ser	Asn	Ala	Ser	275	280	285	
Tyr	Gln	Tyr	Thr	Leu	Leu	Ser	Asp	Asp	Leu	Ala	Ala	Leu	Arg	Glu	Trp	290	295	300	
Glu	Pro	Lys	Ile	Arg	Lys	Lys	Leu	Ala	Thr	Leu	Pro	Glu	Leu	Ala	Asp	305	310	315	320
Val	Asn	Ser	Asp	Gln	Gln	Asp	Asn	Gly	Ala	Glu	Met	Asn	Leu	Val	Tyr	325	330	335	
Asp	Arg	Asp	Thr	Met	Ala	Arg	Leu	Gly	Ile	Asp	Val	Gln	Ala	Ala	Asn	340	345	350	
Ser	Leu	Leu	Asn	Asn	Ala	Phe	Gly	Gln	Arg	Gln	Ile	Ser	Thr	Ile	Tyr	355	360	365	
Gln	Pro	Met	Asn	Gln	Tyr	Lys	Val	Val	Met	Glu	Val	Asp	Pro	Arg	Tyr	370	375	380	
Thr	Gln	Asp	Ile	Ser	Ala	Leu	Glu	Lys	Met	Phe	Val	Ile	Asn	Asn	Glu	385	390	395	400
Gly	Lys	Ala	Ile	Pro	Leu	Ser	Tyr	Phe	Ala	Lys	Trp	Gln	Pro	Ala	Asn	405	410	415	
Ala	Pro	Leu	Ser	Val	Asn	His	Gln	Gly	Leu	Ser	Ala	Ala	Leu	Thr	Ile	420	425	430	
Ser	Phe	Asn	Leu	Pro	Thr	Gly	Lys	Ser	Leu	Ser	Asp	Ala	Ser	Ala	Ala	435	440	445	
Ile	Asp	Arg	Ala	Met	Ser	Gln	Leu	Gly	Val	Pro	Ser	Thr	Val	Arg	Gly	450	455	460	
Ser	Phe	Ala	Gly	Pro	Ala	Gln	Val	Phe	Gln	Glu	Thr	Met	Asn	Ser	Gln	465	470	475	480
Val	Ile	Leu	Ile	Ile	Ala	Ala	Ile	Ala	Thr	Val	Tyr	Ile	Val	Leu	Gly				

485 490 495
 Ile Pro Tyr Glu Arg Tyr Val His Pro Pro Thr Ile Leu Leu
 500 505 510

<210> 858
 <211> 137
 <212> Amino acid
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(137)
 <223> X = any amino acid or stop code

<400> 858
 Ile Ile Thr Pro Asp Ala Met Gly Cys Gln Lys Asp Ile Ala Glu Lys
 1 5 10 15
 Ile Gln Lys Gln Gly Gly Asp Tyr Leu Phe Ala Val Lys Gly Asn Gln
 20 25 30
 Gly Arg Leu Asn Lys Ala Phe Glu Glu Lys Phe Pro Leu Lys Glu Leu
 35 40 45
 Asn Asn Pro Glu His Asp Ser Tyr Ala Ile Ser Glu Lys Ser His Gly
 50 55 60
 Arg Glu Glu Ile Arg Leu His Ile Val Cys Asp Val Pro Asp Glu Leu
 65 70 75 80
 Ile Asp Phe Thr Phe Glu Trp Lys Gly Leu Lys Lys Leu Cys Val Ala
 85 90 95
 Val Ser Phe Arg Ser Ile Ile Ala Glu Gln Lys Lys Glu Pro Glu Met
 100 105 110
 Thr Val Arg Tyr Asn Ile Ser Xaa Leu Gly Ile Ala Gly Asp Ile Ser
 115 120 125
 Val Thr Ala Ile Ser Gly Thr Asp Asp
 130 135 137

<210> 859
 <211> 123
 <212> Amino acid
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(123)
 <223> X = any amino acid or stop code

<400> 859
 His Tyr Leu Lys Met Leu Thr Gln Ala Arg Arg Glu Val Ile Ile Ala
 1 5 10 15
 Asn Ala Tyr Phe Phe Pro Gly Tyr Arg Phe Leu His Ala Leu Arg Lys
 20 25 30
 Ala Ala Arg Arg Gly Val Arg Ile Lys Leu Ile Ile Gln Gly Glu Pro
 35 40 45
 Asp Met Pro Ile Val Arg Val Gly Ala Arg Leu Leu Tyr Asn Tyr Leu
 50 55 60
 Val Lys Gly Gly Val Gln Val Phe Glu Tyr Arg Arg Arg Pro Leu His

```

65          70          75          80
Gly Lys Val Ala Leu Met Asp Asp His Trp Ala Thr Val Gly Ser Ser
      85          90          95
Asn Leu His Pro Val Ser Xaa Ser Gly Asn Leu Gln Ala Asn Val Ile
      100          105          110
Leu His Val Leu Arg Val Pro Thr Leu Asn Pro
      115          120          123

```

<210> 860

<211> 190

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(190)

<223> X = any amino acid or stop code

<400> 860

```

Cys Trp Ser Lys Ser Ala Ala Phe His Ser Lys Leu Ala Thr Thr Cys
1          5          10          15
Ile Val Pro Val Cys Ala Ala Gly His Cys Ser Ala Ala Trp Xaa Ser
      20          25          30
Leu Arg Pro Ile Glu Ala Leu Ala Lys Glu Val Arg Glu Leu Lys Xaa
      35          40          45
His Thr Arg Xaa Leu Leu Asn Pro Ala Thr Thr Arg Glu Leu Thr Ser
      50          55          60
Leu Gly Arg Asn Leu Asn Arg Leu Leu Lys Ser Glu Arg Glu Arg Tyr
      65          70          75          80
Asp Lys Tyr Arg Thr Leu Thr Asp Leu Thr His Ser Leu Lys Thr
      85          90          95
Pro Leu Ala Val Leu Gln Ser Thr Leu Arg Ser Leu Arg Ser Glu Lys
      100          105          110
Met Ser Val Ser Asp Ala Glu Pro Val Met Leu Glu Gln Ile Ser Arg
      115          120          125
Ile Ser Gln Gln Ile Gly Tyr Tyr Leu His Arg Ala Ser Met Arg Gly
      130          135          140
Gly Thr Leu Leu Ser Arg Glu Leu His Pro Val Ala Pro Leu Leu Asp
      145          150          155          160
Asn Leu Thr Ser Ala Leu Ile Lys Gly Lys Pro Arg Lys Gly Gly Asn
      165          170          175
Val Thr Val Phe Pro Phe Thr Ala Met Tyr Arg Asp Gly His
      180          185          190

```

<210> 861

<211> 241

<212>Amino acid

<213> Homo sapiens

<400> 861

```

Gly Asn Thr Val Met Phe Gln His Leu Met Gln Lys Arg Lys His Thr
1          5          10          15
Gln Trp Thr Tyr Gly Pro Leu Thr Ser Thr Leu Tyr Asp Leu Thr Glu
      20          25          30

```

```

Ile Asp Ser Ser Gly Asp Glu Gln Ser Leu Leu Glu Leu Ile Ile Thr
      35              40              45
Thr Lys Lys Arg Glu Ala Arg Gln Ile Leu Asp Gln Thr Pro Val Lys
      50              55              60
Glu Leu Val Ser Leu Lys Trp Lys Arg Tyr Gly Arg Pro Tyr Phe Cys
      65              70              75              80
Met Leu Gly Ala Ile Tyr Leu Leu Tyr Ile Ile Cys Phe Thr Met Cys
              85              90              95
Cys Ile Tyr Arg Pro Leu Lys Pro Arg Thr Asn Asn Arg Thr Ser Pro
              100              105              110
Arg Asp Asn Thr Leu Leu Gln Gln Lys Leu Leu Gln Glu Ala Tyr Met
              115              120              125
Thr Pro Lys Asp Asp Ile Arg Leu Val Gly Glu Leu Val Thr Val Ile
      130              135              140
Gly Ala Ile Ile Ile Leu Leu Val Glu Val Pro Asp Ile Phe Arg Met
      145              150              155              160
Gly Val Thr Arg Phe Phe Gly Gln Thr Ile Leu Gly Gly Pro Phe His
              165              170              175
Val Leu Ile Ile Thr Tyr Ala Phe Met Val Leu Val Thr Met Val Met
              180              185              190
Arg Leu Ile Ser Ala Ser Gly Glu Val Val Pro Met Ser Phe Ala Leu
              195              200              205
Val Leu Gly Trp Cys Asn Val Met Tyr Phe Ala Arg Gly Phe Gln Met
      210              215              220
Leu Gly Pro Phe Thr Ile Met Ile Gln Lys Met Ile Phe Gly Asp Leu
      225              230              235              240
Met
      241

```

<210> 862
 <211> 45
 <212> Amino acid
 <213> Homo sapiens

```

<400> 862
Glu Lys Ala Ala Ala Ala Asn Ile Asp Glu Val Gln Lys Ser Asp Val
  1              5              10              15
Ser Ser Thr Gly Gln Gly Val Ile Asp Lys Asp Ala Leu Gly Pro Met
              20              25              30
Met Leu Glu Val Ala His Leu His Phe Ser Ala Val Phe
      35              40              45

```

<210> 863
 <211> 120
 <212> Amino acid
 <213> Homo sapiens

```

<400> 863
Leu Glu Val Pro Ser Glu Val Thr Pro Leu Gly Phe Ala Met Gln Ala
  1              5              10              15
Thr Lys Thr Leu Leu Arg Thr Cys Cys Leu Gln Glu Phe Asn Ile
              20              25              30
Met Glu Lys Asn Lys Gly Trp Ala Leu Leu Gly Gly Lys Asp Gly His
      35              40              45

```

Leu Gln Gly Leu Phe Leu Leu Ala Asn Ala Leu Leu Glu Arg Asn Gln
 50 55 60
 Leu Leu Ala Gln Lys Val Met Tyr Leu Leu Val Pro Leu Leu Asn Arg
 65 70 75 80
 Gly Asn Asp Lys His Lys Leu Thr Ser Ala Gly Phe Phe Val Glu Leu
 85 90 95
 Leu Arg Ser Pro Val Ala Lys Arg Leu Pro Ser Ile Tyr Ser Val Ala
 100 105 110
 Arg Phe Lys Asp Trp Leu Gln Asp
 115 120

<210> 864

<211> 124

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(124)

<223> X = any amino acid or stop code

<400> 864

Arg Pro Ala Pro Ala Pro Ser Ala Ala Pro Glu Glu Ala Pro Ser Pro
 1 5 10 15
 Gly Val Lys Gly Arg Gly Met Ala Lys Arg Arg Val Pro Ala Pro Val
 20 25 30
 Trp Gly Gly Ala Gly Gly Gly Thr Lys Ser Ala Arg Arg Ala Ala Ala
 35 40 45
 Ala Pro Asp Thr Glu Arg Ser Glu Glu Gly Gly Arg Ala Val Lys Glu
 50 55 60
 Ala Tyr Pro Ser Ser Arg Gln Pro Pro Pro Pro Ser Pro Xaa Pro Leu
 65 70 75 80
 Arg Cys Ala Arg Arg Cys His Pro Asn Leu Ala Pro Ser Met Pro Ile
 85 90 95
 Ser Asn Arg Glu Gly Lys Gly Lys Arg Arg Glu Glu Lys Ile Arg Pro
 100 105 110
 Leu Ser Pro Ala Ser Thr His Thr Ser Ala Arg Ala
 115 120 124

<210> 865

<211> 120

<212> Amino acid

<213> Homo sapiens

<400> 865

Leu Gln Gly Val His Gly Ser Ser Ser Thr Phe Cys Ser Ser Leu Ser
 1 5 10 15
 Ser Asp Phe Asp Pro Leu Glu Tyr Cys Ser Pro Lys Gly Asp Pro Gln
 20 25 30
 Arg Val Asp Met Gln Pro Ser Val Thr Ser Arg Pro Arg Ser Leu Asp
 35 40 45
 Ser Glu Val Pro Thr Gly Glu Thr Gln Val Ser Ser His Val His Tyr
 50 55 60
 His Arg His Arg His His His Tyr Lys Lys Arg Phe Gln Arg His Gly


```

      65              70              75              80
Arg Lys Pro Gly Pro Glu Thr Gly Val Pro Gln Ser Arg Pro Pro Ile
      85              90              95
Pro Arg Thr Gln Pro Gln Pro Glu Pro Pro Ser Pro Asp Gln Gln Val
      100            105            110
Thr Arg Ser Asn Ser Ala Ala Pro
      115              120

```

<210> 866
 <211> 82
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 866
Met Ala Asp Pro Asp Pro Arg Tyr Pro Arg Ser Ser Ile Glu Asp Asp
  1              5              10              15
Phe Asn Tyr Gly Ser Ser Glu Ala Ser Asp Thr Val His Ile Arg Met
      20              25              30
Ala Phe Leu Arg Arg Val Tyr Ser Ile Leu Ser Leu Gln Asp Leu Leu
      35              40              45
Ala Thr Val Thr Ser Thr Asp Asn Leu Ala Phe Glu Asp Gly Arg Thr
      50              55              60
Asp Trp Leu Gln Arg Pro Asp Cys Val Ser Phe Lys Ile His Val Leu
      65              70              75              80
Pro Met
      82

```

<210> 867
 <211> 60
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 867
Ala Gly Met Ser Val Val Val Val Pro Pro Ile Gly Ser Ser Tyr Leu
  1              5              10              15
Gly Leu Ile Ser Gln Glu His Phe Pro Asn Glu Phe Thr Ser Gly Asp
      20              25              30
Gly Lys Lys Ala His Gln Asp Phe Gly Tyr Phe Tyr Gly Ser Ser Tyr
      35              40              45
Val Ala Ala Ser Asp Ser Ser Arg Thr Pro Gly Leu
      50              55              60

```

<210> 868
 <211> 78
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 868
Val Ala Ala Ala Leu Thr Leu Phe Pro Gln Gln Leu Ser Pro Pro Gly

```

```

      1           5           10           15
Ala Trp Gly Leu Gly Leu Ser Ala Cys Phe Cys Cys Ala Glu Gly Phe
      20           25           30
Ser Arg Leu Asn Gln Gln Val Leu Ser Ser Ser Leu Leu Leu Ser
      35           40           45
Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn Leu Lys Lys
      50           55           60
Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Val Arg
      65           70           75           78

```

<210> 869
 <211> 119
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 869
Arg Asp Asp Ala Cys Leu Tyr Ser Pro Ala Ser Ala Pro Glu Val Ile
      1           5           10           15
Thr Val Gly Ala Thr Asn Ala Gln Asp Gln Pro Val Thr Leu Gly Thr
      20           25           30
Leu Gly Thr Asn Phe Gly Arg Cys Val Asp Leu Phe Ala Pro Gly Glu
      35           40           45
Asp Ile Ile Gly Ala Ser Ser Asp Cys Ser Thr Cys Phe Val Ser Gln
      50           55           60
Ser Gly Thr Ser Gln Ala Ala Ala His Val Ala Gly Ile Ala Ala Met
      65           70           75           80
Met Leu Ser Ala Glu Pro Glu Leu Thr Leu Ala Glu Leu Arg Gln Arg
      85           90           95
Leu Ile His Phe Ser Ala Lys Asp Val Ile Asn Glu Ala Trp Phe Pro
      100          105          110
Glu Asp Gln Arg Val Leu Thr
      115          119

```

<210> 870
 <211> 34
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 870
Leu Glu Ile Lys Phe Leu Glu Gln Val Asp Gln Phe Tyr Asp Asp Asn
      1           5           10           15
Phe Pro Met Glu Ile Arg His Leu Leu Ala Gln Trp Ile Glu Asn Gln
      20           25           30
Asp Trp
      34

```

<210> 871
 <211> 154
 <212>Amino acid
 <213> Homo sapiens

<400> 871

```

Glu Ala Gly Asp Ala Asp Glu Asp Glu Ala Asp Ala Asn Ser Ser Asp
 1          5          10          15
Cys Glu Pro Glu Gly Pro Val Glu Ala Glu Glu Pro Pro Gln Glu Asp
          20          25          30
Ser Ser Ser Gln Ser Asp Ser Val Glu Asp Arg Ser Glu Asp Glu Glu
          35          40          45
Asp Glu His Ser Glu Glu Glu Glu Thr Ser Gly Ser Ser Ala Ser Glu
          50          55          60
Glu Ser Glu Ser Glu Glu Ser Glu Asp Ala Gln Ser Gln Ser Gln Ala
          65          70          75          80
Asp Glu Glu Glu Glu Asp Asp Asp Phe Gly Val Glu Tyr Leu Leu Ala
          85          90          95
Arg Asp Glu Glu Gln Ser Glu Ala Asp Ala Gly Ser Gly Pro Pro Thr
          100          105          110
Pro Gly Pro Thr Thr Leu Gly Pro Lys Lys Glu Ile Thr Asp Ile Ala
          115          120          125
Ala Ala Ala Glu Ser Leu Gln Pro Lys Gly Tyr Thr Leu Ala Thr Thr
          130          135          140
Gln Val Lys Thr Pro Ile Pro Leu Leu Leu
145          150          154

```

<210> 872

<211> 118

<212>Amino acid

<213> Homo sapiens

<400> 872

```

Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn Gln Leu Pro Gln
 1          5          10          15
Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu Leu Ser Leu Ile Gln
          20          25          30
Thr Asn Ile Tyr Asn Ile Thr Lys Glu Gly Ile Ser Arg Leu Ile Asn
          35          40          45
Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys Tyr Phe Asn Lys Val Cys
          50          55          60
Glu Lys Thr Asn Ile Glu Asp Gly Val Phe Glu Thr Leu Thr Asn Leu
          65          70          75          80
Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu Ser His Val Pro Pro Lys
          85          90          95
Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu Ser Asn Thr Gln Ile Lys
          100          105          110
Tyr Ile Ser Glu Glu Asp
          115          118

```

<210> 873

<211> 42

<212>Amino acid

<213> Homo sapiens

<400> 873

```

Met Arg Ser Gln Ala Leu Gly Gln Ser Ala Pro Ser Leu Thr Ala Ser

```

```

      1             5             10             15
Leu Lys Glu Leu Ser Leu Pro Arg Arg Gly Ser Phe Pro Val Cys Pro
      20             25             30
Asn Ala Gly Arg Thr Ser Pro Leu Gly *
      35             40 41

```

<210> 874
 <211> 70
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 874
Leu Leu Cys Val Cys Leu Pro Val Gly Ala Cys Pro Ser Leu Ser Leu
      1             5             10             15
Leu Thr Ala Pro Leu Asn Gln Leu Met Arg Cys Leu Arg Lys Tyr Gln
      20             25             30
Ser Arg Thr Pro Ser Pro Leu Leu His Ser Val Pro Ser Glu Ile Val
      35             40             45
Phe Asp Phe Glu Pro Gly Pro Val Phe Arg Gly Ser Trp Ala Leu Leu
      50             55             60
Ser Trp Ser Thr Arg Pro
      65             70

```

<210> 875
 <211> 41
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 875
Gln Thr Pro Asp Lys Lys Gln Asn Asp Gln Arg Asn Arg Lys Arg Lys
      1             5             10             15
Ala Glu Pro Tyr Glu Thr Ser Gln Gly Ser Asn Asn Phe Val Ser Thr
      20             25             30
Lys Val Leu Asn Ser Asn Val Leu Arg
      35             40 41

```

<210> 876
 <211> 139
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 876
Tyr Phe Ile Ile Lys Gly Met Val Glu Leu Val Pro Ala Ser Asp Thr
      1             5             10             15
Leu Arg Lys Ile Gln Val Glu Tyr Gly Val Thr Gly Ser Phe Lys Asp
      20             25             30
Lys Pro Leu Ala Glu Trp Leu Arg Lys Tyr Asn Pro Ser Glu Glu Glu
      35             40             45
Tyr Glu Lys Ala Ser Glu Asn Phe Ile Tyr Ser Cys Ala Gly Cys Cys

```

50	55	60
Val Ala Thr Tyr Val Leu Gly Ile Cys Asp Arg His Asn Asp Asn Ile		
65	70	75
Met Leu Arg Ser Thr Gly His Met Phe His Ile Asp Phe Gly Lys Phe		80
	85	90
Leu Gly His Ala Gln Met Phe Gly Ser Phe Lys Arg Asp Arg Ala Pro		95
	100	105
Phe Val Leu Thr Ser Asp Met Ala Tyr Val Ile Asn Gly Gly Glu Lys		110
	115	120
Pro Thr Ile Arg Phe Gln Leu Phe Val Asp Leu		125
130	135	139

<210> 877

<211> 350

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(350)

<223> X = any amino acid or stop code

<400> 877

Pro Ser Pro Leu Pro Ser Leu Ser Leu Pro Pro Pro Val Ala Pro Gly		
1	5	10
Gly Gln Glu Ser Pro Ser Pro His Thr Ala Glu Val Glu Ser Glu Ala		15
	20	25
Ser Pro Pro Pro Ala Arg Pro Leu Pro Gly Glu Ala Arg Leu Ala Pro		30
	35	40
Ile Ser Glu Glu Gly Lys Pro Gln Leu Val Gly Arg Phe Gln Val Thr		45
	50	55
Ser Ser Lys Asn Arg Leu Ser Leu Phe Pro Cys Ser Gln His Pro Pro		60
	65	70
Leu Ser Leu Val Leu Gln Asn Leu Gln Pro Leu Ser Ser Leu Gln Arg		75
	85	90
Ala Gln Ile Gln Arg Thr Val Pro Gly Gly Gly Pro Glu Thr Arg Glu		95
	100	105
Ala Leu Ala Glu Ser Asp Arg Ala Ala Glu Gly Leu Gly Ala Gly Val		110
	115	120
Glu Glu Glu Gly Asp Asp Gly Lys Glu Pro Gln Val Gly Gly Ser Pro		125
	130	135
Gln Pro Leu Ser His Pro Ser Pro Val Trp Met Asn Tyr Ser Tyr Ser		140
	145	150
Ser Leu Cys Leu Ser Ser Glu Glu Ser Glu Ser Ser Gly Glu Asp Glu		155
	165	170
Glu Phe Trp Ala Glu Leu Gln Ser Leu Arg Gln Lys His Leu Ser Glu		175
	180	185
Val Glu Thr Leu Gln Thr Leu Gln Lys Lys Glu Ile Glu Asp Leu Tyr		190
	195	200
Ser Arg Leu Gly Lys Gln Pro Pro Pro Gly Ile Val Ala Pro Ala Ala		205
	210	215
Met Leu Ser Ser Arg Gln Arg Arg Leu Ser Lys Gly Ser Phe Pro Thr		220
	225	230
Ser Arg Arg Asn Ser Leu Gln Arg Ser Glu Pro Pro Gly Pro Gly Glu		235
	245	250
Thr Ala Gly His Pro Ala Ser Ile Phe Ser Leu Arg Pro Leu Ser Val		255
	260	265
Asp Cys Phe Ser Pro Gly Pro Gly Gly Leu Pro Arg Gly Asn Arg Pro		270
	275	280
		285

Pro Leu Pro Thr Ser Pro Phe Leu Thr Xaa Cys Ser Pro Ser Pro His
 290 295 300
 Thr Ala Glu Val Glu Ser Glu Ala Ser Pro Pro Ala Arg Pro Leu
 305 310 315 320
 Pro Gly Glu Ala Arg Leu Ala Pro Ile Ser Glu Glu Gly Lys Pro Gln
 325 330 335
 Leu Val Gly Arg Phe Pro Ser Asp Phe Ile Gln Gly Thr Gly
 340 345 350

<210> 878
 <211> 112
 <212> Amino acid
 <213> Homo sapiens

<400> 878
 Arg Arg Phe Val Ser Gln Glu Thr Gly Asn Leu Tyr Ile Ala Lys Val
 1 5 10 15
 Glu Lys Ser Asp Val Gly Asn Tyr Thr Cys Val Val Thr Asn Thr Val
 20 25 30
 Thr Asn His Lys Val Leu Gly Pro Pro Thr Pro Leu Ile Leu Arg Asn
 35 40 45
 Asp Gly Val Met Gly Glu Tyr Glu Pro Lys Ile Glu Val Gln Phe Pro
 50 55 60
 Glu Thr Val Pro Thr Ala Lys Gly Ala Thr Val Lys Leu Glu Cys Phe
 65 70 75 80
 Ala Leu Gly Asn Pro Val Pro Thr Ile Ile Trp Arg Arg Ala Asp Gly
 85 90 95
 Lys Pro Ile Ala Arg Lys Ala Arg Arg His Lys Ser Arg Val Gly Lys
 100 105 110 112

<210> 879
 <211> 282
 <212> Amino acid
 <213> Homo sapiens

<400> 879
 Met Leu Arg Thr Cys Tyr Val Leu Cys Ser Gln Ala Gly Pro Arg Ser
 1 5 10 15
 Arg Gly Trp Gln Ser Leu Ser Phe Asp Gly Gly Ala Phe His Leu Lys
 20 25 30
 Gly Thr Gly Glu Leu Thr Arg Ala Leu Leu Val Leu Arg Leu Cys Ala
 35 40 45
 Trp Pro Pro Leu Val Thr His Gly Leu Leu Leu Gln Ala Trp Ser Arg
 50 55 60
 Arg Leu Leu Gly Ser Arg Leu Ser Gly Ala Phe Leu Arg Ala Ser Val
 65 70 75 80
 Tyr Gly Gln Phe Val Ala Gly Glu Thr Ala Glu Glu Val Lys Gly Cys
 85 90 95
 Val Gln Gln Leu Arg Thr Leu Ser Leu Arg Pro Leu Leu Ala Val Pro
 100 105 110
 Thr Glu Glu Glu Pro Asp Ser Ala Ala Lys Ser Gly Glu Ala Trp Tyr
 115 120 125

Glu Gly Asn Leu Gly Ala Met Leu Arg Cys Val Asp Leu Ser Arg Gly
 130 135 140
 Leu Leu Glu Pro Pro Ser Leu Ala Glu Ala Ser Leu Met Gln Leu Lys
 145 150 155 160
 Val Thr Ala Leu Thr Ser Thr Arg Leu Cys Lys Glu Leu Ala Ser Trp
 165 170 175
 Val Arg Arg Pro Gly Ala Ser Leu Glu Leu Ser Pro Glu Arg Leu Ala
 180 185 190
 Glu Ala Met Asp Ser Gly Gln Asn Leu Gln Val Ser Cys Leu Asn Ala
 195 200 205
 Glu Gln Asn Gln His Leu Arg Ala Ser Leu Ser Arg Leu His Arg Val
 210 215 220
 Ala Gln Tyr Ala Arg Ala Gln His Val Arg Leu Leu Val Asp Ala Glu
 225 230 235 240
 Tyr Thr Ser Leu Asn Pro Ala Leu Ser Leu Leu Val Ala Ala Leu Ala
 245 250 255
 Val Arg Trp Asn Ser Pro Gly Glu Gly Pro Trp Val Trp Asn Thr
 260 265 270
 Tyr Gln Ala Cys Leu Lys Asp Thr Phe *
 275 280 281

<210> 880
 <211> 29
 <212> Amino acid
 <213> Homo sapiens

<400> 880
 Pro His His Arg Ile Ala Gly Asp Thr Ala Ile Asp Lys Asn Ile His
 1 5 10 15
 Gln Ser Val Ser Glu Gln Ile Lys Lys Asn Phe Ala Lys
 20 25 29

<210> 881
 <211> 45
 <212> Amino acid
 <213> Homo sapiens

<400> 881
 Gln Met Thr Asn Pro Phe Phe Leu Cys Phe Thr Thr Met Ile Ser Asn
 1 5 10 15
 Cys Asn Phe Phe Lys Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Asp
 20 25 30
 Arg Gly Pro Thr Gly Glu Ser Gly Pro Arg Gly Phe Pro
 35 40 45

<210> 882
 <211> 54
 <212> Amino acid
 <213> Homo sapiens

<400> 882

Asn Gly Ile Ile Ala Ser Phe Phe Leu Arg Thr Phe Ile Phe Cys Phe
 1 5 10 15
 Ile His Ile Gln Gly Cys Gln Ala Gly Gln Thr Ile Lys Val Gln Val
 20 25 30
 Ser Phe Asp Leu Leu Ser Leu Met Phe Thr Phe Val Ser Pro Cys Thr
 35 40 45
 Asn Asp Leu Ile Ile His
 50 54

<210> 883

<211> 479

<212> Amino acid

<213> Homo sapiens

<400> 883

Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys Leu Met His
 1 5 10 15
 Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe Gln Lys Thr
 20 25 30
 Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys Val Phe Phe
 35 40 45
 Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met Asn Met Asp
 50 55 60
 Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala Tyr Asp Ser
 65 70 75 80
 Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser Ile Gly Pro
 85 90 95
 Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln Asn Tyr Asp
 100 105 110
 Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile Ser Val Ser
 115 120 125
 Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys Ile Thr Phe
 130 135 140
 Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser Leu Cys Ala
 145 150 155 160
 Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp Ser Ser Glu
 165 170 175
 Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser Cys Arg Cys
 180 185 190
 Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly Pro Ser Ile
 195 200 205
 Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln Leu Gly Ile
 210 215 220
 Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr Phe Trp Phe
 225 230 235 240
 Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys Asn Leu Cys
 245 250 255
 Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly Ile Asn Thr
 260 265 270
 Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu Leu His Tyr
 275 280 285
 Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly Ile His Leu
 290 295 300
 Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe Leu His Lys
 305 310 315 320
 Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val Val Gly Phe
 325 330 335

Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys Val Cys Trp
 340 345 350
 Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly Pro Ala Cys
 355 360 365
 Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile Ile Tyr Lys
 370 375 380
 Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser Cys Phe Glu
 385 390 395 400
 Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu Phe Leu Leu
 405 410 415
 Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His Ala Ser Val
 420 425 430
 Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln Gly Met Phe
 435 440 445
 Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln Glu Glu Tyr
 450 455 460
 Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys Leu Arg
 465 470 475 479

<210> 884
 <211> 143
 <212> Amino acid
 <213> Homo sapiens

<400> 884
 Gly Thr Arg Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu
 1 5 10 15
 Leu Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser
 20 25 30
 Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp Val
 35 40 45
 Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val Ile Gly
 50 55 60
 Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu His Ser Met
 65 70 75 80
 Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser Thr Asp Ser Glu
 85 90 95
 Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr Ile Cys Leu Phe Arg
 100 105 110
 Leu Val Asp Asn Glu Gln Leu Asn Leu Glu Asp Glu Asp Ile Glu Ser
 115 120 125
 Ile Asp Ala Thr Lys Leu Ser Arg Phe Ile Glu Ile Asn Ser Leu
 130 135 140 143

<210> 885
 <211> 52
 <212> Amino acid
 <213> Homo sapiens

<400> 885
 Asp Glu Thr Ser Gly Leu Ile Val Arg Glu Val Ser Ile Glu Ile Ser
 1 5 10 15
 Arg Gln Gln Val Glu Glu Leu Phe Gly Pro Glu Asp Tyr Trp Cys Gln
 20 25 30

Cys Val Ala Trp Ser Ser Ala Gly Thr Thr Lys Ser Arg Lys Ala Tyr
 35 40 45
 Val Arg Ile Ala
 50 52

<210> 886
 <211> 40
 <212> Amino acid
 <213> Homo sapiens

<400> 886
 Gly Thr Arg Ser Ile His Val Lys Leu Asp Val Gly Lys Leu His Thr
 1 5 10 15
 Gln Pro Lys Leu Ala Ala Gln Leu Arg Met Val Asp Asp Gly Ser Gly
 20 25 30
 Lys Val Glu Gly Leu Pro Gly Ile
 35 40

<210> 887
 <211> 177
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(177)
 <223> X = any amino acid or stop code

<400> 887
 Xaa Cys Gly Glu Asp Gly Ser Phe Thr Gln Val Gln Cys His Thr Tyr
 1 5 10 15
 Thr Gly Tyr Cys Trp Cys Val Thr Pro Asp Gly Lys Pro Ile Ser Gly
 20 25 30
 Ser Ser Val Gln Asn Lys Thr Pro Val Cys Ser Gly Ser Val Thr Asp
 35 40 45
 Lys Pro Leu Ser Gln Gly Asn Ser Gly Arg Lys Asp Asp Gly Ser Lys
 50 55 60
 Pro Thr Pro Thr Met Glu Thr Gln Pro Val Phe Asp Gly Asp Glu Ile
 65 70 75 80
 Thr Ala Pro Thr Leu Trp Ile Lys His Leu Val Ile Lys Asp Ser Lys
 85 90 95
 Leu Asn Asn Thr Asn Ile Arg Asn Ser Glu Lys Val Tyr Ser Cys Asp
 100 105 110
 Gln Glu Arg Gln Ser Ala Leu Glu Glu Ala Gln Gln Asn Pro Arg Glu
 115 120 125
 Gly Ile Val Ile Pro Glu Cys Ala Pro Gly Gly Leu Tyr Lys Pro Val
 130 135 140
 Gln Cys His Gln Ser Thr Gly Tyr Cys Trp Cys Val Leu Val Asp Thr
 145 150 155 160
 Gly Arg Pro Leu Pro Gly Thr Ser Thr Arg Tyr Val Met Pro Ser Xaa
 165 170 175 176

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<210> 888
 <211> 48
 <212> Amino acid
 <213> Homo sapiens

<400> 888
 Val Leu Gln Leu Ile Lys Ser Gln Lys Phe Leu Asn Lys Leu Val Ile
 1 5 10 15
 Leu Val Glu Thr Glu Lys Glu Lys Ile Leu Arg Lys Glu Tyr Val Phe
 20 25 30
 Ala Asp Ser Lys Val Ser Asp Ser Lys Leu Leu Lys Trp Ala Val Arg
 35 40 45 48

<210> 889
 <211> 316
 <212> Amino acid
 <213> Homo sapiens

<400> 889
 Arg Arg Leu Ser Leu Leu Asp Leu Gln Leu Gly Pro Leu Gly Arg Asp
 1 5 10 15
 Pro Pro Gln Glu Cys Ser Thr Phe Ser Pro Thr Asp Ser Gly Glu Glu
 20 25 30
 Pro Gly Gln Leu Ser Pro Gly Val Gln Phe Gln Arg Arg Gln Asn Gln
 35 40 45
 Arg Arg Phe Ser Met Glu Asp Val Ser Lys Arg Leu Ser Leu Pro Met
 50 55 60
 Asp Ile Arg Leu Pro Gln Glu Phe Leu Gln Lys Leu Gln Met Glu Ser
 65 70 75 80
 Pro Asp Leu Pro Lys Pro Leu Ser Arg Met Ser Arg Arg Ala Ser Leu
 85 90 95
 Ser Asp Ile Gly Phe Gly Lys Leu Glu Thr Tyr Val Lys Leu Asp Lys
 100 105 110
 Leu Gly Glu Gly Thr Tyr Ala Thr Val Phe Lys Gly Arg Ser Lys Leu
 115 120 125
 Thr Glu Asn Leu Val Ala Leu Lys Glu Ile Arg Leu Glu His Glu Glu
 130 135 140
 Gly Ala Pro Cys Thr Ala Ile Arg Glu Val Ser Leu Leu Lys Asn Leu
 145 150 155 160
 Lys His Ala Asn Ile Val Thr Leu His Asp Leu Ile His Thr Asp Arg
 165 170 175
 Ser Leu Thr Leu Val Phe Glu Tyr Leu Asp Ser Asp Leu Lys Gln Tyr
 180 185 190
 Leu Asp His Cys Gly Asn Leu Met Ser Met His Asn Val Lys Val Arg
 195 200 205
 Pro Arg Gly Gln Gly Pro Pro Ile Leu Ala Ala Thr Cys Pro Glu Ala
 210 215 220
 Gln Cys Gly Asp Pro Leu Ser Pro Pro Gly Ile Arg Leu Leu Arg Trp
 225 230 235 240
 Leu Lys Pro Ser His Val Gly Lys Arg Glu Arg Ala Met Pro Ser Thr
 245 250 255
 Ser Pro Gly Thr Gly Leu Ser Ala Leu Pro Gln Glu Gln Thr His Thr

260 265 270
 Val Cys His Cys Leu Ala Val Gly Ile Lys Pro Thr Leu Asn Ser Glu
 275 280 285
 His Gln Phe Pro Ser Leu Ser Asn Gly Ser Val Ser Tyr Leu Pro Lys
 290 295 300
 Cys Arg Glu Ala Ser Gly Glu Ala Arg Gly Tyr Glu
 305 310 315 316

<210> 890
 <211> 34
 <212> Amino acid
 <213> Homo sapiens

<400> 890
 His Glu Arg His Glu Pro Ser Pro Thr Ala Leu Ala Phe Gly Asp His
 1 5 10 15
 Pro Ile Val Gln Pro Lys Gln Leu Ser Phe Lys Ile Ile Gln Val Asn
 20 25 30
 Asp Asn
 34

<210> 891
 <211> 68
 <212> Amino acid
 <213> Homo sapiens

<400> 891
 Ala Arg Gly Pro Ser Leu Leu Ser Glu Phe His Pro Gly Ser Asp Arg
 1 5 10 15
 Pro Gln Glu Arg Arg Thr Ser Tyr Glu Pro Ile His Pro Gly Pro Ser
 20 25 30
 Pro Val Asp His Asp Ser Leu Glu Ser Lys Arg Pro Arg Leu Glu Gln
 35 40 45
 Ala Ser Asp Ser His Tyr Gln Gly His Ile Thr Gly Glu Ser Leu Pro
 50 55 60
 Gly Arg Val His
 65 68

<210> 892
 <211> 38
 <212> Amino acid
 <213> Homo sapiens

<400> 892
 Gly Thr Arg Lys Glu Glu Phe Ser Ala Glu Glu Asn Phe Leu Ile Leu
 1 5 10 15
 Thr Glu Met Ala Thr Asn His Val Gln Val Leu Val Glu Phe Thr Lys
 20 25 30
 Lys Leu Pro Gly Ile Phe

35

38

<210> 893
 <211> 195
 <212>Amino acid
 <213> Homo sapiens

<400> 893
 His Thr His Lys Leu Val Ala Pro Arg Pro Gly Leu Pro Pro Thr Ser
 1 5 10 15
 Gln Trp Pro Arg Asp Ala Gly Arg Gln Ala Ser Gly Gly Leu Pro Ser
 20 25 30
 Leu Ser Thr Gly Pro Pro Lys Gly Pro Arg Asp Gly Leu Ala Arg Gly
 35 40 45
 His Pro Ala Glu Trp Leu Ala Gly Ser Pro Gly Asn Asn Ser Pro Thr
 50 55 60
 Gln Gly Ser Leu Pro Pro Gln Leu Asp Leu Tyr Ala Gly Ala Leu Phe
 65 70 75 80
 Val His Ile Cys Leu Gly Trp Asn Phe Tyr Leu Ser Thr Ile Leu Thr
 85 90 95
 Leu Gly Ile Thr Ala Leu Tyr Thr Ile Ala Gly Met Val Pro Ala Ala
 100 105 110
 Gly Arg Ser Thr Gln Gly Thr Cys Lys Gly Val Arg Arg Pro Pro Pro
 115 120 125
 Pro Thr Gly Pro Arg Glu Gln Pro Arg Lys Trp Pro Gln Gln Glu Pro
 130 135 140
 Gln Lys Phe Leu Pro Val Ser Leu Leu Pro Gly Ala Arg Ala Pro Ser
 145 150 155 160
 Ser Asn Leu Ala Ser Thr Gly Arg Gly Pro Gly Cys Cys Asn Leu His
 165 170 175
 Gly Arg Pro Ala Asp Ala His His Gly Gly Gly Cys His Pro Asp
 180 185 190
 Asn Gln Arg
 195

<210> 894
 <211> 87
 <212>Amino acid
 <213> Homo sapiens

<400> 894
 Met Val Asn His Ser Leu Gln Glu Thr Ser Glu Gln Asn Val Ile Leu
 1 5 10 15
 Gln His Thr Leu Gln Gln Gln Gln Met Leu Gln Gln Glu Thr Ile
 20 25 30
 Arg Asn Gly Glu Leu Glu Asp Thr Gln Thr Lys Leu Glu Lys Gln Val
 35 40 45
 Ser Lys Leu Glu Gln Glu Leu Gln Lys Gln Arg Glu Ser Ser Ala Glu
 50 55 60
 Lys Leu Arg Lys Met Glu Glu Lys Cys Glu Ser Ala Ala His Glu Ala
 65 70 75 80
 Asp Leu Lys Arg Gln Lys *
 85 86

<210> 895
 <211> 49
 <212>Amino acid
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(49)
 <223> X = any amino acid or stop code

<400> 895
 Val Cys Pro Lys Trp Cys Arg Phe Leu Thr Met Leu Gly His Cys Cys
 1 5 10 15
 Tyr Phe Trp His Val Trp Pro Ala Ser Xaa Ala Leu Ser Ala Gly Pro
 20 25 30
 Thr Pro Thr Ser Arg Ser Phe Ser Pro Ser Pro Leu Arg Ser Ile Ser
 35 40 45
 Thr
 49

<210> 896
 <211> 128
 <212>Amino acid
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(128)
 <223> X = any amino acid or stop code

<400> 896
 Met Arg Gly Pro Pro Val Leu Leu Leu Gln Ala Ala Pro Met Glu Cys
 1 5 10 15
 Pro Val Pro Gln Gly Ile Pro Ala Gly Ser Ser Pro Glu Pro Ala Pro
 20 25 30
 Asp Pro Pro Gly Pro His Phe Leu Arg Gln Glu Arg Ser Phe Glu Cys
 35 40 45
 Arg Met Cys Gly Lys Ala Phe Lys Arg Ser Ser Thr Leu Ser Thr His
 50 55 60
 Leu Leu Ile His Ser Asp Thr Arg Pro Tyr Pro Cys Gln Phe Cys Gly
 65 70 75 80
 Lys Arg Phe His Gln Lys Ser Asp Met Lys Lys His Thr Tyr Ile His
 85 90 95
 Thr Gly Glu Lys Pro His Lys Cys Gln Thr Gln Arg Glu Pro Thr Met
 100 105 110
 Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Xaa *
 115 120 125 127

<210> 897
 <211> 57
 <212>Amino acid
 <213> Homo sapiens

<400> 897

```

His Glu Gln Leu Thr Asn Asn Thr Ala Thr Ala Pro Ser Ala Thr Pro
 1          5          10          15
Val Phe Gly Gln Val Ala Ala Ser Thr Ala Pro Ser Leu Phe Gly Gln
          20          25          30
Gln Thr Gly Ile Thr Ala Ser Thr Ala Val Ala Thr Pro Gln Val Ile
          35          40          45
Ser Ser Arg Phe Ile Asn Leu Asp Phe
 50          55          57

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<210> 898

<211> 163

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(163)

<223> X = any amino acid or stop code

<400> 898

```

Val Ser Val Phe Lys Asn Cys Pro Met Tyr Xaa Ile Cys Ile Phe Leu
 1          5          10          15
Thr Lys Met Phe Cys Val Leu Ile Ile Xaa Asn Lys Phe Xaa Val His
          20          25          30
Lys Lys Pro Leu Gln Glu Val Glu Ile Ala Ala Ile Thr His Gly Ala
          35          40          45
Leu Gln Gly Leu Ala Tyr Leu His Ser His Thr Met Ile His Arg Asp
          50          55          60
Ile Lys Ala Gly Asn Ile Leu Leu Thr Glu Pro Gly Gln Val Lys Leu
          65          70          75          80
Ala Asp Phe Gly Ser Ala Ser Met Ala Ser Pro Ala Asn Ser Phe Val
          85          90          95
Gly Thr Pro Tyr Trp Met Ala Pro Glu Val Ile Leu Ala Met Asp Glu
          100          105          110
Gly Gln Tyr Asp Gly Lys Val Asp Val Trp Ser Leu Gly Ile Thr Cys
          115          120          125
Ile Glu Leu Ala Glu Arg Lys Pro Pro Leu Phe Asn Met Asn Ala Met
          130          135          140
Ser Ala Leu Tyr His Ile Ala Gln Asn Glu Ser Pro Thr Leu Gln Ser
          145          150          155          160
Asn Glu Trp
          163

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<210> 899

<211> 352

<212>Amino acid

<213> Homo sapiens

<400> 899

```

Arg His Ala Arg Pro Gly Gly Gly Gly His Ser Asn Gln Arg Lys Met
 1          5          10          15
Ser Leu Glu Gln Glu Glu Glu Thr Gln Pro Gly Arg Leu Leu Gly Arg
      20          25          30
Arg Asp Ala Val Pro Ala Phe Ile Glu Pro Asn Val Arg Phe Trp Ile
      35          40          45
Thr Glu Arg Gln Ser Phe Ile Arg Arg Phe Leu Gln Trp Thr Glu Leu
      50          55          60
Leu Asp Pro Thr Asn Val Phe Ile Ser Val Glu Ser Ile Glu Asn Ser
      65          70          75          80
Arg Gln Leu Leu Cys Thr Asn Glu Asp Val Ser Ser Pro Ala Ser Ala
      85          90          95
Asp Gln Arg Ile Gln Glu Ala Trp Lys Arg Ser Leu Ala Thr Val His
      100          105          110
Pro Asp Ser Ser Asn Leu Ile Pro Lys Leu Phe Arg Pro Ala Ala Phe
      115          120          125
Leu Pro Phe Met Ala Pro Thr Val Phe Leu Ser Met Thr Pro Leu Lys
      130          135          140
Gly Ile Lys Ser Val Ile Leu Pro Gln Val Phe Leu Cys Ala Tyr Met
      145          150          155          160
Ala Ala Phe Asn Ser Ile Asn Gly Asn Arg Ser Tyr Thr Cys Lys Pro
      165          170          175
Leu Glu Arg Ser Leu Leu Met Ala Gly Ala Val Ala Ser Ser Thr Phe
      180          185          190
Leu Gly Val Ile Pro Gln Phe Val Gln Met Lys Tyr Gly Leu Thr Gly
      195          200          205
Pro Trp Ile Lys Arg Leu Leu Pro Val Ile Phe Leu Val Gln Ala Ser
      210          215          220
Gly Met Asn Val Tyr Met Ser Arg Ser Leu Glu Ser Ile Lys Gly Ile
      225          230          235          240
Ala Val Met Asp Lys Glu Gly Asn Val Leu Gly His Ser Arg Ile Ala
      245          250          255
Gly Thr Lys Ala Val Arg Glu Thr Leu Ala Ser Arg Ile Val Leu Phe
      260          265          270
Gly Thr Ser Ala Leu Ile Pro Glu Val Phe Thr Tyr Phe Phe Lys Arg
      275          280          285
Thr Gln Tyr Phe Arg Lys Asn Pro Gly Ser Leu Trp Ile Leu Lys Leu
      290          295          300
Ser Cys Thr Val Leu Ala Met Gly Leu Met Val Pro Phe Ser Phe Ser
      305          310          315          320
Ile Phe Pro Gln Ile Gly Gln Ile Gln Tyr Cys Ser Leu Glu Glu Lys
      325          330          335
Ile Gln Ser Pro Thr Glu Glu Thr Glu Ile Phe Tyr His Arg Gly Val
      340          345          350          352

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<210> 900

<211> 186

<212> Amino acid

<213> Homo sapiens

<400> 900

```

His Ala Ser Gly Arg Leu Glu Val Phe Tyr Asn Gly Thr Trp Gly Ser
 1          5          10          15
Val Gly Arg Arg Asn Ile Thr Thr Ala Ile Ala Gly Ile Val Cys Arg
      20          25          30
Gln Leu Gly Cys Gly Glu Asn Gly Val Val Ser Leu Ala Pro Leu Ser
      35          40          45

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Lys Thr Gly Ser Gly Phe Met Trp Val Asp Asp Ile Gln Cys Pro Lys
  50          55          60
Thr His Ile Ser Ile Trp Gln Cys Leu Ser Ala Pro Trp Glu Arg Arg
  65          70          75          80
Ile Ser Ser Pro Ala Glu Glu Thr Trp Ile Thr Cys Glu Asp Arg Ile
          85          90          95
Arg Val Arg Gly Gly Asp Thr Glu Cys Ser Gly Arg Val Glu Ile Trp
          100          105          110
His Ala Gly Ser Trp Gly Thr Val Cys Asp Asp Ser Trp Asp Leu Ala
          115          120          125
Glu Ala Glu Val Val Cys Gln Gln Leu Gly Cys Gly Ser Ala Leu Ala
          130          135          140
Ala Leu Arg Asp Ala Ser Phe Gly Gln Gly Thr Gly Thr Ile Trp Leu
          145          150          155          160
Asp Asp Met Arg Cys Lys Gly Asn Glu Ser Phe Leu Trp Asp Cys His
          165          170          175
Ala Lys Pro Trp Gly Gln Ser Asp Cys Gly
          180          185 186

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<210> 901
 <211> 365
 <212> Amino acid
 <213> Homo sapiens

```

          <400> 901
Leu Gly Asp Phe Pro Gln Pro Gln Arg Gln Arg Arg Pro Gly Ala Ser
  1          5          10          15
Asp Leu Pro Pro His Leu Ala Gly Ala Arg Gln Trp Glu Val Arg Phe
          20          25          30
Phe Arg His Leu Pro Ala Arg Thr Leu Pro Pro Ser Leu Arg Met Pro
          35          40          45
Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu Ala Cys
          50          55          60
Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val Ser Arg
          65          70          75          80
Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser Ala Ser
          85          90          95
Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro Gly Ala
          100          105          110
Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly Met Ser
          115          120          125
Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His Ala His
          130          135          140
Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu Cys Phe
          145          150          155          160
Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys Trp Gln
          165          170          175
Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe Arg Glu
          180          185          190
Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro Ile Cys
          195          200          205
Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn Tyr Leu
          210          215          220
Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala
          225          230          235          240
Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro Glu Leu
          245          250          255
Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp Leu Leu
          260          265          270

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Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly Gly Arg
 275 280 285
 Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe Arg Ala
 290 295 300
 Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln Asp Arg
 305 310 315 320
 His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu Ala Pro
 325 330 335
 Lys Gly Arg Lys Ser Arg Lys Lys Lys Ser Lys Ala Thr Gln Leu Ser
 340 345 350
 Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys
 355 360 365

<210> 902
 <211> 110
 <212> Amino acid
 <213> Homo sapiens

<400> 902
 Leu Thr Trp Ser Ala Cys Tyr Trp Arg Asp Ile Leu Arg Ile Gln Leu
 1 5 10 15
 Trp Ile Ala Ala Asp Ile Leu Leu Arg Met Leu Glu Lys Ala Leu Leu
 20 25 30
 Tyr Ser Glu His Gln Asn Ile Ser Asn Thr Gly Leu Ser Ser Gln Gly
 35 40 45
 Leu Leu Ile Phe Ala Glu Leu Ile Pro Ala Ile Lys Arg Thr Leu Ala
 50 55 60
 Arg Leu Leu Val Ile Ile Ala Ser Leu Asp Tyr Gly Ile Glu Lys Pro
 65 70 75 80
 His Leu Gly Thr Gly Met His Arg Val Ile Gly Leu Met Leu Leu Tyr
 85 90 95
 Leu Ile Phe Ala Asn Ala Glu Ser Val Ile Arg Val Ile Gly
 100 105 110

<210> 903
 <211> 44
 <212> Amino acid
 <213> Homo sapiens

<400> 903
 Phe Phe Phe Glu Met Glu Ser Arg Ser Ala Ala Gln Ala Gly Val Gln
 1 5 10 15
 Trp Cys Asn Leu Gly Ser Leu Gln Ala Leu Pro Pro Arg Phe Thr Pro
 20 25 30
 Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr
 35 40 44

<210> 904
 <211> 190
 <212> Amino acid
 <213> Homo sapiens

<400> 904

```

Tyr Glu Cys Glu Glu Leu Ala Lys Lys Leu Glu Asn Ser Gln Arg Asp
 1          5          10          15
Gly Ile Ser Arg Asn Lys Leu Ala Leu Ala Glu Leu Tyr Glu Asp Glu
          20          25          30
Val Lys Cys Lys Ser Ser Lys Ser Asn Arg Pro Lys Ala Thr Val Phe
          35          40          45
Lys Ser Pro Arg Thr Pro Pro Gln Arg Phe Tyr Ser Ser Glu His Glu
          50          55          60
Tyr Ser Gly Leu Asn Ile Val Arg Pro Ser Thr Gly Lys Ile Val Asn
          65          70          75          80
Glu Leu Phe Lys Glu Ala Arg Glu His Gly Ala Val Pro Leu Asn Glu
          85          90          95
Ala Thr Arg Ala Ser Gly Asp Asp Lys Ser Lys Ser Phe Thr Gly Gly
          100          105          110
Gly Tyr Arg Leu Gly Ser Ser Phe Cys Lys Arg Ser Glu Tyr Ile Tyr
          115          120          125
Gly Glu Asn Gln Leu Gln Asp Val Gln Ile Leu Leu Lys Leu Trp Ser
          130          135          140
Asn Gly Phe Ser Leu Asp Asp Gly Glu Leu Arg Pro Tyr Asn Glu Pro
          145          150          155          160
Thr Asn Ala Gln Phe Leu Glu Ser Val Lys Arg Gly Val Thr Leu Ile
          165          170          175
Ala Cys Met Pro Glu Ile Gln Gln Leu Met Leu Glu Ile Phe
          180          185          190

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<210> 905

<211> 414

<212> Amino acid

<213> Homo sapiens

<400> 905

```

Trp Pro Cys Gly Ala Ala Pro Gly Leu Thr His Ala Ser Glu Arg Met
 1          5          10          15
Phe Thr Leu Thr Thr Met Ile Gln Ala Leu Ala Pro Val Met Gly Trp
          20          25          30
Asp Arg Lys Pro Leu Lys Met Phe Ser Ser Glu Glu Met Arg Gly His
          35          40          45
Leu His His His His Lys Cys Leu Thr Lys Ile Leu Lys Val Glu Gly
          50          55          60
Gln Val Pro Asp Leu Pro Ser Cys Leu Pro Leu Thr Asp Asn Thr Arg
          65          70          75          80
Met Leu Ala Ser Ile Leu Ile Asn Met Leu Tyr Asp Asp Leu Arg Cys
          85          90          95
Asp Pro Glu Arg Asp His Phe Arg Lys Ile Cys Glu Glu Tyr Ile Thr
          100          105          110
Gly Lys Phe Asp Pro Gln Asp Met Asp Lys Asn Leu Asn Ala Ile Gln
          115          120          125
Thr Val Ser Gly Ile Leu Gln Gly Pro Phe Asp Leu Gly Asn Gln Leu
          130          135          140
Leu Gly Leu Lys Gly Val Met Glu Met Met Val Ala Leu Cys Gly Ser
          145          150          155          160
Glu Arg Glu Thr Asp Gln Leu Val Ala Val Glu Ala Leu Ile His Ala
          165          170          175
Ser Thr Lys Leu Ser Arg Ala Thr Phe Ile Ile Thr Asn Gly Val Ser
          180          185          190

```

Leu Leu Lys Gln Ile Tyr Lys Thr Thr Lys Asn Glu Lys Ile Lys Ile
 195 200 205
 Arg Thr Leu Val Gly Leu Cys Lys Leu Gly Ser Ala Gly Gly Thr Asp
 210 215 220
 Tyr Gly Leu Arg Gln Phe Ala Glu Gly Ser Thr Glu Lys Leu Ala Lys
 225 230 235 240
 Gln Cys Arg Lys Trp Leu Cys Asn Met Ser Ile Asp Thr Arg Thr Arg
 245 250 255
 Arg Trp Ala Val Glu Gly Leu Ala Tyr Leu Thr Leu Asp Ala Asp Val
 260 265 270
 Lys Asp Asp Phe Val Gln Asp Val Pro Ala Leu Gln Ala Met Phe Glu
 275 280 285
 Leu Ala Lys Thr Ser Asp Lys Thr Ile Leu Tyr Ser Val Ala Thr Thr
 290 295 300
 Leu Val Asn Cys Thr Asn Ser Tyr Asp Val Lys Glu Val Ile Pro Glu
 305 310 315 320
 Leu Val Gln Leu Ala Lys Phe Ser Lys Gln His Val Pro Glu Glu His
 325 330 335
 Pro Lys Asp Lys Lys Asp Phe Ile Asp Met Arg Val Lys Arg Leu Leu
 340 345 350
 Lys Ala Gly Val Ile Ser Ala Leu Ala Cys Met Val Lys Ala Asp Ser
 355 360 365
 Ala Ile Leu Thr Asp Gln Thr Lys Glu Leu Leu Ala Arg Val Phe Leu
 370 375 380
 Ala Leu Cys Asp Asn Pro Lys Asp Arg Gly Thr Ile Val Ala Gln Gly
 385 390 395 400
 Gly Gly Lys Ala Leu Ile Pro Leu Ala Leu Glu Gly Thr Asp
 405 410 414

<210> 906
 <211> 296
 <212> Amino acid
 <213> Homo sapiens

<400> 906
 Val Asp Ser Val Gly Gly Gly Ser Glu Ser Arg Ser Leu Asp Ser Pro
 1 5 10 15
 Thr Ser Ser Pro Gly Ala Gly Thr Arg Gln Leu Val Lys Ala Ser Ser
 20 25 30
 Thr Gly Thr Glu Ser Ser Asp Asp Phe Glu Glu Arg Asp Pro Asp Leu
 35 40 45
 Gly Asp Gly Leu Glu Asn Gly Leu Gly Ser Pro Phe Gly Lys Trp Thr
 50 55 60
 Leu Ser Ser Ala Ala Gln Thr His Gln Leu Arg Arg Leu Arg Gly Pro
 65 70 75 80
 Ala Lys Cys Arg Glu Cys Glu Ala Phe Met Val Ser Gly Thr Glu Cys
 85 90 95
 Glu Glu Cys Phe Leu Thr Cys His Lys Arg Cys Leu Glu Thr Leu Leu
 100 105 110
 Ile Leu Cys Gly His Arg Arg Leu Pro Ala Arg Thr Pro Leu Phe Gly
 115 120 125
 Val Asp Phe Leu Gln Leu Pro Arg Asp Phe Pro Glu Val Pro Phe
 130 135 140
 Val Val Thr Lys Cys Thr Ala Glu Ile Glu His Arg Ala Leu Asp Val
 145 150 155 160
 Gln Gly Ile Tyr Arg Val Ser Gly Ser Arg Val Arg Val Glu Arg Leu
 165 170 175
 Cys Gln Ala Phe Glu Asn Gly Arg Ala Leu Val Glu Leu Ser Gly Asn
 180 185 190

```

Ser Pro His Asp Val Ser Ser Val Leu Lys Arg Phe Leu Gln Glu Leu
      195                200                205
Thr Glu Pro Val Ile Pro Phe His Leu Tyr Asp Ala Phe Ile Ser Leu
      210                215                220
Ala Lys Thr Leu His Ala Asp Pro Gly Asp Asp Pro Gly Thr Pro Ser
225                230                235                240
Pro Ser Pro Glu Val Ile Arg Ser Leu Lys Thr Leu Leu Val Gln Leu
      245                250                255
Pro Asp Ser Asn Tyr Asn Thr Leu Arg His Leu Val Ala His Leu Phe
      260                265                270
Arg Val Ala Ala Arg Phe Met Glu Asn Lys Met Ser Ala Asn Asn Leu
      275                280                285
Gly Ile Val Phe Gly Pro Thr Leu
      290                295 296

```

```

<210> 907
<211> 131
<212>Amino acid
<213> Homo sapiens

```

```

<400> 907
Gly Leu His Val Ile Ser Leu His Ser Ala Asp Gly Arg His Trp Glu
 1                5                10                15
Asp Pro Leu Ser Glu Leu Asp Ser Glu Arg Val Ser Ala Phe Leu Val
      20                25                30
Thr Glu Thr Leu Val Phe Tyr Leu Phe Cys Leu Leu Ala Asp Glu Thr
      35                40                45
Val Val Pro Pro Asp Val Pro Ser Tyr Leu Ser Ser Gln Gly Thr Leu
      50                55                60
Ser Asp Arg Gln Glu Thr Val Val Arg Thr Glu Gly Gly Pro Gln Ala
65                70                75                80
Asn Gly His Ile Glu Ser Asn Gly Lys Ala Ser Val Thr Val Lys Gln
      85                90                95
Ser Ser Ala Val Thr Val Ser Leu Gly Ala Gly Gly Gly Leu Gln Val
      100                105                110
Phe Thr Gly Gln Val Pro Gly Ile Arg Trp Gly Lys Leu Gly Glu Ala
      115                120                125
His Ala Ser
130 131

```

```

<210> 908
<211> 124
<212>Amino acid
<213> Homo sapiens

```

```

<400> 908
Lys Ile Lys His Arg Pro Glu Glu Glu Pro Arg Trp Ala Ala Ala Gly
 1                5                10                15
Ala Gln Ser Ala Gly Pro Gly Ala Ala Glu Val Ala Pro Pro Arg Pro
      20                25                30
Gly Thr Val Ala Pro Gly Ala Asn Gly Met Thr Asp Ser Ala Thr Ala
      35                40                45
Asn Gly Asp Asp Arg Asp Pro Glu Ile Glu Leu Phe Val Lys Ala Gly
      50                55                60

```

Ile Asp Gly Glu Ser Ile Gly Asn Cys Pro Phe Ser Gln Arg Leu Phe
 65 70 75 80
 Met Ile Leu Trp Leu Lys Gly Val Val Phe Asn Val Thr Thr Val Asp
 85 90 95
 Leu Lys Arg Lys Pro Ala Asp Leu Arg Asn Leu Ala Pro Gly Thr His
 100 105 110
 Pro Pro Phe Leu Ala Phe Asn Trp Tyr Val Lys Thr
 115 120 124

<210> 909

<211> 111

<212>Amino acid

<213> Homo sapiens

<400> 909

Leu Gly Phe Ser Asp Gly Gln Glu Ala Arg Pro Glu Glu Ile Gly Trp
 1 5 10 15
 Leu Asn Gly Tyr Asn Glu Thr Thr Gly Glu Arg Gly Asp Phe Pro Gly
 20 25 30
 Thr Tyr Val Glu Tyr Ile Gly Arg Lys Lys Ile Ser Pro Pro Thr Pro
 35 40 45
 Lys Pro Arg Pro Pro Arg Pro Leu Pro Val Ala Pro Gly Ser Ser Lys
 50 55 60
 Thr Glu Ala Asp Val Glu Gln Gln Val Leu Tyr Lys Tyr Arg Lys Lys
 65 70 75 80
 Pro Ser Ser Ser His Arg Pro Gln Thr Pro His Asn Gly Lys Ser Lys
 85 90 95
 Asn Phe Leu His Lys Gln Gly Leu Lys Lys Lys Lys Ala Ser Leu
 100 105 110 111

<210> 910

<211> 298

<212>Amino acid

<213> Homo sapiens

<400> 910

Arg Thr Arg Gly Val Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro
 1 5 10 15
 Arg Trp Leu Leu Leu Leu Pro Leu Leu Gly Leu Asn Ala Gly Ala
 20 25 30
 Val Ile Asp Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val
 35 40 45
 Thr Val Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr
 50 55 60
 Asn Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln
 65 70 75 80
 Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile
 85 90 95
 Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln
 100 105 110
 Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr Gly Phe Ser
 115 120 125
 Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu Ala Met Val Ala
 130 135 140

```

Ser Asp Met Met Gly Leu Leu Lys Thr Phe Phe Ser Cys His Lys Glu
145          150          155          160
Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu Ser Tyr Gly Gly Lys
          165          170          175
Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly
          180          185          190
Thr Ile Lys Cys Asn Phe Ala Gly Val Ala Leu Gly Asp Ser Trp Ile
          195          200          205
Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met
          210          215          220
Ser Leu Leu Glu Asp Lys Gly Leu Ala Glu Val Ser Lys Val Ala Glu
225          230          235          240
Gln Val Leu Asn Ala Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu
          245          250          255
Leu Trp Gly Lys Ala Glu Met Ile Ile Glu Gln Val Lys Arg Gly Asn
          260          265          270
Thr Gln Arg Arg Ala Cys Leu Ala Phe Ser Gly Gly Tyr Arg Ala His
          275          280          285
Gly Trp Cys Cys Gln Thr Trp Ser Leu His
          290          295          298

```

<210> 911

<211> 213

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(213)

<223> X = any amino acid or stop code

<400> 911

```

Pro Gly Trp Ser Arg Ser Pro Asp Leu Val Ile Arg Leu Pro Arg Pro
1          5          10          15
Pro Lys Val Leu Gly Leu Gln Tyr Tyr His Phe Phe Phe Phe Leu Arg
          20          25          30
Trp Ser Leu Asp Ser Val Ala Gln Ala Glu Val Gln Trp His Asp Leu
          35          40          45
Arg Ser Leu Gln Ala Pro Pro Pro Gly Phe Thr Pro Phe Ser Cys Leu
          50          55          60
Ser Leu Pro Gly Ser Trp Asp Tyr Arg Cys Pro Pro Arg Pro Ala
          65          70          75          80
Asn Phe Leu Tyr Phe Xaa Xaa Arg Arg Gly Phe Thr Val Leu Ala Arg
          85          90          95
Met Val Ser Ile Ser Xaa Pro Arg Asp Pro Pro Ala Ser Ala Ser Gln
          100          105          110
Ser Ala Gly Ile Thr Val Leu Ser Leu Phe Phe Phe Phe Glu Met Glu
          115          120          125
Ser Cys Ser Val Ala Gln Ala Gly Val Gln Trp Arg Tyr Leu Gly Ser
          130          135          140
Leu Gln Ala Leu Pro Pro Gly Phe Thr Pro Phe Ser Cys Leu Ser Leu
145          150          155          160
Pro Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Pro Ala Asn Phe
          165          170          175
Phe Val Phe Leu Val Glu Thr Gly Val Ser Pro Cys Xaa Pro Gly Trp
          180          185          190
Ser Arg Ser Pro Asp Leu Val Ile Arg Leu Pro Gln Pro Pro Lys Val
          195          200          205
Leu Gly Leu Gln Val

```

210

213

<210> 912

<211> 583

<212>Amino acid

<213> Homo sapiens

<400> 912

```

Pro Ser Met Lys Thr Gly Glu Leu Glu Lys Glu Thr Ala Pro Leu Arg
 1      5      10      15
Lys Asp Ala Asp Ser Ser Ile Ser Val Leu Glu Ile His Ser Gln Lys
      20      25      30
Ala Gln Ile Glu Glu Pro Asp Pro Pro Glu Met Glu Thr Ser Leu Asp
      35      40      45
Ser Ser Glu Met Ala Lys Asp Leu Ser Ser Lys Thr Ala Leu Ser Ser
      50      55      60
Thr Glu Ser Cys Thr Met Lys Gly Glu Glu Lys Ser Pro Lys Thr Lys
      65      70      75      80
Lys Asp Lys Arg Pro Pro Ile Leu Glu Cys Leu Glu Lys Leu Glu Lys
      85      90      95
Ser Lys Lys Thr Phe Leu Asp Lys Asp Ala Gln Arg Leu Ser Pro Ile
      100      105      110
Pro Glu Glu Val Pro Lys Ser Thr Leu Glu Ser Glu Lys Pro Gly Ser
      115      120      125
Pro Glu Ala Ala Glu Thr Ser Pro Pro Ser Asn Ile Ile Asp His Cys
      130      135      140
Glu Lys Leu Ala Ser Glu Lys Glu Val Val Glu Cys Gln Ser Thr Ser
145      150      155      160
Thr Val Gly Gly Gln Ser Val Lys Lys Val Asp Leu Glu Thr Leu Lys
      165      170      175
Glu Asp Ser Glu Phe Thr Lys Val Glu Met Asp Asn Leu Asp Asn Ala
      180      185      190
Gln Thr Ser Gly Ile Glu Glu Pro Ser Glu Thr Lys Gly Ser Met Gln
      195      200      205
Lys Ser Lys Phe Lys Tyr Lys Leu Val Pro Glu Glu Glu Thr Thr Ala
      210      215      220
Ser Glu Asn Thr Glu Ile Thr Ser Glu Arg Gln Lys Glu Gly Ile Lys
225      230      235      240
Leu Thr Ile Arg Ile Ser Ser Arg Lys Lys Lys Pro Asp Ser Pro Pro
      245      250      255
Lys Val Leu Glu Pro Glu Asn Lys Gln Glu Lys Thr Glu Lys Glu Glu
      260      265      270
Glu Lys Thr Asn Val Gly Arg Thr Leu Arg Arg Ser Pro Arg Ile Ser
      275      280      285
Arg Pro Thr Ala Lys Val Ala Glu Ile Arg Asp Gln Lys Ala Asp Lys
      290      295      300
Lys Arg Gly Glu Gly Glu Asp Glu Val Glu Glu Glu Ser Thr Ala Leu
305      310      315      320
Gln Lys Thr Asp Lys Lys Glu Ile Leu Lys Lys Ser Glu Lys Asp Thr
      325      330      335
Asn Ser Lys Val Ser Lys Val Lys Pro Lys Gly Lys Val Arg Trp Thr
      340      345      350
Gly Ser Arg Thr Arg Gly Arg Trp Lys Tyr Ser Ser Asn Asp Glu Ser
      355      360      365
Glu Gly Ser Gly Ser Glu Lys Ser Ser Ala Ala Ser Glu Glu Glu
      370      375      380
Glu Lys Glu Ser Glu Glu Ala Ile Leu Ala Asp Asp Asp Glu Pro Cys
385      390      395      400
Lys Lys Cys Gly Leu Pro Asn His Pro Glu Leu Ile Leu Leu Cys Asp

```



```
<210> 913
<211> 178
<212> Amino acid
<213> Homo sapiens
```

<210> 914
<211> 158
<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(158)

<223> X = any amino acid or stop code

<400> 914

```

Met Pro Glu Tyr Leu Arg Lys Arg Phe Gly Gly Ile Arg Ile Pro Ile
 1           5           10           15
Ile Leu Ala Val Leu Tyr Leu Phe Ile Tyr Ile Phe Thr Lys Ile Ser
      20           25           30
Val Asp Met Tyr Ala Gly Ala Ile Phe Ile Gln Gln Ser Leu His Leu
      35           40           45
Asp Leu Tyr Leu Ala Ile Val Gly Leu Leu Ala Ile Thr Ala Val Tyr
      50           55           60
Thr Val Ala Gly Gly Leu Ala Ala Val Ile Tyr Thr Asp Ala Leu Gln
      65           70           75           80
Thr Leu Ile Met Leu Ile Gly Ala Leu Thr Leu Met Gly Tyr Ser Phe
      85           90           95
Ala Ala Val Gly Gly Met Glu Gly Leu Lys Glu Lys Tyr Phe Leu Ala
      100          105          110
Leu Ala Ser Asn Arg Ser Glu Asn Ser Ser Cys Gly Leu Pro Arg Glu
      115          120          125
Asp Ala Phe His Ile Phe Arg Asp Pro Leu Thr Ser Asp Leu Pro Trp
      130          135          140
Pro Gly Val Leu Phe Gly Met Ser Ile Pro Ser Leu Xaa *
145          150          155          157

```

<210> 915

<211> 108

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(108)

<223> X = any amino acid or stop code

<400> 915

```

Xaa Ser Ala Ser Ala Thr Ser Leu Thr Leu Ser His Cys Val Asp Val
 1           5           10           15
Val Lys Gly Leu Leu Asp Phe Lys Lys Arg Arg Gly His Ser Ile Gly
      20           25           30
Gly Ala Pro Glu Gln Arg Tyr Gln Ile Ile Pro Val Met Cys Cys Ser
      35           40           45
Leu Leu Ala Thr Gly Gly Ala Asp Arg Leu Ile His Leu Trp Asn Val
      50           55           60
Val Gly Ser Arg Leu Glu Ala Asn Gln Thr Leu Glu Gly Ala Gly Gly
      65           70           75           80
Ser Ile Thr Ser Val Asp Phe Asp Pro Ser Gly Tyr Gln Val Leu Ala
      85           90           95
Ala Thr Tyr Asn Gln Val Ala Gln Phe Trp Lys *
      100          105          107

```

<210> 916
 <211> 45
 <212>Amino acid
 <213> Homo sapiens

<400> 916
 Gln Lys Arg Phe Pro Ser Asn Cys Gly Arg Asp Gly Lys Leu Phe Leu
 1 5 10 15
 Trp Gly Gln Ala Leu His Ile Ile Ala Lys Leu Leu Gly Lys Trp Arg
 20 25 30
 Arg Leu Gly Met Val Phe Phe Ser Leu Leu Leu Ser Tyr
 35 40 45

<210> 917
 <211> 180
 <212>Amino acid
 <213> Homo sapiens

<400> 917
 Val His Val Cys Ser Ser Lys Met Gly Ala Leu Ser Thr Glu Arg Leu
 1 5 10 15
 Gln Tyr Tyr Thr Gln Glu Leu Gly Val Arg Glu Arg Ser Gly His Ser
 20 25 30
 Val Ser Leu Ile Asp Leu Trp Gly Leu Leu Val Glu Tyr Leu Leu Tyr
 35 40 45
 Gln Glu Glu Asn Pro Ala Lys Leu Ser Asp Gln Gln Glu Ala Val Arg
 50 55 60
 Gln Gly Gln Asn Pro Tyr Pro Ile Tyr Thr Ser Val Asn Val Arg Thr
 65 70 75 80
 Asn Leu Ser Gly Glu Asp Phe Ala Glu Trp Cys Glu Phe Thr Pro Tyr
 85 90 95
 Glu Val Gly Phe Pro Lys Tyr Gly Ala Tyr Val Pro Thr Glu Leu Phe
 100 105 110
 Gly Ser Glu Leu Phe Met Gly Arg Leu Leu Gln Leu Gln Pro Glu Pro
 115 120 125
 Arg Ile Cys Tyr Leu Gln Gly Met Trp Gly Ser Ala Phe Ala Thr Ser
 130 135 140
 Leu Asp Glu Ile Phe Leu Lys Thr Ala Gly Ser Gly Leu Ser Phe Leu
 145 150 155 160
 Glu Trp Tyr Arg Gly Ser Val Asn Ile Thr Asp Asp Cys Gln Lys Pro
 165 170 175
 Gln Leu His Asn
 180

<210> 918
 <211> 281
 <212>Amino acid
 <213> Homo sapiens

<400> 918

Glu Phe Leu Gly Arg Pro Thr Arg Pro Ala Lys Asp Glu Gly Asn Asp
 1 5 10 15
 Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp
 20 25 30
 Glu Gly Lys Asp Glu Gly Lys Asp Glu Arg Lys Asp Glu Gly Lys Asp
 35 40 45
 Glu Gly Lys Asp Glu Arg Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp
 50 55 60
 Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp
 65 70 75 80
 Glu Gly Lys Asp Glu Gly Asn Asp Glu Gly Lys Asp Glu Gly Lys Asp
 85 90 95
 Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp
 100 105 110
 Glu Arg Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp Glu Arg Lys Asp
 115 120 125
 Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp
 130 135 140
 Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Asn Asp
 145 150 155 160
 Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp
 165 170 175
 Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Asn Asp Glu Gly Asn Asp
 180 185 190
 Glu Gly Asn Asp Glu Gly Lys Asp Glu Gly Lys Asp Glu Arg Asn Asp
 195 200 205
 Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp
 210 215 220
 Glu Arg Asn Asp Glu Gly Lys Asp Glu Arg Lys Asp Glu Gly Lys Asp
 225 230 235 240
 Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp Glu Gly Lys Asp
 245 250 255
 Glu Gly Asn Asp Glu Gly Lys Asp Glu Arg Lys Asp Glu Gly Lys Asp
 260 265 270
 Glu Gly Lys Asp Glu Gly Lys Asp Lys
 275 280 281

<210> 919

<211> 147

<212> Amino acid

<213> Homo sapiens

<400> 919

Pro Ser Leu Arg Pro Ala Trp His Glu Gly Glu Asp Phe Ser Tyr Gly
 1 5 10 15
 Leu Gln Pro Tyr Cys Gly Tyr Ser Phe Gln Val Val Gly Glu Met Ile
 20 25 30
 Arg Asn Arg Glu Val Leu Pro Cys Pro Asp Asp Cys Pro Ala Trp Ala
 35 40 45
 Tyr Ala Leu Met Ile Glu Gly Trp Asn Glu Phe Pro Ser Arg Arg Ala
 50 55 60
 Arg Phe Lys Asp Ile His Ser Arg Leu Arg Ala Trp Gly Asn Leu Ser
 65 70 75 80
 Asn Tyr Asn Ser Ser Glu Gln Thr Ser Gly Gly Arg Asn Thr Thr Gln
 85 90 95
 Thr Ser Ser Leu Ser Thr Ser Pro Leu Cys Asn Val Ser Asn Ala Pro
 100 105 110
 Tyr Val Gly Pro Lys Gln Lys Val Pro Pro Phe Pro Gln Thr Gln Val

115 120 125
 Ile Pro Met Lys Gly Gln Ile Arg Pro Met Val Pro Pro Pro Gln Leu
 130 135 140
 Tyr Val Pro
 145 147

<210> 920
 <211> 150
 <212> Amino acid
 <213> Homo sapiens

<400> 920
 Arg Asn Ser Gly Arg His Pro Arg Val Arg Trp Ile Leu Glu Glu Arg
 1 5 10 15
 Lys Arg Val Met Gln Glu Ala Cys Ala Lys Tyr Arg Ala Ser Ser Ser
 20 25 30
 Arg Arg Ala Val Thr Pro Arg His Val Ser Arg Ile Phe Val Glu Asp
 35 40 45
 Arg His Arg Val Leu Tyr Cys Glu Val Pro Lys Ala Gly Cys Ser Asn
 50 55 60
 Trp Lys Arg Val Leu Met Val Leu Ala Gly Leu Ala Ser Ser Thr Ala
 65 70 75 80
 Asp Ile Gln His Asn Thr Val His Tyr Gly Ser Ala Leu Lys Arg Leu
 85 90 95
 Asp Thr Phe Asp Arg Gln Gly Ile Leu His Arg Leu Ser Thr Tyr Thr
 100 105 110
 Lys Met Leu Phe Val Arg Glu Pro Phe Glu Arg Leu Val Ser Ala Phe
 115 120 125
 Arg Asp Lys Phe Glu His Pro Asn Ser Tyr Tyr His Pro Val Phe Cys
 130 135 140
 Met Ala Ile Leu Ala Arg
 145 150

<210> 921
 <211> 125
 <212> Amino acid
 <213> Homo sapiens

<400> 921
 Ile Met Tyr Ser Ile Ser Pro Ala Asn Ser Glu Glu Gly Gln Glu Leu
 1 5 10 15
 Tyr Val Cys Thr Val Lys Asp Asp Val Asn Leu Asp Thr Val Leu Leu
 20 25 30
 Leu Pro Phe Leu Lys Glu Ile Ala Val Ser Gln Leu Asp Gln Leu Ser
 35 40 45
 Pro Glu Glu Gln Leu Leu Val Lys Cys Ala Ala Ile Ile Gly His Ser
 50 55 60
 Phe His Ile Asp Leu Leu Gln His Leu Leu Pro Gly Trp Asp Lys Asn
 65 70 75 80
 Lys Leu Leu Gln Val Leu Arg Ala Leu Val Asp Ile His Val Leu Cys
 85 90 95
 Trp Ser Asp Lys Ser Gln Glu Leu Pro Ala Glu Pro Ile Leu Met Pro
 100 105 110
 Ser Ser Ile Asp Ile Ile Asp Gly Thr Lys Glu Lys Lys

115

120

125

<210> 922

<211> 111

<212>Amino acid

<213> Homo sapiens

<400> 922

```

Gly Pro His Val Val Leu Val Leu Arg Arg Cys Phe Leu Leu Ser Tyr
 1          5          10          15
Phe Lys Gly Val Glu Lys Ala Lys Ala Met Pro Ser Pro Arg Ile Leu
          20          25          30
Lys Thr His Leu Ser Thr Gln Leu Leu Pro Pro Ser Phe Trp Glu Asn
          35          40          45
Asn Cys Lys Val Arg Tyr Gln Gln Leu Pro Val Thr Glu Gly Lys Val
          50          55          60
Ser Gln Pro Lys Arg Val Leu Gln Thr Pro Thr Gln Ser Ile Arg Asp
          65          70          75          80
His Leu Cys Leu Ser Thr Val Ser Asp Ala Tyr Gln Gln Arg Glu Asn
          85          90          95
Ile Lys Phe Tyr Ile Gln Gln Asp Ile His Leu Asn Ser Phe Lys
          100          105          110 111

```

<210> 923

<211> 69

<212>Amino acid

<213> Homo sapiens

<400> 923

```

Phe Tyr Tyr Ile Cys Arg Leu Ser Lys Glu Asp Lys Ala Phe Leu Trp
 1          5          10          15
Glu Lys Arg Tyr Tyr Cys Phe Lys His Pro Asn Cys Leu Pro Lys Ile
          20          25          30
Leu Ala Ser Ala Pro Asn Trp Lys Trp Val Asn Leu Ala Lys Thr Tyr
          35          40          45
Ser Leu Leu His Gln Trp Pro Ala Leu Tyr Pro Leu Ile Ala Leu Glu
          50          55          60
Leu Leu Asp Ser Lys
          65          69

```

<210> 924

<211> 120

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(120)

<223> X = any amino acid or stop code

<400> 924

```

Lys Met Met Ile Xaa Gly Leu Phe Glu Ile Gln Gln Cys Pro Ile Gly
 1           5           10           15
Lys His Cys Asn Phe Leu Gln Val Leu Arg Asn Pro Asn Arg Asp Leu
           20           25           30
Trp Leu Val Ser Ser Phe Gly Lys Ser Ser Lys Gly Arg Glu Arg Met
           35           40           45
Gly His His Asp Glu Tyr Tyr Arg Leu Arg Gly Arg His Asn Pro Ser
 50           55           60
Pro Asp His Ser Tyr Lys Arg Asn Gly Glu Ser Glu Arg Lys Arg Lys
 65           70           75           80
Lys Ser His Xaa His Met Ser Lys Ser Gln Glu Arg His Asn Ser Pro
           85           90           95
Ser Arg Gly Arg Asn Ser Asp Arg Ser Gly Gly Arg Cys Ser Arg Ser
           100          105          110
Asp Asn Gly Arg Ser Arg Tyr Arg
      115          120

```

<210> 925

<211> 108

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(108)

<223> X = any amino acid or stop code

<400> 925

```

Pro Leu Ser Leu Phe Ala Arg Val Ala Gly Ser Arg Val Glu Met Pro
 1           5           10           15
Glu Pro Pro Gly Leu Gly Asp Glu Gly Arg Pro Leu Leu His Pro Gly
           20           25           30
Arg Arg Glu Ala Val Gly Ser Trp Val Ser Ala Phe Ala Gly Asp Ser
           35           40           45
Thr Pro Cys Gly Pro Gly Asp Leu Ser Val Pro Arg Arg Glu Pro Phe
 50           55           60
Arg Leu Thr Ala Leu Xaa Pro His Arg Ser Pro Val Val Arg Thr Ser
 65           70           75           80
Leu Ile Gly Leu Leu Leu Gly Phe Ser Val Lys Glu Glu Leu Arg Gly
           85           90           95
Val Gly Trp Ala Ala Arg Thr Pro Leu Gly Ile Arg
           100          105          108

```

<210> 926

<211> 305

<212>Amino acid

<213> Homo sapiens

<400> 926

```

Phe Asp Lys Arg Gln His Glu Ala Arg Ile Gln Gln Met Glu Asn Glu
 1           5           10           15
Ile His Tyr Leu Gln Glu Asn Leu Lys Ser Met Glu Glu Ile Gln Gly

```

20 25 30
 Leu Thr Asp Leu Gln Leu Gln Glu Ala Asp Glu Glu Lys Glu Arg Ile
 35 40 45
 Leu Ala Gln Leu Arg Glu Leu Glu Lys Lys Lys Lys Leu Glu Asp Ala
 50 55 60
 Lys Ser Gln Glu Gln Val Phe Gly Leu Asp Lys Glu Leu Lys Lys Leu
 65 70 75 80
 Lys Lys Ala Val Ala Thr Ser Asp Lys Leu Ala Thr Ala Glu Leu Thr
 85 90 95
 Ile Ala Lys Asp Gln Leu Lys Ser Leu His Gly Thr Val Met Lys Ile
 100 105 110
 Asn Gln Glu Arg Ala Glu Glu Leu Gln Glu Ala Glu Arg Phe Ser Arg
 115 120 125
 Lys Ala Ala Gln Ala Ala Arg Asp Leu Thr Arg Ala Glu Ala Glu Ile
 130 135 140
 Glu Leu Leu Gln Asn Leu Leu Arg Gln Lys Gly Glu Gln Phe Arg Leu
 145 150 155 160
 Glu Met Glu Lys Thr Gly Val Gly Thr Gly Ala Asn Ser Gln Val Leu
 165 170 175
 Glu Ile Glu Lys Leu Asn Glu Thr Met Glu Arg Gln Arg Thr Glu Ile
 180 185 190
 Ala Arg Leu Gln Asn Val Leu Tyr Leu Thr Gly Ser Asp Asn Lys Gly
 195 200 205
 Gly Phe Glu Asn Val Leu Glu Glu Ile Ala Glu Leu Arg Arg Glu Gly
 210 215 220
 Ser Tyr Gln Asn Asp Tyr Ile Ser Ser Met Ala Asp Pro Phe Lys Arg
 225 230 235 240
 Arg Gly Tyr Trp Tyr Phe Met Pro Pro Pro Ser Ser Lys Val Ser
 245 250 255
 Ser His Ser Ser Gln Ala Thr Lys Asp Ser Gly Val Gly Leu Lys Tyr
 260 265 270
 Ser Ala Ser Thr Pro Val Arg Lys Pro Arg Pro Gly Gln Gln Asp Gly
 275 280 285
 Lys Glu Gly Ser Gln Pro Pro Pro Ala Ser Gly Tyr Trp Val Tyr Ser
 290 295 300
 Pro
 305

<210> 927
 <211> 303
 <212> Amino acid
 <213> Homo sapiens

<400> 927
 Ser Asp Ala Ser Ser Phe Lys Thr Arg Val Ile Val Val Pro Arg Pro
 1 5 10 15
 Arg Val Phe Pro Leu Gly Ser Ala Ile Thr Glu Asn Ser Leu Glu Ser
 20 25 30
 Asp Ser Gln Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu
 35 40 45
 Val Ala Asp Lys Val Ile Val Thr Ser Lys His Asn Asn Asp Thr Gln
 50 55 60
 His Ile Trp Glu Ser Asp Ser Asn Glu Phe Ser Val Ile Ala Asp Pro
 65 70 75 80
 Arg Gly Asn Thr Leu Gly Arg Gly Thr Thr Ile Thr Leu Val Leu Lys
 85 90 95
 Glu Glu Ala Ser Asp Tyr Leu Glu Leu Asp Thr Ile Lys Asn Leu Val
 100 105 110
 Lys Lys Tyr Ser Gln Phe Ile Asn Phe Pro Ile Tyr Val Trp Ser Ser

115	120	125
Lys Thr Glu Thr Val Glu Glu Pro Met Glu Glu Glu Glu Ala Ala Lys		
130	135	140
Glu Glu Lys Glu Glu Ser Asp Asp Glu Ala Ala Val Glu Glu Glu Glu		
145	150	155
Glu Glu Lys Lys Pro Lys Thr Lys Lys Val Glu Lys Thr Val Trp Asp		160
	165	170
Trp Glu Leu Met Asn Asp Ile Lys Pro Ile Trp Gln Arg Pro Ser Lys		175
	180	185
Glu Val Glu Glu Asp Glu Tyr Lys Ala Phe Tyr Lys Ser Phe Ser Lys		190
	195	200
Glu Ser Asp Asp Pro Met Ala Tyr Ile His Phe Thr Ala Glu Gly Glu		205
210	215	220
Val Thr Phe Lys Ser Ile Leu Phe Val Pro Thr Ser Ala Pro Arg Gly		
225	230	235
Leu Phe Asp Glu Tyr Gly Ser Lys Lys Ser Asp Tyr Ile Lys Leu Tyr		240
	245	250
Val Arg Arg Val Phe Ile Thr Asp Asp Phe His Asp Met Met Pro Lys		255
	260	265
Tyr Leu Asn Phe Val Lys Gly Val Val Asp Ser Asp Asp Leu Pro Leu		270
	275	280
Asn Val Ser Arg Glu Thr Leu Gln Gln His Lys Leu Leu Lys Val		285
290	295	300
		303

<210> 928
 <211> 147
 <212> Amino acid
 <213> Homo sapiens

<400> 928
Cys Gly Ser Trp Met Arg Arg Ala Leu Ile Pro Pro Cys Arg Gly Gly
1 5 10 15
Pro Ser Ala Ser Asp Arg Cys Cys Ser Cys Ser Pro Ser Gly Phe Ser
20 25 30
Ala Gly Arg Gly Arg Cys Pro Val Gln Gly Cys Leu Arg Pro His Arg
35 40 45
Val Gln Leu Leu Arg Arg Trp Gly Pro Gly Ser Pro Ala Gly Gln Arg
50 55 60
Leu Ser Lys Gly Phe Gln Leu Leu Arg Trp Trp Gly Pro Gly Ser Pro
65 70 75 80
Ala Pro Glu Pro Arg Lys Gly Pro Phe Pro Pro Pro Asp Pro Pro Trp
85 90 95
Pro Val Thr Ala Val Thr Val Met Ala Gly Ser Val Pro Ser Ala Gln
100 105 110
Ser Val Asp Ala Leu Glu Ser Pro Gly Pro Leu Ala Leu Glu Gly Pro
115 120 125
Ser Ser Pro Arg Asn Leu Leu Trp Arg Glu Met Ser Ile Phe Leu Pro
130 135 140
Gly Ile Phe
145 147

<210> 929
 <211> 183
 <212> Amino acid
 <213> Homo sapiens

<400> 929

```

Pro Gly Pro Thr Pro Pro Pro Arg His Gly Ser Pro Pro His Arg Leu
 1          5          10          15
Ile Arg Val Glu Thr Pro Gly Pro Pro Ala Pro Pro Ala Asp Glu Arg
          20          25          30
Ile Ser Gly Pro Pro Ala Ser Ser Asp Arg Leu Ala Ile Leu Glu Asp
          35          40          45
Tyr Ala Asp Pro Phe Asp Val Gln Glu Thr Gly Glu Gly Ser Ala Gly
          50          55          60
Ala Ser Gly Ala Pro Glu Lys Val Pro Glu Asn Asp Gly Tyr Met Glu
          65          70          75          80
Pro Tyr Glu Ala Gln Lys Met Met Ala Glu Ile Arg Gly Ser Lys Glu
          85          90          95
Thr Ala Thr Gln Pro Leu Pro Leu Tyr Asp Thr Pro Tyr Glu Pro Glu
          100          105          110
Glu Asp Gly Ala Thr Pro Glu Gly Glu Gly Ala Pro Trp Pro Arg Glu
          115          120          125
Ser Arg Leu Pro Glu Asp Asp Glu Arg Pro Pro Glu Glu Tyr Asp Gln
          130          135          140
Pro Trp Glu Trp Lys Lys Glu Arg Ile Ser Lys Ala Phe Ala Val Asp
          145          150          155          160
Ile Lys Val Ile Lys Asp Leu Pro Trp Pro Pro Pro Val Gly Gln Leu
          165          170          175
Asp Ser Ser Pro Ser Leu Pro
          180          183

```

<210> 930

<211> 187

<212>Amino acid

<213> Homo sapiens

<400> 930

```

Gln Phe Phe Ser Leu Phe Leu Arg Tyr Gln Ile His Thr Gly Leu Gln
 1          5          10          15
His Ser Ile Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro Leu Asp Asn
          20          25          30
Ala Thr Leu Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser Thr His Met
          35          40          45
Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys Met Pro Thr
          50          55          60
Arg Arg Gly Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp
          65          70          75          80
Tyr Tyr Thr His Tyr Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp
          85          90          95
Leu Tyr Glu Asn Asp Asn Ala Ala Trp Asp Tyr Asp Asn Gly Ile Tyr
          100          105          110
Ser Thr Gln Met Tyr Thr Gln Arg Val Gln Gln Ile Leu Ala Ser His
          115          120          125
Asn Pro Thr Lys Pro Ile Phe Leu Tyr Ile Ala Tyr Gln Ala Val His
          130          135          140
Ser Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr Arg Ser Ile
          145          150          155          160
Ile Asn Ile Asn Arg Arg Tyr Ala Ala Met Leu Ser Cys Leu Asp
          165          170          175
Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys
          180          185          187

```

<210> 931
 <211> 192
 <212> Amino acid
 <213> Homo sapiens

<400> 931
 Arg Val Arg Lys Gly Arg Gly Gly Glu Arg Leu Gln Ser Pro Leu Arg
 1 5 10 15
 Val Pro Gln Lys Pro Glu Arg Pro Pro Leu Pro Pro Lys Pro Gln Phe
 20 25 30
 Leu Asn Ser Gly Ala Tyr Pro Gln Lys Pro Leu Arg Asn Gln Gly Val
 35 40 45
 Val Arg Thr Leu Ser Ser Ser Ala Gln Glu Asp Ile Ile Arg Trp Phe
 50 55 60
 Lys Glu Glu Gln Leu Pro Leu Arg Ala Gly Tyr Gln Lys Thr Ser Asp
 65 70 75 80
 Thr Ile Ala Pro Trp Phe His Gly Ile Leu Thr Leu Lys Lys Ala Asn
 85 90 95
 Glu Leu Leu Leu Ser Thr Gly Met Pro Gly Ser Phe Leu Ile Arg Val
 100 105 110
 Ser Glu Arg Ile Lys Gly Tyr Ala Leu Ser Tyr Leu Ser Glu Asp Gly
 115 120 125
 Cys Lys His Phe Leu Ile Asp Ala Ser Ala Asp Ala Tyr Ser Phe Leu
 130 135 140
 Gly Val Asp Gln Leu Gln His Ala Thr Leu Ala Asp Leu Val Glu Tyr
 145 150 155 160
 His Lys Glu Glu Pro Ile Thr Ser Leu Gly Lys Glu Leu Leu Leu Tyr
 165 170 175
 Pro Cys Gly Gln Gln Asp Gln Leu Pro Asp Tyr Leu Glu Leu Phe Glu
 180 185 190 192

<210> 932
 <211> 545
 <212> Amino acid
 <213> Homo sapiens

<400> 932
 Gly Ser Leu Glu Lys Ala Leu Phe Gln Leu Leu Lys Val Trp Gly Gln
 1 5 10 15
 Trp Ala Glu Gln Thr Arg Arg Leu Gln Arg Leu Asp Val Ser Leu Ser
 20 25 30
 Val Ala Arg Val Arg Ser Ala Gly Pro Ser Cys Gln Asn Lys Gly Asp
 35 40 45
 Leu Val Met Glu Ala Leu Leu Glu Gly Ile Gln Asn Arg Gly His Gly
 50 55 60
 Gly Gly Phe Leu Thr Ser Cys Glu Ala Glu Leu Gln Glu Leu Met Lys
 65 70 75 80
 Gln Ile Asp Ile Met Val Ala His Lys Lys Ser Glu Trp Glu Gly Arg
 85 90 95
 Thr His Ala Leu Glu Thr Cys Leu Lys Ile Arg Glu Gln Glu Leu Lys
 100 105 110
 Ser Leu Arg Ser Gln Leu Asp Val Thr His Lys Glu Val Gly Met Leu

115	120	125
His Gln Gln Val Glu Glu	His Glu Lys Ile Lys	Gln Glu Met Thr Met
130	135	140
Glu Tyr Lys Gln Glu Leu	Lys Lys Leu His Glu	Glu Leu Cys Ile Leu
145	150	155
Lys Arg Ser Tyr Glu Lys	Leu Gln Lys Lys Gln	Met Arg Glu Phe Arg
165	170	175
Gly Asn Thr Lys Asn His	Arg Glu Asp Arg Ser	Glu Ile Glu Arg Leu
180	185	190
Thr Ala Lys Ile Glu Glu	Phe Arg Gln Lys Ser	Leu Asp Trp Glu Lys
195	200	205
Gln Arg Leu Ile Tyr Gln	Gln Gln Val Ser Ser	Leu Glu Ala Gln Arg
210	215	220
Lys Ala Leu Ala Glu Gln	Ser Glu Ile Ile Gln	Ala Gln Leu Val Asn
225	230	235
Arg Lys Gln Lys Leu Glu	Ser Val Glu Leu Ser	Ser Gln Ser Glu Ile
245	250	255
Gln His Leu Ser Ser Lys	Leu Glu Arg Ala Asn	Asp Thr Ile Cys Ala
260	265	270
Asn Glu Leu Glu Ile Glu	Arg Leu Thr Met Arg	Val Asn Asp Leu Val
275	280	285
Gly Thr Ser Met Thr Val	Leu Gln Glu Gln Gln	Lys Glu Glu Lys
290	295	300
Leu Arg Glu Ser Glu Lys	Leu Leu Glu Ala Leu	Gln Glu Glu Lys Arg
305	310	315
Glu Leu Lys Ala Ala Leu	Gln Ser Gln Glu Asn	Leu Ile His Glu Ala
325	330	335
Arg Ile Gln Lys Glu Lys	Leu Gln Glu Lys Val	Lys Ala Thr Asn Thr
340	345	350
Gln His Ala Val Glu Ala	Ile Ser Leu Glu Ser	Val Ser Ala Thr Cys
355	360	365
Lys Gln Leu Ser Gln Glu	Leu Met Glu Lys Tyr	Glu Glu Leu Lys Arg
370	375	380
Met Glu Ala His Asn Asn	Glu Tyr Lys Ala Glu	Ile Lys Lys Leu Lys
385	390	395
Glu Gln Ile Leu Gln Gly	Glu Gln Ser Tyr Ser	Ser Ala Leu Glu Gly
405	410	415
Met Lys Met Glu Ile Ser	His Leu Thr Gln Glu	Leu His Gln Arg Asp
420	425	430
Ile Thr Ile Ala Ser Thr	Lys Gly Ser Ser Ser	Asp Met Glu Lys Arg
435	440	445
Leu Arg Ala Glu Met Gln	Lys Ala Glu Asp Lys	Ala Val Glu His Lys
450	455	460
Glu Ile Leu Asp Gln Leu	Glu Ser Leu Lys Leu	Glu Asn Arg His Leu
465	470	475
Ser Glu Met Val Met Lys	Leu Glu Leu Gly Leu	His Glu Cys Ser Leu
485	490	495
Pro Val Ser Pro Leu Gly	Ser Ile Ala Thr Arg	Phe Leu Glu Glu Glu
500	505	510
Glu Leu Arg Ser His His	Ile Leu Glu Arg Leu	Asp Ala His Ile Glu
515	520	525
Glu Leu Lys Arg Glu Ser	Glu Lys Thr Val Arg	Gln Phe Thr Ala Leu
530	535	540
Lys		
545		

<210> 933

<211> 297

<212> Amino acid

<213> Homo sapiens

<400> 933

Thr	Gly	Phe	Leu	Gly	Trp	Ser	Gln	Gly	Pro	Ser	Leu	Thr	Pro	Thr	Ser
1				5					10					15	
Leu	Ser	Ala	Leu	Tyr	Pro	Ser	Gln	Val	Glu	Glu	Thr	Gly	Val	Val	Leu
			20					25					30		
Ser	Leu	Glu	Gln	Thr	Glu	Gln	His	Ser	Arg	Arg	Pro	Ile	Gln	Arg	Gly
		35					40					45			
Ala	Pro	Ser	Gln	Lys	Asp	Thr	Pro	Asn	Pro	Gly	Asp	Ser	Leu	Asp	Thr
	50					55					60				
Pro	Gly	Pro	Arg	Ile	Leu	Ala	Phe	Leu	His	Pro	Pro	Ser	Leu	Ser	Glu
65				70						75				80	
Ala	Ala	Leu	Ala	Ala	Asp	Pro	Arg	Arg	Phe	Cys	Ser	Pro	Asp	Leu	Arg
			85						90					95	
Arg	Leu	Leu	Gly	Pro	Ile	Leu	Asp	Gly	Ala	Ser	Val	Ala	Ala	Thr	Pro
			100					105					110		
Ser	Thr	Pro	Leu	Ala	Thr	Arg	His	Pro	Gln	Ser	Pro	Leu	Ser	Ala	Asp
		115					120					125			
Leu	Pro	Asp	Glu	Leu	Pro	Val	Gly	Thr	Glu	Asn	Val	His	Arg	Leu	Phe
	130					135					140				
Thr	Ser	Gly	Lys	Asp	Thr	Glu	Ala	Val	Glu	Thr	Asp	Leu	Asp	Ile	Ala
145					150					155				160	
Gln	Asp	Ala	Asp	Ala	Leu	Asp	Leu	Glu	Met	Leu	Ala	Pro	Tyr	Ile	Ser
			165					170						175	
Met	Asp	Asp	Asp	Phe	Gln	Leu	Asn	Ala	Ser	Glu	Gln	Leu	Pro	Arg	Ala
		180						185					190		
Tyr	His	Arg	Pro	Leu	Gly	Ala	Val	Pro	Arg	Pro	Arg	Ala	Arg	Ser	Phe
		195				200						205			
His	Gly	Leu	Ser	Pro	Pro	Ala	Leu	Glu	Pro	Ser	Leu	Leu	Pro	Arg	Trp
	210					215					220				
Gly	Ser	Asp	Pro	Arg	Leu	Ser	Cys	Ser	Ser	Pro	Ser	Arg	Gly	Asp	Pro
225					230					235				240	
Ser	Ala	Ser	Ser	Pro	Met	Ala	Gly	Ala	Arg	Lys	Arg	Thr	Leu	Ala	Gln
			245					250						255	
Ser	Ser	Lys	Asp	Glu	Asp	Glu	Gly	Val	Glu	Leu	Leu	Gly	Val	Arg	Pro
		260						265				270			
Pro	Lys	Arg	Ser	Pro	Ser	Pro	Glu	His	Glu	Asn	Phe	Leu	Leu	Phe	Pro
		275					280					285			
Leu	Ser	Leu	Ser	Phe	Leu	Leu	Thr	Gly							
	290					295		297							

<210> 934
 <211> 140
 <212> Amino acid
 <213> Homo sapiens

<400> 934

Glu	Leu	Gln	Asp	Cys	Phe	Asp	Val	His	Asp	Ala	Ser	Trp	Glu	Glu	Gln
1				5					10					15	
Ile	Phe	Trp	Gly	Trp	His	Asn	Asp	Val	His	Ile	Phe	Asp	Thr	Lys	Thr
		20						25					30		
Gln	Thr	Trp	Phe	Gln	Pro	Glu	Ile	Lys	Gly	Gly	Val	Pro	Pro	Gln	Pro
		35					40					45			
Arg	Ala	Ala	His	Thr	Cys	Ala	Val	Leu	Gly	Asn	Lys	Gly	Tyr	Ile	Phe
	50					55					60				
Gly	Gly	Arg	Val	Leu	Gln	Thr	Arg	Met	Asn	Asp	Leu	His	Tyr	Leu	Asn
65				70						75				80	
Leu	Asp	Thr	Trp	Thr	Trp	Ser	Gly	Arg	Ile	Thr	Ile	Asn	Gly	Glu	Ser

```
<210> 935
<211> 97
<212> Amino acid
<213> Homo sapiens
```

```
<210> 936
<211> 245
<212> Amino acid
<213> Homo sapiens
```

516

145		150		155		160									
Ile	Ser	Cys	Cys	Val	Leu	Ser	Pro	Arg	Ala	Gly	Glu	Ala	Arg	Gly	Gln
			165						170					175	
His	Gly	Arg	Ala	Ala	Ala	Ser	Val	Pro	Pro	Thr	Ala	Arg	Pro	Gln	Ala
			180					185					190		
His	Cys	Ser	Phe	Leu	Cys	Asp	Trp	Leu	His	Ser	Pro	Val	Arg	Thr	Lys
		195					200					205			
Trp	Glu	Glu	Val	Ser	Leu	Phe	Ser	Arg	Val	Val	Ser	Ser	Val	Cys	Asp
	210					215					220				
Leu	Pro	Leu	Leu	Ser	Ser	Ser	Arg	Gly	Thr	Trp	Pro	Phe	Ser	Pro	Leu
225					230					235					240
Thr	Ser	Pro	Phe	His											
			245												

<210> 937
 <211> 211
 <212> Amino acid
 <213> Homo sapiens

<400> 937

Ala	Glu	Cys	Leu	Glu	Ala	Ser	Ile	Ala	Arg	Tyr	Ala	His	Arg	Val	Ala
1				5					10					15	
Asn	Ser	Arg	Tyr	Thr	Phe	Asp	Gly	Glu	Thr	Val	Thr	Leu	Ser	Pro	Ser
		20					25					30			
Gln	Gly	Val	Asn	Gln	Leu	His	Gly	Gly	Pro	Glu	Gly	Phe	Asp	Lys	Arg
		35					40					45			
Arg	Trp	Gln	Ile	Val	Asn	Gln	Asn	Asp	Arg	Gln	Val	Leu	Phe	Ala	Leu
	50				55					60					
Ser	Ser	Asp	Asp	Gly	Asp	Gln	Gly	Phe	Pro	Gly	Asn	Leu	Gly	Ala	Thr
	65				70				75					80	
Val	Gln	Tyr	Arg	Leu	Thr	Asp	Asp	Asn	Arg	Ile	Ser	Ile	Thr	Tyr	Arg
			85					90					95		
Ala	Thr	Val	Asp	Lys	Pro	Cys	Pro	Val	Asn	Met	Thr	Asn	His	Val	Tyr
		100						105				110			
Phe	Asn	Leu	Asp	Gly	Glu	Gln	Ser	Asp	Val	Arg	Asn	His	Lys	Leu	Gln
	115					120					125				
Ile	Leu	Ala	Asp	Glu	Tyr	Leu	Pro	Val	Asp	Glu	Gly	Gly	Ile	Pro	His
	130					135				140					
Asp	Gly	Leu	Lys	Ser	Val	Ala	Gly	Thr	Ser	Phe	Asp	Phe	Arg	Ser	Ala
145				150					155					160	
Lys	Ile	Ile	Ala	Ser	Glu	Phe	Leu	Ala	Asp	Asp	Gln	Arg	Lys	Val	
			165					170					175		
Lys	Gly	Tyr	Asp	His	Ala	Phe	Leu	Leu	Gln	Ala	Lys	Gly	Asp	Gly	Lys
		180						185					190		
Lys	Val	Ala	Ala	His	Val	Trp	Ser	Ala	Asp	Glu	Lys	Leu	Gln	Leu	Lys
	195						200					205			
Val	Tyr	Thr													
	210	211													

<210> 938
 <211> 118
 <212> Amino acid
 <213> Homo sapiens

<400> 938

```

Pro Leu Ser Arg Phe Leu Ser Lys Glu Ser Gln Glu Asp Trp Gly Met
 1           5           10           15
Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe Gln
           20           25           30
His Gln Gly Ala Val Glu Leu Leu Val Phe Asn Phe Leu Leu Ile Leu
          35           40           45
Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe Leu
          50           55           60
His Glu Thr Gly Gly Ala Met Val Tyr Asp Lys Pro Pro Lys Phe Ala
          65           70           75           80
Met Ser Arg Glu Gln Met Ser Gln Ser Cys Ser His Thr Ala His Asn
           85           90           95
Ala Ser Leu Leu Thr Asp Ala Gly Pro Leu Ser Cys Gly Glu Ser Arg
          100          105          110
Ala Ser Cys Leu Phe Leu
          115          118

```

<210> 939

<211> 143

<212> Amino acid

<213> Homo sapiens

<400> 939

```

Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu Glu Glu Glu
 1           5           10           15
Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys Ser Leu
          20           25           30
Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu Ser Phe
          35           40           45
Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro Ser Ser
          50           55           60
Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn Leu Thr
          65           70           75           80
Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys Leu Gln
          85           90           95
Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu
          100          105          110
Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Trp Leu
          115          120          125
Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Met Gln Glu
          130          135          140          143

```

<210> 940

<211> 63

<212> Amino acid

<213> Homo sapiens

<400> 940

```

Met Gln Ser Ile Ala Trp Gly His Arg Arg Asp Arg Gly Glu Ser Pro
 1           5           10           15
Leu Gly Trp Gly Gln Glu Ser Glu Ala Ser Pro Ser Ala Leu Thr Glu
          20           25           30
Ala Pro Lys Ala Ala His Thr Thr Arg Leu Gly Phe Leu Ala Ala Asn

```



```
<210> 941
<211> 238
<212> Amino acid
<213> Homo sapiens
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```
<210> 942
<211> 158 :
<212> Amino acid
<213> Homo sapiens
```

519

```
<210> 943
<211> 235
<212> Amino acid
<213> Homo sapiens
```

```
<210> 944
<211> 284
<212> Amino acid
<213> Homo sapiens
```

<400> 944

```

Gly Phe His Pro Asn Thr Thr His Tyr Arg Ala Arg Ala Ala Arg
 1          5          10          15
Ala Gly Ala Gly Ser Phe Val Gly Glu Val Ser Ala Val Asp Lys Asp
          20          25          30
Phe Gly Pro Asn Gly Glu Val Arg Tyr Ser Phe Glu Met Val Gln Pro
          35          40          45
Asp Phe Glu Leu His Ala Ile Ser Gly Glu Ile Thr Asn Thr His Gln
          50          55          60
Phe Asp Arg Glu Ser Leu Met Arg Arg Arg Gly Thr Ala Val Phe Ser
          65          70          75          80
Phe Thr Val Ile Ala Thr Asp Gln Gly Ile Pro Gln Pro Leu Lys Asp
          85          90          95
Gln Ala Thr Val His Val Tyr Met Lys Asp Ile Asn Asp Asn Ala Pro
          100          105          110
Lys Phe Leu Lys Asp Phe Tyr Gln Ala Thr Ile Ser Glu Ser Ala Ala
          115          120          125
Asn Leu Thr Gln Val Leu Arg Val Ser Ala Ser Asp Val Asp Glu Gly
          130          135          140
Asn Asn Gly Leu Ile His Tyr Ser Ile Ile Lys Gly Asn Glu Glu Arg
          145          150          155          160
Gln Phe Ala Ile Asp Ser Thr Ser Gly Gln Val Thr Leu Ile Gly Lys
          165          170          175
Leu Asp Tyr Glu Ala Thr Pro Ala Tyr Ser Leu Val Ile Gln Ala Val
          180          185          190
Asp Ser Gly Thr Ile Pro Leu Asn Ser Thr Cys Thr Leu Asn Ile Asp
          195          200          205
Ile Leu Asp Glu Asn Asp Asn Thr Pro Phe Phe Leu Leu Asn Gln His
          210          215          220
Phe Phe Val Asp Val Leu Glu Asn Met Arg Ile Gly Glu Leu Gly Ala
          225          230          235          240
Ser Gly Thr Ala Thr Asp Ser Asp Ser Gly Asp Ile Ala Asp Leu Tyr
          245          250          255
Tyr Lys Phe Thr Gly Thr Lys His Pro Pro Gly Thr Phe Ser Ile Ser
          260          265          270
Pro Lys His Leu Gly Val Phe Phe Leu Ala Gln Lys
          275          280          284

```

<210> 945

<211> 119

<212> Amino acid

<213> Homo sapiens

<400> 945

```

Gly Asp Cys Tyr Asp Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu Ala
 1          5          10          15
Glu Leu Val Gln Tyr Tyr Met Glu His His Gly Gln Leu Lys Glu Lys
          20          25          30
Asn Gly Asp Val Ile Glu Leu Lys Asn Pro Leu Asn Cys Ala Asp Pro
          35          40          45
Thr Ser Gln Arg Trp Phe His Gly His Leu Ser Gly Lys Glu Ala Glu
          50          55          60
Lys Leu Leu Thr Glu Lys Gly Lys His Ser Ser Phe Leu Val Arg Glu
          65          70          75          80
Ser Gln Ser His Pro Gly Asp Phe Val Leu Ser Val Cys Thr Gly Asp
          85          90          95
Asp Lys Gly Glu Ser Asn Asp Gly Lys Ser Lys Val Thr His Val Met

```

	100		105		110
Ile His Cys Gln Glu Leu Lys					
	115		119		

<210> 946
 <211> 166
 <212> Amino acid
 <213> Homo sapiens

<400> 946

Ile	Asp	Ser	Gly	Asn	Gln	Asn	Gly	Gly	Asn	Asp	Asp	Lys	Thr	Lys	Asn
1				5					10					15	
Ala	Glu	Arg	Asn	Tyr	Leu	Asn	Val	Leu	Pro	Gly	Glu	Phe	Tyr	Ile	Thr
			20					25					30		
Arg	His	Ser	Asn	Leu	Ser	Glu	Ile	His	Val	Ala	Phe	His	Leu	Cys	Val
			35				40					45			
Asp	Asp	His	Val	Lys	Ser	Gly	Asn	Ile	Thr	Ala	Arg	Asp	Pro	Ala	Ile
	50					55					60				
Met	Gly	Leu	Arg	Asn	Ile	Leu	Lys	Val	Cys	Cys	Thr	His	Asp	Ile	Thr
65					70					75				80	
Thr	Ile	Ser	Ile	Pro	Leu	Leu	Leu	Val	His	Asp	Met	Ser	Glu	Glu	Met
				85					90					95	
Thr	Ile	Pro	Trp	Cys	Leu	Arg	Arg	Ala	Glu	Leu	Val	Phe	Lys	Cys	Val
			100					105					110		
Lys	Gly	Phe	Met	Met	Glu	Met	Ala	Ser	Trp	Asp	Gly	Gly	Ile	Ser	Arg
		115					120				125				
Thr	Val	Gln	Phe	Leu	Val	Pro	Gln	Ser	Ile	Ser	Glu	Glu	Met	Phe	Tyr
	130					135					140				
Gln	Leu	Ser	Asn	Met	Leu	Pro	Gln	Ile	Phe	Arg	Val	Ser	Ser	Thr	Leu
145					150					155					160
Thr	Leu	Thr	Ser	Lys	His										
				165	166										

<210> 947
 <211> 121
 <212> Amino acid
 <213> Homo sapiens

<400> 947

Ser	Ile	Leu	Pro	Ala	Leu	Leu	Val	Thr	Ile	Leu	Ile	Phe	Met	Asp	Gln
1				5					10					15	
Gln	Ile	Thr	Ala	Val	Ile	Val	Asn	Arg	Lys	Glu	Asn	Lys	Leu	Lys	Lys
			20					25					30		
Ala	Ala	Gly	Tyr	His	Leu	Asp	Leu	Phe	Trp	Val	Gly	Ile	Leu	Met	Ala
		35					40					45			
Leu	Cys	Ser	Phe	Met	Gly	Leu	Pro	Trp	Tyr	Val	Ala	Ala	Thr	Val	Ile
	50					55					60				
Ser	Ile	Ala	His	Ile	Asp	Ser	Leu	Lys	Met	Glu	Thr	Glu	Thr	Ser	Ala
65					70					75				80	
Pro	Gly	Glu	Gln	Pro	Gln	Phe	Leu	Gly	Val	Arg	Glu	Gln	Arg	Val	Thr
			85					90					95		
Gly	Ile	Ile	Val	Phe	Ile	Leu	Thr	Gly	Ile	Ser	Val	Phe	Leu	Ala	Pro
			100					105					110		
Ile	Leu	Lys	Cys	Ile	Pro	Leu	Pro	Val							

115

120 121

<210> 948
 <211> 191
 <212>Amino acid
 <213> Homo sapiens

<400> 948
 Gly Ala Ser Arg Val Glu Ala Gly Ser Ala Asn Gly Met Leu Ile Asp
 1 5 10 15
 Gly Gly Ser Gln Ile Val Lys Val Gln Gly His Ala Asp Gly Thr Thr
 20 25 30
 Ile Asn Lys Ser Gly Ser Gln Asp Val Val Gln Gly Ser Leu Ala Thr
 35 40 45
 Asn Thr Thr Ile Asn Gly Gly Arg Gln Tyr Val Glu Gln Ser Thr Val
 50 55 60
 Glu Thr Thr Thr Ile Lys Asn Gly Gly Glu Gln Arg Val Tyr Glu Ser
 65 70 75 80
 Arg Ala Leu Asp Thr Thr Ile Glu Gly Gly Thr Gln Ser Leu Asn Ser
 85 90 95
 Lys Ser Thr Ala Lys Asn Thr His Ile Tyr Ser Gly Gly Thr Gln Ile
 100 105 110
 Val Asp Asn Thr Ser Thr Ser Asp Val Ile Glu Val Tyr Ser Gly Gly
 115 120 125
 Val Leu Asp Val Arg Gly Gly Thr Ala Thr Asn Val Thr Gln His Asp
 130 135 140
 Gly Ala Ile Leu Lys Thr Asn Thr Asn Gly Thr Thr Val Ser Gly Thr
 145 150 155 160
 Asn Ser Glu Gly Ala Phe Ser Ile His Asn His Val Ala Asp Asn Val
 165 170 175
 Leu Leu Glu Asn Gly Gly His Leu Asp Ile Asn Ala Tyr Gly Ser
 180 185 190 191

<210> 949
 <211> 98
 <212>Amino acid
 <213> Homo sapiens

<400> 949
 Phe Phe Ser Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met
 1 5 10 15
 Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser
 20 25 30
 Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu
 35 40 45
 Leu Leu Lys Thr Ile Pro Lys Tyr Lys Val Met Asn Asp Leu Ile Pro
 50 55 60
 Glu Ile Lys Ala Thr Glu Met Pro Arg Ala Leu Phe Ser Gln Ser Ser
 65 70 75 80
 Gly Phe Lys Leu Tyr Phe Gly Ala Met Phe Leu Leu Thr Thr Ile Thr
 85 90 95
 Ala Cys
 98

<210> 950
 <211> 196
 <212> Amino acid
 <213> Homo sapiens

<400> 950
 Ser Cys Ser Gly Thr Gly Thr Asn Ala Cys Tyr Met Glu Asp Met Ser
 1 5 10 15
 Asn Ile Asp Leu Val Glu Gly Asp Glu Gly Arg Met Cys Ile Asn Thr
 20 25 30
 Glu Trp Gly Ala Phe Gly Asp Asp Gly Ala Leu Glu Asp Ile Arg Thr
 35 40 45
 Glu Phe Asp Arg Glu Leu Asp Leu Gly Ser Leu Asn Pro Gly Lys Gln
 50 55 60
 Leu Phe Glu Lys Met Ile Ser Gly Leu Tyr Leu Gly Glu Leu Val Arg
 65 70 75 80
 Leu Ile Leu Leu Lys Met Ala Lys Ala Gly Leu Leu Phe Gly Gly Glu
 85 90 95
 Lys Ser Ser Ala Leu His Thr Lys Gly Lys Ile Glu Thr Arg His Val
 100 105 110
 Ala Ala Met Glu Lys Tyr Lys Glu Gly Leu Ala Asn Thr Arg Glu Ile
 115 120 125
 Leu Val Asp Leu Gly Leu Glu Pro Ser Glu Ala Asp Cys Ile Ala Val
 130 135 140
 Gln His Val Cys Thr Ile Val Ser Phe Arg Ser Ala Asn Leu Cys Ala
 145 150 155 160
 Ala Ala Leu Ala Ala Ile Leu Thr Arg Leu Arg Glu Asn Lys Lys Val
 165 170 175
 Glu Arg Leu Arg Thr Thr Val Gly Met Asp Gly Thr Leu Tyr Lys Ile
 180 185 190
 His Pro Gln Tyr
 195 196

<210> 951
 <211> 721
 <212> Amino acid
 <213> Homo sapiens

<400> 951
 Phe Val Ala Ile Ala Thr Asn Gly Val Val Pro Ala Gly Gly Ser Tyr
 1 5 10 15
 Tyr Met Ile Ser Arg Ser Leu Gly Pro Glu Phe Gly Gly Ala Val Gly
 20 25 30
 Leu Cys Phe Tyr Leu Gly Thr Thr Phe Ala Gly Ala Met Tyr Ile Leu
 35 40 45
 Gly Thr Ile Glu Ile Leu Leu Ala Tyr Leu Phe Pro Ala Met Ala Ile
 50 55 60
 Phe Lys Ala Glu Asp Ala Ser Gly Glu Ala Ala Met Leu Asn Asn
 65 70 75 80
 Met Arg Val Tyr Gly Thr Cys Val Leu Thr Cys Met Ala Thr Val Val
 85 90 95
 Phe Val Gly Val Lys Tyr Val Asn Lys Phe Ala Leu Val Phe Leu Gly
 100 105 110
 Cys Val Ile Leu Ser Ile Leu Ala Ile Tyr Ala Gly Val Ile Lys Ser

115	120	125
Ala Phe Asp Pro Pro Asn Phe Pro Ile Cys Leu Leu Gly Asn Arg Thr		
130	135	140
Leu Ser Arg His Gly Phe Asp Val Cys Ala Lys Leu Ala Trp Glu Gly		
145	150	155
Asn Glu Thr Val Thr Thr Arg Leu Trp Gly Leu Phe Cys Ser Ser Arg		
165	170	175
Phe Leu Asn Ala Thr Cys Asp Glu Tyr Phe Thr Arg Asn Asn Val Thr		
180	185	190
Glu Ile Gln Gly Ile Pro Gly Ala Ala Ser Gly Leu Ile Lys Glu Asn		
195	200	205
Leu Trp Ser Ser Tyr Leu Thr Lys Gly Val Ile Val Glu Arg Ser Gly		
210	215	220
Met Thr Ser Val Gly Leu Ala Asp Gly Thr Pro Ile Asp Met Asp His		
225	230	235
Pro Tyr Val Phe Ser Asp Met Thr Ser Tyr Phe Thr Leu Leu Val Gly		
245	250	255
Ile Tyr Phe Pro Ser Val Thr Gly Ile Met Ala Gly Ser Asn Arg Ser		
260	265	270
Gly Asp Leu Arg Asp Ala Gln Lys Ser Ile Pro Thr Gly Thr Ile Leu		
275	280	285
Ala Ile Ala Thr Thr Ser Ala Val Tyr Ile Ser Ser Val Val Leu Phe		
290	295	300
Gly Ala Cys Ile Glu Gly Val Val Leu Arg Asp Lys Phe Gly Glu Ala		
305	310	315
Val Asn Gly Asn Leu Val Val Gly Thr Leu Ala Trp Pro Ser Pro Trp		
325	330	335
Val Ile Val Ile Gly Ser Phe Phe Ser Thr Cys Gly Ala Gly Leu Gln		
340	345	350
Ser Leu Thr Gly Ala Pro Arg Leu Leu Gln Ala Ile Ser Arg Asp Gly		
355	360	365
Ile Val Pro Phe Leu Gln Val Phe Gly His Gly Lys Ala Asn Gly Glu		
370	375	380
Pro Thr Trp Ala Leu Leu Leu Thr Ala Cys Ile Cys Glu Ile Gly Ile		
385	390	395
Leu Ile Ala Ser Leu Asp Glu Val Ala Pro Ile Leu Ser Met Phe Phe		
405	410	415
Leu Met Cys Tyr Met Phe Val Asn Leu Ala Cys Ala Val Gln Thr Leu		
420	425	430
Leu Arg Thr Pro Asn Trp Arg Pro Arg Phe Arg Tyr Tyr His Trp Thr		
435	440	445
Leu Ser Phe Leu Gly Met Ser Leu Cys Leu Ala Leu Met Phe Ile Cys		
450	455	460
Ser Trp Tyr Tyr Ala Leu Val Ala Met Leu Ile Ala Gly Leu Ile Tyr		
465	470	475
Lys Tyr Ile Glu Tyr Arg Gly Ala Lys Lys Glu Trp Gly Asp Gly Ile		
485	490	495
Arg Gly Leu Ser Leu Ser Ala Ala Arg Tyr Ala Leu Leu Arg Leu Glu		
500	505	510
Glu Gly Pro Pro His Thr Lys Asn Trp Arg Pro Gln Leu Leu Val Leu		
515	520	525
Val Arg Val Asp Gln Asp Gln Asn Val Val His Pro Gln Leu Leu Ser		
530	535	540
Leu Thr Ser Gln Leu Lys Ala Gly Lys Gly Leu Thr Ile Val Gly Ser		
545	550	555
Val Leu Glu Gly Thr Phe Leu Glu Asn His Pro Gln Ala Gln Arg Ala		
565	570	575
Glu Glu Ser Ile Arg Arg Leu Met Glu Ala Glu Lys Val Lys Gly Phe		
580	585	590
Cys Gln Val Val Ile Ser Ser Asn Leu Arg Asp Gly Val Ser His Leu		
595	600	605
Ile Gln Ser Gly Gly Leu Gly Gly Leu Gln His Asn Thr Val Leu Val		
610	615	620
Gly Trp Pro Arg Asn Trp Arg Gln Lys Glu Asp His Gln Thr Trp Arg		

625 630 635 640
 Asn Phe Ile Glu Leu Val Arg Glu Thr Thr Ala Gly His Leu Ala Leu
 645 650 655
 Leu Val Thr Lys Asn Val Ser Met Phe Pro Gly Asn Pro Glu Arg Phe
 660 665 670
 Ser Glu Gly Ser Ile Asp Arg Trp Gly Ile Gly His Asp Gly Gly Met
 675 680 685
 Leu Met Leu Val Pro Phe Leu Leu Arg His His Lys Val Trp Arg Lys
 690 695 700
 Cys Lys Met Arg Ile Phe Thr Val Ala Gln Met Val Asp Met His Ala
 705 710 715 720
 Met
 721

<210> 952
 <211> 42
 <212> Amino acid
 <213> Homo sapiens

<400> 952
 Phe Tyr Leu Arg Leu Leu Ser Phe Phe Cys Phe Gln Glu His Glu Lys
 1 5 10 15
 Arg Cys Trp Ser Val Asp Phe Asn Leu Met Asp Pro Lys Leu Ala
 20 25 30
 Ser Gly Ser Asp Asp Ala Lys Gly Thr Val
 35 40 42

<210> 953
 <211> 80
 <212> Amino acid
 <213> Homo sapiens

<400> 953
 Arg Asn Ser Lys Ala Met His Arg Ser Ser Cys Asp Gly Pro Leu Leu
 1 5 10 15
 Ser Leu Pro Ser Val Gly Arg Ser Ala Thr His Ala Leu Val Gln Ala
 20 25 30
 Gln Leu Ile Cys Ser Gly Ala Arg Arg Gly Met His Ala Phe Ile Val
 35 40 45
 Pro Ile Arg Ser Leu Gln Asp His Thr Pro Leu Pro Gly Lys Pro Ile
 50 55 60
 Met Leu Pro Gln Gly Thr Leu Pro Gly Gly Glu Pro Arg Trp Pro Pro
 65 70 75 80

<210> 954
 <211> 202
 <212> Amino acid
 <213> Homo sapiens

<400> 954

Cys Gly Thr Leu Ile Leu Gln Ala Arg Ala Tyr Val Gly Pro His Val
 1 5 10 15
 Leu Ala Val Val Thr Arg Thr Gly Phe Cys Thr Ala Lys Gly Gly Leu
 20 25 30
 Val Ser Ser Ile Leu His Pro Arg Pro Ile Asn Phe Lys Phe Tyr Lys
 35 40 45
 His Ser Met Lys Phe Val Ala Ala Leu Ser Val Leu Ala Leu Leu Gly
 50 55 60
 Thr Ile Tyr Ser Ile Phe Ile Leu Tyr Arg Asn Arg Val Pro Leu Asn
 65 70 75 80
 Glu Ile Val Ile Arg Ala Leu Asp Leu Val Thr Val Val Val Pro Pro
 85 90 95
 Ala Leu Pro Ala Ala Met Thr Val Cys Thr Leu Tyr Ala Gln Ser Arg
 100 105 110
 Leu Arg Arg Gln Gly Ile Phe Cys Ile His Pro Leu Arg Ile Asn Leu
 115 120 125
 Gly Gly Lys Leu Gln Leu Val Cys Phe Asp Lys Thr Gly Thr Leu Thr
 130 135 140
 Glu Asp Gly Leu Asp Val Met Gly Val Val Pro Leu Lys Gly Gln Ala
 145 150 155 160
 Phe Leu Pro Leu Val Pro Glu Pro Arg Arg Leu Pro Val Gly Pro Leu
 165 170 175
 Leu Arg Ala Leu Ala Thr Cys His Ala Leu Ser Arg Leu Gln Asp Thr
 180 185 190
 Pro Val Gly Asp Pro Met Asp Leu Lys Met
 195 200 202

<210> 955

<211> 188

<212> Amino acid

<213> Homo sapiens

<400> 955

Gln Ile Glu Tyr Phe Arg Ser Leu Leu Asp Glu His His Ile Ser Tyr
 1 5 10 15
 Val Ile Asp Glu Asp Val Lys Ser Gly Arg Tyr Met Glu Leu Glu Gln
 20 25 30
 Arg Tyr Met Asp Leu Ala Glu Asn Ala Arg Phe Glu Arg Glu Gln Leu
 35 40 45
 Leu Gly Val Gln Gln His Leu Ser Asn Thr Leu Lys Met Ala Glu Gln
 50 55 60
 Asp Asn Lys Glu Ala Gln Glu Met Ile Gly Ala Leu Lys Glu Arg Ser
 65 70 75 80
 His His Met Glu Arg Ile Ile Glu Ser Glu Gln Lys Gly Lys Ala Ala
 85 90 95
 Leu Ala Ala Thr Leu Glu Glu Tyr Lys Ala Thr Val Ala Ser Asp Gln
 100 105 110
 Ile Glu Met Asn Arg Leu Lys Ala Gln Leu Glu Asn Glu Lys Gln Lys
 115 120 125
 Val Ala Glu Leu Tyr Ser Ile His Asn Ser Gly Asp Lys Ser Asp Ile
 130 135 140
 Gln Asp Leu Leu Glu Ser Val Arg Leu Asp Lys Glu Lys Ala Glu Thr
 145 150 155 160
 Leu Ala Ser Ser Leu Gln Glu Asp Leu Ala His Thr Arg Asn Asp Ala
 165 170 175
 Asn Arg Leu Gln Asp Ala Ile Ala Lys Gly Arg Gly

180

185

188

<210> 956
 <211> 132
 <212> Amino acid
 <213> Homo sapiens

<400> 956

Ala	Arg	Tyr	Arg	Phe	Thr	Leu	Ser	Ala	Arg	Thr	Gln	Val	Gly	Ser	Gly
1				5					10					15	
Glu	Ala	Val	Thr	Glu	Glu	Ser	Pro	Ala	Pro	Pro	Asn	Glu	Ala	Thr	Pro
			20					25					30		
Thr	Ala	Ala	Pro	Pro	Thr	Leu	Pro	Pro	Thr	Thr	Val	Gly	Ala	Thr	Gly
			35				40					45			
Ala	Val	Ser	Ser	Thr	Asp	Ala	Thr	Ala	Ile	Ala	Ala	Thr	Thr	Glu	Ala
	50					55				60					
Thr	Thr	Val	Pro	Ile	Ile	Pro	Thr	Val	Ala	Pro	Thr	Thr	Met	Ala	Thr
65					70					75					80
Thr	Thr	Thr	Val	Ala	Thr	Thr	Thr	Thr	Thr	Thr	Ala	Ala	Ala	Thr	Thr
				85					90					95	
Thr	Thr	Glu	Ser	Pro	Pro	Thr	Thr	Thr	Ser	Gly	Thr	Lys	Ile	His	Glu
			100				105						110		
Ser	Ala	Pro	Asp	Glu	Gln	Ser	Ile	Trp	Asn	Val	Thr	Val	Leu	Pro	Asn
		115					120					125			
Ser	Lys	Trp	Ala												
130			132												

<210> 957
 <211> 220
 <212> Amino acid
 <213> Homo sapiens

<400> 957

Leu	Lys	Ser	Thr	Gln	Asp	Glu	Ile	Asn	Gln	Ala	Arg	Ser	Lys	Leu	Ser
1				5					10					15	
Gln	Leu	His	Glu	Ser	Arg	Gln	Glu	Ala	His	Arg	Ser	Leu	Glu	Gln	Tyr
			20					25					30		
Asp	Gln	Val	Leu	Asp	Gly	Ala	His	Gly	Ala	Ser	Leu	Thr	Asp	Leu	Ala
			35				40					45			
Asn	Leu	Ser	Glu	Gly	Val	Ser	Leu	Ala	Glu	Arg	Gly	Ser	Phe	Gly	Ala
	50					55				60					
Met	Asp	Asp	Pro	Phe	Lys	Asn	Lys	Ala	Leu	Leu	Phe	Ser	Asn	Asn	Thr
65					70					75					80
Gln	Glu	Leu	His	Pro	Asp	Pro	Phe	Gln	Thr	Glu	Asp	Pro	Phe	Lys	Ser
			85						90					95	
Asp	Pro	Phe	Lys	Gly	Ala	Asp	Pro	Phe	Lys	Gly	Asp	Pro	Phe	Gln	Asn
			100				105						110		
Asp	Pro	Phe	Ala	Glu	Gln	Gln	Thr	Ser	Thr	Asp	Pro	Phe	Gly	Gly	
		115					120				125				
Asp	Pro	Phe	Lys	Glu	Ser	Asp	Pro	Phe	Arg	Gly	Ser	Ala	Thr	Asp	Asp
	130					135				140					
Phe	Phe	Lys	Lys	Gln	Thr	Lys	Asn	Asp	Pro	Phe	Thr	Ser	Asp	Pro	Phe
145				150					155					160	
Thr	Lys	Asn	Pro	Ser	Leu	Pro	Ser	Lys	Leu	Asp	Pro	Phe	Glu	Ser	Ser

				165					170					175			
Asp	Pro	Phe	Ser	Ser	Ser	Ser	Val	Ser	Ser	Lys	Gly	Ser	Asp	Pro	Phe		
			180						185				190				
Gly	Thr	Leu	Asp	Pro	Phe	Gly	Ser	Gly	Ser	Phe	Asn	Ser	Ala	Glu	Gly		
		195					200					205					
Phe	Ala	Asp	Phe	Ser	Thr	Ile	Glu	Gly	Arg	Arg	Gly						
	210					215					220						

<210> 958
 <211> 250
 <212> Amino acid
 <213> Homo sapiens

Arg	Thr	Arg	Gly	Gly	Ser	Gly	Asn	Ser	Ser	Gln	Pro	Ser	Leu	Arg	Glu		
1				5					10					15			
Gly	His	Asp	Lys	Pro	Val	Phe	Asn	Gly	Ala	Gly	Lys	Pro	His	Ser	Ser		
			20					25					30				
Thr	Ser	Ser	Pro	Ser	Val	Pro	Lys	Thr	Ser	Ala	Ser	Arg	Thr	Gln	Lys		
		35					40					45					
Ser	Ala	Val	Glu	His	Lys	Ala	Lys	Lys	Ser	Leu	Ser	His	Pro	Ser	His		
	50					55					60						
Ser	Arg	Pro	Gly	Pro	Met	Val	Thr	Pro	His	Asn	Lys	Ala	Lys	Ser	Pro		
	65				70					75					80		
Gly	Val	Arg	Gln	Pro	Gly	Ser	Ser	Ser	Ser	Ser	Ala	Pro	Gly	Gln	Pro		
			85					90						95			
Ser	Thr	Gly	Val	Ala	Arg	Pro	Thr	Val	Ser	Ser	Gly	Pro	Val	Pro	Arg		
			100					105					110				
Arg	Gln	Asn	Gly	Ser	Ser	Ser	Ser	Gly	Pro	Glu	Arg	Ser	Ile	Ser	Gly		
	115					120						125					
Ser	Lys	Lys	Pro	Thr	Asn	Asp	Ser	Asn	Pro	Ser	Arg	Arg	Thr	Val	Ser		
	130				135						140						
Gly	Thr	Cys	Gly	Pro	Gly	Gln	Pro	Ala	Ser	Ser	Ser	Gly	Gly	Pro	Gly		
145					150					155				160			
Arg	Pro	Ile	Ser	Gly	Ser	Val	Ser	Ser	Ala	Arg	Pro	Leu	Gly	Ser	Ser		
			165					170					175				
Arg	Gly	Pro	Gly	Arg	Pro	Val	Ser	Ser	Pro	His	Glu	Leu	Arg	Arg	Pro		
			180					185					190				
Val	Ser	Gly	Leu	Gly	Pro	Pro	Gly	Arg	Ser	Val	Ser	Gly	Pro	Gly	Arg		
		195				200						205					
Ser	Ile	Ser	Gly	Ser	Ile	Pro	Ala	Gly	Arg	Thr	Val	Ser	Asn	Ser	Val		
	210				215					220							
Pro	Gly	Arg	Pro	Val	Ser	Ser	Leu	Gly	Pro	Gly	Gln	Thr	Val	Ser	Ser		
225				230						235					240		
Ser	Gly	Pro	Thr	Ile	Lys	Pro	Lys	Cys	Thr								
			245					250									

<210> 959
 <211> 48
 <212> Amino acid
 <213> Homo sapiens

Arg	Gly	Lys	Gly	Ile	Thr	Pro	Arg	Tyr	His	Leu	Cys	Ile	Ser	Asp	Pro		

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      1             5             10             15
His Asn Leu Lys Ile Cys Cys Arg Val Asn Gly Glu Val Val Gln Ser
      20             25             30
Ser Asn Thr Asn Gln Met Val Phe Lys Thr Glu Asp Leu Ile Ala Trp
      35             40             45             48

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<210> 960
 <211> 63
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 960
Val Val Ala Val Thr Arg Trp Leu Cys Glu Asn Gly Val Ser Tyr Leu
      1             5             10             15
Arg Lys Cys Val Cys Ser Ala Cys Arg His Gly Thr Arg Cys Ala Gly
      20             25             30
Glu Val Ala Ala Ala Asn Asn Ser His Cys Thr Val Gly Ile Ala
      35             40             45
Phe Asn Ala Lys Ile Gly Gly Met Gly Asn Gln Leu Thr Trp Met
      50             55             60             63

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<210> 961
 <211> 59
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 961
Gly Ala Pro Pro Pro Phe Val Pro Thr Leu Lys Ser Asp Asp Asp Thr
      1             5             10             15
Ser Asn Phe Asp Glu Pro Lys Lys Asn Ser Trp Val Ser Ser Ser Pro
      20             25             30
Cys Gln Leu Ser Pro Ser Gly Phe Ser Gly Glu Glu Leu Pro Phe Val
      35             40             45
Gly Phe Ser Tyr Ser Lys Ala Leu Gly Ile Leu
      50             55             59

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<210> 962
 <211> 140
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 962
Phe Val Glu Arg Leu Ala His Leu His Ala Ala Cys Ala Pro Arg Arg
      1             5             10             15
Lys Val Ala Leu Leu Leu Glu Val Cys Arg Asp Val Tyr Ala Gly Leu
      20             25             30
Ala Arg Gly Glu Asn Gln Asp Pro Leu Gly Ala Asp Ala Phe Leu Pro

```

```

      35      40      45
Ala Leu Thr Glu Glu Leu Ile Trp Ser Pro Asp Ile Gly Asp Thr Gln
  50      55      60
Leu Asp Val Glu Phe Leu Met Glu Leu Leu Asp Pro Asp Glu Leu Arg
  65      70      75      80
Gly Glu Ala Gly Tyr Tyr Leu Thr Thr Trp Phe Gly Ala Leu His His
      85      90      95
Ile Ala His Tyr Gln Pro Glu Thr Asp Arg Ala Pro Arg Gly Leu Ser
      100      105      110
Ser Glu Ala Arg Ala Ser Leu His Gln Trp His Arg Arg Arg Thr Leu
      115      120      125
His Arg Lys Asp His Pro Arg Ala Gln Gln Leu Asp
      130      135      140

```

<210> 963
 <211> 153
 <212> Amino acid
 <213> Homo sapiens

```

<400> 963
Phe Trp Met Asp Pro Tyr Asn Pro Leu Asn Phe Lys Ala Pro Phe Gln
  1      5      10      15
Thr Ser Gly Glu Asn Glu Lys Gly Cys Arg Asp Ser Lys Thr Pro Ser
      20      25      30
Glu Ser Ile Val Ala Ile Ser Glu Cys His Thr Leu Leu Ser Cys Lys
      35      40      45
Val Gln Leu Leu Gly Ser Gln Glu Ser Glu Cys Pro Asp Ser Val Gln
      50      55      60
Arg Asp Val Leu Ser Gly Gly Arg His Thr His Val Lys Arg Lys Lys
      65      70      75      80
Val Thr Phe Leu Glu Glu Val Thr Glu Tyr Tyr Ile Ser Gly Asp Glu
      85      90      95
Asp Arg Lys Gly Pro Trp Glu Glu Phe Ala Arg Asp Gly Cys Arg Phe
      100      105      110
Gln Lys Arg Ile Gln Glu Thr Glu Asp Ala Ile Gly Tyr Cys Leu Thr
      115      120      125
Phe Glu His Arg Glu Arg Met Phe Asn Arg Leu Gln Gly Thr Cys Phe
      130      135      140
Lys Gly Leu Asn Val Leu Lys Gln Cys
      145      150      153

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<210> 964
 <211> 54
 <212> Amino acid
 <213> Homo sapiens

```

<400> 964
Ala Ala Ser Thr Ala Tyr Ser Phe Phe Gly Thr Val Glu Asn Met Ala
  1      5      10      15
Pro Lys Val Val Asn Arg Pro Gly His Thr Gln Ser Ala Asp Trp Gly
      20      25      30
Ser Phe Gly Gly Leu Met Gly Arg Phe Glu Phe Gly Ile Phe Leu Lys
      35      40      45
Gly Lys Glu Ile Val Lys

```

50

54

<210> 965
 <211> 39
 <212>Amino acid
 <213> Homo sapiens

<400> 965
 Gly Phe Val Phe Leu Pro Gly Pro Met Ser Val Gly Leu Asp Phe Ser
 1 5 10 15
 Leu Pro Gly Met Glu His Val Tyr Gly Ile Pro Glu His Ala Asp Asn
 20 25 30
 Leu Arg Leu Lys Val Thr Glu
 35 39

<210> 966
 <211> 130
 <212>Amino acid
 <213> Homo sapiens

<400> 966
 Gly Ser Glu Cys Gln Gly Thr Asp Leu Asp Thr Arg Asn Cys Thr Ser
 1 5 10 15
 Asp Leu Cys Val His Thr Ala Ser Gly Pro Glu Asp Val Ala Leu Tyr
 20 25 30
 Val Gly Leu Ile Ala Val Ala Val Cys Leu Val Leu Leu Leu Val
 35 40 45
 Leu Ile Leu Val Tyr Cys Arg Lys Lys Glu Gly Leu Asp Ser Asp Val
 50 55 60
 Ala Asp Ser Ser Ile Leu Thr Ser Gly Phe Gln Pro Val Ser Ile Lys
 65 70 75 80
 Pro Ser Lys Ala Asp Asn Pro His Leu Leu Thr Ile Gln Pro Asp Leu
 85 90 95
 Ser Thr Thr Thr Thr Thr Tyr Gln Gly Ser Leu Cys Pro Arg Gln Asp
 100 105 110
 Gly Pro Ser Pro Lys Phe Gln Leu Thr Asn Gly His Leu Leu Ser Pro
 115 120 125
 Leu Gly
 130

<210> 967
 <211> 259
 <212>Amino acid
 <213> Homo sapiens

<400> 967
 Leu Ile Tyr Asn Glu Asp Met Ile Cys Trp Ile Glu Ser Arg Glu Ser
 1 5 10 15
 Ser Asn Gln Leu Lys Cys Ile Gln Ile Thr Lys Ala Gly Gly Leu Thr

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<210> 968
<211> 161
<212> Amino acid
<213> Homo sapiens
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533

161

<210> 969
 <211> 76
 <212> Amino acid
 <213> Homo sapiens

<400> 969
 Phe Phe Phe Phe Lys Met Gly Ser Arg Ser Val Thr Gln Ala Gly Val
 1 5 10 15
 Gln Trp Cys Asp Val Ser Ser Leu Gln Ala Pro Pro Pro Arg Phe Thr
 20 25 30
 Leu Phe Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Cys Val Pro
 35 40 45
 Pro Cys Pro Ala Asn Phe Phe Val Phe Leu Val Glu Thr Gly Phe His
 50 55 60
 Arg Val Ser Gln Tyr Gly Leu Asp Leu Leu Thr Ser
 65 70 75 76

<210> 970
 <211> 267
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(267)
 <223> X = any amino acid or stop code

<400> 970
 Gln Leu Ser Leu Ala Arg Gly Lys Val Phe Leu Cys Ala Leu Ser Phe
 1 5 10 15
 Val Tyr Phe Ala Lys Ala Leu Ala Glu Gly Tyr Leu Lys Ser Thr Ile
 20 25 30
 Thr Gln Ile Glu Arg Arg Val Asp Ile Pro Ser Ser Leu Val Gly Val
 35 40 45
 Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val Ile Thr Phe Val
 50 55 60
 Ser Tyr Phe Gly Ala Lys Leu His Arg Pro Lys Ile Ile Gly Ala Gly
 65 70 75 80
 Cys Val Ile Met Gly Val Gly Thr Leu Leu Ile Ala Met Pro Gln Phe
 85 90 95
 Phe Met Glu Gln Tyr Lys Tyr Glu Arg Tyr Ser Pro Ser Ser Asn Ser
 100 105 110
 Thr Leu Ser Ile Ser Pro Cys Leu Leu Glu Ser Ser Ser Gln Leu Pro
 115 120 125
 Val Ser Val Met Glu Lys Ser Lys Ser Lys Ile Ser Asn Glu Cys Glu
 130 135 140
 Val Asp Thr Ser Ser Ser Met Trp Ile Tyr Val Phe Leu Gly Asn Leu
 145 150 155 160
 Leu Arg Gly Ile Gly Glu Thr Pro Ile Gln Pro Leu Gly Ile Ala Tyr
 165 170 175
 Leu Asp Asp Phe Ala Ser Glu Asp Asn Ala Ala Phe Tyr Ile Gly Cys
 180 185 190

Val Gln Thr Val Ala Ile Ile Gly Pro Ile Phe Gly Phe Leu Leu Gly
 195 200 205
 Ser Leu Cys Ala Lys Leu Tyr Val Asp Ile Gly Phe Val Asn Leu Asp
 210 215 220
 His Phe Xaa Val Ser Ala Gln Leu Gly Thr Arg Lys Gly Val Leu Val
 225 230 235 240
 Cys Leu Val Phe Cys Leu Leu Cys Gln Ser Ile Gly Arg Arg Leu Ser
 245 250 255
 Glu Glu His His His Ser Asp Arg Glu Lys Gly
 260 265 267

<210> 971
 <211> 282
 <212> Amino acid
 <213> Homo sapiens

<400> 971
 Gln Pro Ala Gly Arg Val Glu Ala Phe Cys Lys Phe His Met Trp Ala
 1 5 10 15
 Glu Gly Met Thr Ser Leu Met Lys Ala Ala Leu Asp Leu Thr Tyr Pro
 20 25 30
 Ile Thr Ser Met Phe Ser Gly Ala Gly Phe Asn Ser Ser Ile Phe Ser
 35 40 45
 Val Phe Lys Asp Gln Gln Ile Glu Asp Leu Trp Ile Pro Tyr Phe Ala
 50 55 60
 Ile Thr Thr Asp Ile Thr Ala Ser Ala Met Arg Val His Thr Asp Gly
 65 70 75 80
 Ser Leu Trp Arg Tyr Val Arg Ala Ser Met Ser Leu Ser Gly Tyr Met
 85 90 95
 Pro Pro Leu Cys Asp Pro Lys Asp Gly His Leu Leu Met Asp Gly Gly
 100 105 110
 Tyr Ile Asn Asn Leu Pro Ala Asp Val Ala Arg Ser Met Gly Ala Lys
 115 120 125
 Val Val Ile Ala Ile Asp Val Gly Ser Arg Asp Glu Thr Asp Leu Thr
 130 135 140
 Asn Tyr Gly Asp Ala Leu Ser Gly Trp Trp Leu Leu Trp Lys Arg Trp
 145 150 155 160
 Asn Pro Leu Ala Thr Lys Val Lys Val Leu Asn Met Ala Glu Ile Gln
 165 170 175
 Thr Arg Leu Ala Tyr Val Cys Cys Val Arg Gln Leu Glu Val Val Lys
 180 185 190
 Ser Ser Asp Tyr Cys Glu Tyr Leu Arg Pro Pro Ile Asp Ser Tyr Ser
 195 200 205
 Thr Leu Asp Phe Gly Lys Phe Asn Glu Ile Cys Glu Val Gly Tyr Gln
 210 215 220
 His Gly Arg Thr Val Phe Asp Ile Trp Gly Arg Ser Gly Val Leu Glu
 225 230 235 240
 Lys Met Leu Arg Asp Gln Gln Gly Pro Ser Lys Lys Pro Ala Ser Ala
 245 250 255
 Val Leu Thr Cys Pro Asn Ala Ser Phe Thr Asp Leu Ala Glu Ile Val
 260 265 270
 Ser Arg Ile Glu Pro Ala Lys Pro Ala Met
 275 280 282

<210> 972
 <211> 167
 <212> Amino acid
 <213> Homo sapiens

<400> 972

```

Leu Trp Val Ile Met Phe Val Ser Tyr Leu Ile Leu Thr Leu Leu His
 1           5           10           15
Val Gln Thr Ala Val Leu Ala Arg Pro Gly Gly Glu Ser Ile Gly Cys
          20           25           30
Asp Asp Tyr Leu Gly Ser Asp Lys Val Val Asp Lys Cys Gly Val Cys
          35           40           45
Gly Gly Asp Asn Thr Gly Cys Gln Val Val Ser Gly Val Phe Lys His
          50           55           60
Ala Leu Thr Ser Leu Gly Tyr His Arg Val Val Glu Ile Pro Glu Gly
          65           70           75           80
Ala Thr Lys Ile Asn Ile Thr Glu Met Tyr Lys Ser Asn Asn Tyr Leu
          85           90           95
Ala Leu Arg Ser Arg Ser Gly Arg Ser Ile Ile Asn Gly Asn Trp Ala
          100          105          110
Ile Asp Arg Pro Gly Lys Tyr Glu Gly Gly Gly Thr Met Phe Thr Tyr
          115          120          125
Lys Arg Pro Asn Glu Ile Ser Ser Thr Ala Gly Glu Ser Phe Leu Ala
          130          135          140
Glu Gly Pro Thr Asn Glu Ile Leu Asp Val Tyr Val Ser Leu Asp Val
          145          150          155          160
Ser Gly Leu Phe Phe Gly Phe
          165          167

```

<210> 973

<211> 140

<212>Amino acid

<213> Homo sapiens

<400> 973

```

Ile Ser Gly Gly Thr Arg Ser Ala Gly Pro Leu Arg Arg Asn Tyr Asn
 1           5           10           15
Phe Ile Ala Ala Val Val Glu Lys Val Ala Pro Ser Val Val His Val
          20           25           30
Gln Leu Trp Gly Arg Asn Gln Gln Trp Ile Glu Val Val Leu Gln Asn
          35           40           45
Gly Ala Arg Tyr Glu Ala Val Val Lys Asp Ile Asp Leu Lys Leu Asp
          50           55           60
Leu Ala Val Ile Lys Ile Glu Ser Asn Ala Glu Leu Pro Val Leu Met
          65           70           75           80
Leu Gly Arg Ser Ser Asp Leu Arg Ala Gly Glu Phe Val Val Ala Leu
          85           90           95
Gly Ser Pro Phe Ser Leu Gln Asn Thr Ala Thr Ala Gly Ile Val Ser
          100          105          110
Thr Lys Gln Arg Gly Gly Lys Glu Leu Gly Met Lys Asp Ser Asp Met
          115          120          125
Asp Tyr Val Gln Ile Asp Ala Thr Ile Asn Tyr Gly
          130          135          140

```

<210> 974

<211> 286

<212>Amino acid

<213> Homo sapiens

<400> 974

```

Pro Arg Val Arg Glu Leu Lys Glu Ile Leu Asp Arg Lys Gly His Phe
 1           5           10           15
Ser Glu Asn Glu Thr Arg Trp Ile Ile Gln Ser Leu Ala Ser Ala Ile
           20           25           30
Ala Tyr Leu His Asn Asn Asp Ile Val His Arg Asp Leu Lys Leu Glu
           35           40           45
Asn Ile Met Val Lys Ser Ser Leu Ile Asp Asp Asn Asn Glu Ile Asn
           50           55           60
Leu Asn Ile Lys Val Thr Asp Phe Gly Leu Ala Val Lys Lys Gln Ser
           65           70           75           80
Arg Ser Glu Ala Met Leu Gln Ala Thr Cys Gly Thr Pro Ile Tyr Met
           85           90           95
Ala Pro Glu Val Ile Ser Ala His Asp Tyr Ser Gln Gln Cys Asp Ile
           100           105           110
Trp Ser Ile Gly Val Val Met Tyr Met Leu Leu Arg Gly Glu Pro Pro
           115           120           125
Phe Leu Ala Ser Ser Glu Glu Lys Leu Phe Glu Leu Ile Arg Lys Gly
           130           135           140
Glu Leu His Phe Glu Asn Ala Val Trp Asn Ser Ile Ser Asp Cys Ala
145           150           155           160
Lys Ser Val Leu Lys Gln Leu Met Lys Val Asp Pro Ala His Arg Ile
           165           170           175
Thr Ala Lys Glu Leu Leu Asp Asn Gln Trp Leu Thr Gly Asn Lys Leu
           180           185           190
Ser Ser Val Arg Pro Thr Asn Val Leu Glu Met Met Lys Glu Trp Lys
           195           200           205
Asn Asn Pro Glu Ser Val Glu Glu Asn Thr Thr Glu Glu Lys Asn Lys
           210           215           220
Pro Ser Thr Glu Glu Lys Leu Lys Ser Tyr Gln Pro Trp Gly Asn Val
225           230           235           240
Pro Glu Thr Asn Tyr Thr Ser Asp Glu Glu Glu Lys Gln Val Gly
           245           250           255
Arg Ile Ile Ala Ala Phe Leu Pro Ser Val Lys Tyr Pro His His Thr
           260           265           270
Trp Asn Ile Phe Leu Gln Ile Cys Leu Phe Val Val Ser Leu
           275           280           285           286

```

<210> 975

<211> 155

<212> Amino acid

<213> Homo sapiens

<400> 975

```

Leu Ser Ile Ser Val Ser Asp Val Ser Leu Ser Asp Glu Gly Gln Tyr
 1           5           10           15
Thr Cys Ser Leu Phe Thr Met Pro Val Lys Thr Ser Lys Ala Tyr Leu
           20           25           30
Thr Val Leu Gly Val Pro Glu Lys Pro Gln Ile Ser Gly Phe Ser Ser
           35           40           45
Pro Val Met Glu Gly Asp Leu Met Gln Leu Thr Cys Lys Thr Ser Gly
           50           55           60
Ser Lys Pro Ala Ala Asp Ile Arg Trp Phe Lys Asn Asp Lys Glu Ile
65           70           75           80

```

```
<210> 976
<211> 137
<212> Amino acid
<213> Homo sapiens
```

```
<210> 977
<211> 246
<212> Amino acid
<213> Homo sapiens
```

538

Ala Ala Thr Glu Val Ser Leu Leu Ala Gly Ser Glu Glu Phe Asn Ala
 100 105 110
 Thr Lys Leu Phe Glu Val Asp Thr Asp Ser Cys Glu Arg Trp Met Ser
 115 120 125
 Cys Lys Ser Glu Phe Leu Lys Lys Tyr Met His Lys Val Met Asn Asp
 130 135 140
 Leu Pro Ser Cys Pro Cys Ser Tyr Pro Thr Glu Val Ala Tyr Ser Thr
 145 150 155 160
 Ala Asp Ile Phe Asp Arg Ile Lys Arg Lys Asp Phe Arg Trp Lys Asp
 165 170 175
 Ala Ser Gly Pro Lys Glu Lys Leu Glu Ile Tyr Lys Pro Thr Ala Arg
 180 185 190
 Tyr Cys Ile Arg Ser Met Leu Ser Leu Glu Ser Thr Thr Leu Ala Ala
 195 200 205
 Gln His Cys Cys Tyr Gly Asp Asn Met Gln Leu Ile Thr Arg Gly Lys
 210 215 220
 Gly Ala Gly Thr Pro Asn Leu Ile Ser Thr Glu Phe Ser Ala Glu Leu
 225 230 235 240
 His Tyr Lys Val Asp Val
 245 246

<210> 978
 <211> 203
 <212> Amino acid
 <213> Homo sapiens

<400> 978
 Glu Ser Glu Glu Asn Gly Glu Ser Ala Met Asp Ser Thr Val Ala Lys
 1 5 10 15
 Glu Gly Thr Asn Val Pro Leu Val Ala Ala Gly Pro Cys Asp Asp Glu
 20 25 30
 Gly Ile Val Thr Ser Thr Gly Ala Lys Glu Glu Asp Glu Glu Gly Glu
 35 40 45
 Asp Val Val Thr Ser Thr Gly Arg Gly Asn Glu Ile Gly His Ala Ser
 50 55 60
 Thr Cys Thr Gly Leu Gly Glu Ser Glu Gly Val Leu Ile Cys Glu
 65 70 75 80
 Ser Ala Glu Gly Asp Ser Gln Ile Gly Thr Val Val Glu His Val Glu
 85 90 95
 Ala Glu Ala Gly Ala Ala Ile Met Asn Ala Asn Glu Asn Asn Val Asp
 100 105 110
 Ser Met Ser Gly Thr Glu Lys Gly Ser Lys Asp Thr Asp Ile Cys Ser
 115 120 125
 Ser Ala Lys Gly Ile Val Glu Ser Ser Val Thr Ser Ala Val Ser Gly
 130 135 140
 Lys Asp Glu Val Thr Pro Val Pro Gly Gly Cys Glu Gly Pro Met Thr
 145 150 155 160
 Ser Ala Ala Ser Asp Gln Ser Asp Ser Gln Leu Glu Lys Val Glu Asp
 165 170 175
 Thr Thr Ile Ser Thr Gly Leu Val Gly Gly Ser Tyr Asp Val Leu Val
 180 185 190
 Ser Gly Glu Val Pro Glu Cys Glu Val Ala His
 195 200 203

<210> 979
 <211> 94
 <212> Amino acid
 <213> Homo sapiens

<400> 979

```

Val Cys Ile Ile Cys Leu Ile Phe Ser Tyr Tyr Ser Phe Asp Ser Ala
 1          5          10          15
Leu Gln Ser Ala Lys Ser Ser Leu Gly Gly Asn Asp Glu Leu Ser Ala
          20          25          30
Thr Phe Leu Glu Met Lys Gly His Phe Tyr Met Tyr Ala Gly Ser Leu
          35          40          45
Leu Leu Lys Met Gly Gln His Gly Asn Asn Val Gln Trp Arg Ala Leu
          50          55          60
Ser Glu Leu Ala Ala Leu Cys Tyr Leu Ile Ala Phe Gln Val Ser Leu
          65          70          75          80
Pro Leu Gly Ala Ile Asp Ile Ser Arg Ser Leu Asp Val Phe
          85          90          94

```

<210> 980

<211> 226

<212> Amino acid

<213> Homo sapiens

<400> 980

```

Gln His Pro Ser Gln Glu Lys Pro Gln Val Leu Thr Pro Ser Pro Arg
 1          5          10          15
Lys Gln Lys Leu Asn Arg Lys Tyr Arg Ser His His Asp Gln Met Ile
          20          25          30
Cys Lys Cys Leu Ser Leu Ser Ile Ser Tyr Ser Ala Thr Ile Gly Gly
          35          40          45
Leu Thr Thr Ile Ile Gly Thr Ser Thr Ser Leu Ile Phe Leu Glu His
          50          55          60
Phe Asn Asn Gln Tyr Pro Ala Ser Glu Val Val Asn Phe Gly Thr Trp
          65          70          75          80
Phe Leu Phe Ser Phe Pro Ile Ser Leu Ile Met Leu Val Val Ser Trp
          85          90          95
Phe Trp Met His Trp Leu Phe Leu Gly Cys Asn Phe Lys Glu Thr Cys
          100          105          110
Ser Leu Ser Lys Lys Lys Lys Thr Lys Arg Glu Gln Leu Ser Glu Lys
          115          120          125
Arg Ile Gln Glu Glu Tyr Glu Lys Leu Gly Asp Ile Ser Tyr Pro Glu
          130          135          140
Met Val Thr Gly Phe Phe Phe Ile Leu Met Thr Val Leu Trp Phe Thr
          145          150          155          160
Arg Glu Pro Gly Phe Val Pro Gly Trp Asp Ser Phe Phe Glu Lys Lys
          165          170          175
Gly Tyr Arg Thr Asp Ala Thr Val Ser Val Phe Leu Gly Phe Leu Leu
          180          185          190
Phe Leu Ile Pro Ala Lys Lys Pro Cys Phe Gly Lys Lys Asn Asp Gly
          195          200          205
Glu Asn Gln Glu His Ser Leu Gly Thr Glu Pro Ile Ile Thr Trp Lys
          210          215          220
Asp Phe
225 226

```

<210> 981

<211> 163

<212>Amino acid

<213> Homo sapiens

<400> 981

```

Leu Glu Arg Glu Gly Asp Lys Gly Thr Pro Val Leu Arg Gly Phe Ser
 1          5          10          15
Ser Val Ser Gly Ser Trp Ser Arg Arg Met Pro Pro Phe Leu Leu Leu
          20          25          30
Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro Val Ala Leu Asp
          35          40          45
Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp Arg Asn Thr Asp
          50          55          60
His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys Asp Asn His Val
          65          70          75          80
Asn Gly Glu Trp Tyr His Phe Thr Gly Met Ala Gly Asp Ala Met Pro
          85          90          95
Thr Phe Cys Ile Pro Glu Asn His Cys Gly Thr His Ala Pro Val Trp
          100          105          110
Leu Asn Gly Ser His Pro Leu Glu Gly Asp Gly Ile Val Gln Arg Gln
          115          120          125
Ala Cys Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp Asn Thr Thr Val
          130          135          140
Glu Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr Arg Leu Thr Lys
          145          150          155          160
Pro Ser Val
          163

```

<210> 982

<211> 327

<212>Amino acid

<213> Homo sapiens

<400> 982

```

Cys Gly Arg Thr Met Ser Asp Ile Arg His Ser Leu Leu Arg Arg Asp
 1          5          10          15
Ala Leu Ser Ala Ala Lys Glu Val Leu Tyr His Leu Asp Ile Tyr Phe
          20          25          30
Ser Ser Gln Leu Gln Ser Ala Pro Leu Pro Ile Val Asp Lys Gly Pro
          35          40          45
Val Glu Leu Leu Glu Glu Phe Val Phe Gln Val Pro Lys Glu Arg Ser
          50          55          60
Ala Gln Pro Lys Arg Leu Asn Ser Leu Gln Glu Leu Gln Leu Leu Glu
          65          70          75          80
Ile Met Cys Asn Tyr Phe Gln Glu Gln Thr Lys Asp Ser Val Arg Gln
          85          90          95
Ile Ile Phe Ser Ser Leu Phe Ser Pro Gln Gly Asn Lys Ala Asp Asp
          100          105          110
Ser Arg Met Ser Leu Leu Gly Lys Leu Val Ser Met Ala Val Ala Val
          115          120          125
Cys Arg Ile Pro Val Leu Glu Cys Ala Ala Ser Trp Leu Gln Arg Thr
          130          135          140
Pro Val Val Tyr Cys Val Arg Leu Ala Lys Ala Leu Val Asp Asp Tyr
          145          150          155          160
Cys Cys Leu Val Pro Gly Ser Ile Gln Thr Leu Lys Gln Ile Phe Ser
          165          170          175

```

Ala Ser Pro Arg Phe Cys Cys Gln Phe Ile Thr Ser Val Thr Ala Leu
 180 185 190
 Tyr Asp Leu Ser Ser Asp Asp Leu Ile Pro Pro Met Asp Leu Leu Glu
 195 200 205
 Met Ile Val Thr Trp Ile Phe Glu Asp Pro Arg Leu Ile Leu Ile Thr
 210 215 220
 Phe Leu Asn Thr Pro Ile Ala Ala Asn Leu Pro Ile Gly Phe Leu Glu
 225 230 235 240
 Leu Thr Pro Leu Val Gly Leu Ile Arg Trp Cys Val Lys Ala Pro Leu
 245 250 255
 Ala Tyr Lys Arg Lys Lys Lys Pro Pro Leu Ser Asn Gly His Val Ser
 260 265 270
 Asn Lys Val Thr Lys Asp Pro Gly Val Gly Met Asp Arg Asp Ser His
 275 280 285
 Leu Leu Tyr Ser Lys Leu His Leu Ser Val Leu Gln Val Leu Met Thr
 290 295 300
 Leu Gln Leu His Leu Thr Glu Lys Asn Leu Tyr Gly Pro Pro Gly Ala
 305 310 315 320
 Asp Pro Leu Arg Pro His Gly
 325 327

<210> 983
 <211> 110
 <212> Amino acid
 <213> Homo sapiens

<400> 983
 Ser Ala Cys Ser Thr Gly Pro Glu Leu Pro Gly Arg Ala Thr Arg Ser
 1 5 10 15
 Leu Thr Arg Pro Ala Asn Gln Lys Gly Cys Asp Gly Asp Arg Leu Tyr
 20 25 30
 Tyr Asp Gly Cys Ala Met Ile Ala Met Asn Gly Ser Val Phe Ala Gln
 35 40 45
 Gly Ser Gln Phe Ser Leu Asp Asp Val Glu Val Leu Thr Ala Thr Leu
 50 55 60
 Asp Leu Glu Asp Val Arg Ser Tyr Arg Ala Glu Ile Ser Ser Arg Asn
 65 70 75 80
 Leu Ala Val Ser Ala Pro Val Asp Thr Cys Val Gly Cys Ser Ser Lys
 85 90 95
 Thr Trp Lys Val Ala Pro Phe Val Arg Ala Trp Trp Arg Pro
 100 105 110

<210> 984
 <211> 80
 <212> Amino acid
 <213> Homo sapiens

<400> 984
 Ala Pro Leu Ser Arg Leu Cys Phe Pro Gln Val Leu Val Asn Glu Gly
 1 5 10 15
 Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val Arg Gly
 20 25 30
 Val Tyr Ser Phe Arg Phe His Val Lys Val Tyr Asn Arg Gln Thr
 35 40 45

Val	Gln	Val	Thr	Ser	Ala	Leu	Ala	Pro	Ile	Pro	Gly	Ser	Gly	Gly	Trp
50						55					60				
Gly	Gly	Gly	Arg	Arg	Gly	Ala	Gln	Leu	Thr	Ser	Gly	Trp	Thr	Leu	His
65					70					75					80

<210> 985
 <211> 235
 <212>Amino acid
 <213> Homo sapiens

<400> 985

Pro	His	Ile	Ile	Gly	Ala	Glu	Asp	Asp	Asp	Phe	Gly	Thr	Glu	His	Glu
1				5					10					15	
Gln	Ile	Asn	Gly	Gln	Cys	Ser	Cys	Phe	Gln	Ser	Ile	Glu	Leu	Leu	Lys
		20					25						30		
Ser	Arg	Pro	Ala	His	Leu	Ala	Val	Phe	Leu	Arg	His	Val	Val	Ser	Gln
		35				40						45			
Phe	Asp	Pro	Ala	Thr	Leu	Leu	Cys	Tyr	Leu	Tyr	Ser	Asp	Leu	Tyr	Lys
	50					55					60				
His	Thr	Asn	Ser	Lys	Glu	Thr	Arg	Arg	Ile	Phe	Leu	Glu	Phe	His	Gln
	65				70					75					80
Phe	Phe	Leu	Asp	Arg	Ser	Ala	His	Leu	Lys	Val	Ser	Val	Pro	Asp	Glu
			85						90					95	
Met	Ser	Ala	Asp	Leu	Glu	Lys	Arg	Arg	Pro	Glu	Leu	Ile	Pro	Glu	Asp
		100					105						110		
Leu	His	Arg	His	Tyr	Ile	Gln	Thr	Met	Gln	Glu	Arg	Val	His	Pro	Glu
		115				120						125			
Val	Gln	Arg	His	Leu	Glu	Asp	Phe	Arg	Gln	Lys	Arg	Ser	Met	Gly	Leu
	130					135					140				
Thr	Leu	Ala	Glu	Ser	Glu	Leu	Thr	Lys	Leu	Asp	Ala	Glu	Arg	Asp	Lys
	145				150					155					160
Asp	Arg	Leu	Thr	Leu	Glu	Lys	Glu	Arg	Thr	Cys	Ala	Glu	Gln	Ile	Val
			165					170						175	
Ala	Lys	Ile	Glu	Val	Leu	Met	Thr	Ala	Gln	Ala	Val	Glu	Glu	Asp	
		180				185						190			
Lys	Ser	Ser	Thr	Met	Gln	Tyr	Val	Ile	Leu	Met	Tyr	Met	Lys	His	Leu
		195				200						205			
Gly	Val	Lys	Val	Lys	Glu	Pro	Arg	Asn	Leu	Glu	His	Lys	Arg	Gly	Arg
	210					215					220				
Ile	Gly	Phe	Leu	Pro	Lys	Ile	Lys	Gln	Ser	Met					
225					230					235					

<210> 986
 <211> 140
 <212>Amino acid
 <213> Homo sapiens

<400> 986

Ser	Pro	Gly	Thr	Gly	Arg	Gly	Pro	Gly	Pro	Thr	Ser	Phe	Val	Cys	Leu
1				5				10						15	
Pro	Thr	Pro	Gln	Cys	Pro	Phe	Ile	Asp	Phe	Ile	Leu	Ala	Leu	His	
			20					25					30		

Arg Lys Ile Lys Asn Glu Pro Val Val Phe Pro Glu Gly Pro Glu Ile
 35 40 45
 Ser Glu Glu Leu Lys Asp Leu Ile Leu Lys Met Leu Asp Lys Asn Pro
 50 55 60
 Glu Thr Arg Ile Gly Val Pro Asp Ile Lys Leu His Pro Trp Val Thr
 65 70 75 80
 Lys Asn Gly Glu Glu Pro Leu Pro Ser Glu Glu His Cys Ser Val
 85 90 95
 Val Glu Val Thr Glu Glu Glu Val Lys Asn Ser Val Arg Leu Ile Pro
 100 105 110
 Ser Trp Thr Thr Val Ile Leu Val Lys Ser Met Leu Arg Lys Arg Ser
 115 120 125
 Phe Gly Asn Pro Phe Glu Pro Gln Ala Arg Met Ala
 130 135 140

<210> 987

<211> 242

<212>Amino acid

<213> Homo sapiens

<400> 987

His Ala Ser Gly Ile Lys Ile Asp Lys Thr Ser Asp Gly Pro Lys Leu
 1 5 10 15
 Phe Leu Thr Glu Asp Gln Lys Lys Leu His Asp Phe Glu Glu Gln
 20 25 30
 Cys Val Glu Met Tyr Phe Asn Glu Lys Asp Asp Lys Phe His Ser Gly
 35 40 45
 Ser Glu Glu Arg Ile Arg Val Thr Phe Glu Arg Val Glu Gln Met Cys
 50 55 60
 Ile Gln Ile Lys Glu Val Gly Asp Arg Val Asn Tyr Ile Lys Arg Ser
 65 70 75 80
 Leu Gln Ser Leu Asp Ser Gln Ile Gly His Leu Gln Asp Leu Ser Ala
 85 90 95
 Leu Thr Val Asp Thr Leu Lys Thr Leu Thr Ala Gln Lys Ala Ser Glu
 100 105 110
 Ala Ser Lys Val His Asn Glu Ile Thr Arg Glu Leu Ser Ile Ser Lys
 115 120 125
 His Leu Ala Gln Asn Leu Ile Asp Asp Gly Pro Val Arg Pro Ser Val
 130 135 140
 Trp Lys Lys His Gly Val Val Asn Thr Leu Ser Ser Ser Leu Pro Gln
 145 150 155 160
 Gly Asp Leu Glu Ser Asn Asn Pro Phe His Cys Asn Ile Leu Met Lys
 165 170 175
 Asp Asp Lys Asp Pro Gln Cys Asn Ile Phe Gly Gln Asp Leu Pro Ala
 180 185 190
 Val Pro Gln Arg Lys Glu Phe Asn Phe Pro Glu Ala Gly Ser Ser Ser
 195 200 205
 Gly Ala Leu Phe Pro Ser Ala Val Ser Pro Pro Glu Leu Arg Gln Arg
 210 215 220
 Leu His Gly Val Glu Leu Leu Lys Ile Phe Asn Lys Lys Gln Lys Lys
 225 230 235 240
 Arg Ala
 242

<210> 988

<211> 154

<212>Amino acid

<213> Homo sapiens

<400> 988

```

Cys Cys Arg Trp Ile Asp Cys Phe Ala Leu Tyr Asp Gln Gln Glu Glu
 1           5           10           15
Leu Val Arg His Ile Glu Lys Val His Ile Asp Gln Arg Lys Gly Glu
           20           25           30
Asp Phe Thr Cys Phe Trp Ala Gly Cys Pro Arg Arg Tyr Lys Pro Phe
           35           40           45
Asn Ala Arg Tyr Lys Leu Leu Ile His Met Arg Val His Ser Gly Glu
           50           55           60
Lys Pro Asn Lys Cys Thr Phe Glu Gly Cys Glu Lys Ala Phe Ser Arg
           65           70           75           80
Leu Glu Asn Leu Lys Ile His Leu Arg Ser His Thr Gly Glu Lys Pro
           85           90           95
Tyr Leu Cys Gln His Pro Gly Cys Gln Lys Ala Phe Ser Asn Ser Ser
           100          105          110
Asp Arg Ala Lys His Gln Arg Thr His Leu Asp Thr Lys Pro Tyr Ala
           115          120          125
Cys Gln Ile Pro Gly Cys Thr Lys Arg Tyr Thr Asp Pro Ser Ser Leu
           130          135          140
Arg Lys His Val Lys Ala His Ser Ser Lys
145          150          154

```

<210> 989

<211> 65

<212>Amino acid

<213> Homo sapiens

<400> 989

```

Leu Pro Leu Leu Trp Thr Leu Ser Asp Phe Gly Gly Thr Met Asp Gln
 1           5           10           15
Ser Gly Met Glu Ile Pro Val Thr Leu Ile Ile Lys Ala Pro Asn Gln
           20           25           30
Lys Tyr Ser Asp Gln Thr Ile Ser Cys Phe Leu Asn Trp Thr Val Gly
           35           40           45
Lys Leu Lys Thr His Leu Ser Asn Val Tyr Pro Ser Lys Pro Val Ser
           50           55           60
Val
65

```

<210> 990

<211> 297

<212>Amino acid

<213> Homo sapiens

<400> 990

```

Ala Gly Thr Arg Met Cys Val Val Ala Ala Ala Glu Glu Leu Val Cys
 1           5           10           15
Gly Ala Arg Gly Leu Trp Met Arg Arg Thr Arg Arg Pro Arg Phe Val
           20           25           30

```

```

Leu Met Asn Lys Met Asp Asp Leu Asn Leu His Tyr Arg Phe Leu Asn
   35           40           45
Trp Arg Arg Arg Ile Arg Glu Ile Arg Glu Val Arg Ala Phe Arg Tyr
   50           55           60
Gln Glu Arg Phe Lys His Ile Leu Val Asp Gly Asp Thr Leu Ser Tyr
   65           70           75           80
His Gly Asn Ser Gly Glu Val Gly Cys Tyr Val Ala Ser Arg Pro Leu
           85           90           95
Thr Lys Asp Ser Asn Tyr Phe Glu Val Ser Ile Val Asp Ser Gly Val
           100          105          110
Arg Gly Thr Ile Ala Val Gly Leu Val Pro Gln Tyr Tyr Ser Leu Asp
   115          120          125
His Gln Pro Gly Trp Leu Pro Asp Ser Val Ala Tyr His Ala Asp Asp
   130          135          140
Gly Lys Leu Tyr Asn Gly Arg Ala Lys Gly Arg Gln Phe Gly Ser Lys
   145          150          155          160
Cys Asn Ser Gly Asp Arg Ile Gly Cys Gly Ile Glu Pro Val Ser Phe
           165          170          175
Asp Val Gln Thr Ala Gln Ile Phe Phe Thr Lys Asn Gly Lys Arg Val
           180          185          190
Gly Ser Thr Ile Met Pro Met Ser Pro Asp Gly Leu Phe Pro Ala Val
           195          200          205
Gly Met His Ser Leu Gly Glu Glu Val Arg Leu His Leu Asn Ala Glu
   210          215          220
Leu Gly Arg Glu Asp Asp Ser Val Met Met Val Asp Ser Tyr Glu Asp
   225          230          235          240
Glu Trp Gly Arg Leu His Asp Val Arg Val Cys Gly Thr Leu Leu Glu
           245          250          255
Tyr Leu Gly Lys Gly Lys Ser Ile Val Asp Val Gly Leu Ala Gln Ala
           260          265          270
Arg His Pro Leu Ser Thr Arg Ser His Tyr Phe Glu Val Glu Ile Val
           275          280          285
Asp Pro Gly Glu Lys Cys Tyr Ile Ala
   290          295          297

```

<210> 991
 <211> 207
 <212> Amino acid
 <213> Homo sapiens

```

<400> 991
Gln Gln Ala Glu Glu His Leu Ala Ala Tyr Ser Val Ser Asp Ser Asp
   1           5           10           15
Ser Gly Lys Asp Pro Ser Met Glu Cys Cys Arg Arg Ala Thr Pro Gly
           20           25           30
Thr Leu Leu Phe Leu Ala Phe Leu Leu Ser Ser Arg Thr Ala
   35           40           45
Arg Ser Glu Glu Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp
   50           55           60
Ser Glu Cys Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg
   65           70           75           80
Arg Cys Leu Ser Ser Lys Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg
           85           90           95
Thr Cys Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala
           100          105          110
Gln Gln Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe Tyr
   115          120          125
Glu Trp Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser Leu Lys
   130          135          140

```

Cys Gln Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala Pro Lys Val
 145 150 155 160
 Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser
 165 170 175
 Gly Leu Cys Gln Val Ser Ala Asp Leu Phe Ser Phe Asn Leu Ser Arg
 180 185 190
 Gly Phe Gln Cys Leu Cys Val Asn Gly Leu His Ser Leu Thr Leu
 195 200 205 207

<210> 992
 <211> 184
 <212> Amino acid
 <213> Homo sapiens

<400> 992
 Arg Leu Leu Arg Gln Glu Leu Val Val Leu Cys His Leu His His Pro
 1 5 10 15
 Ser Leu Ile Ser Leu Leu Ala Ala Gly Ile Arg Pro Arg Met Leu Val
 20 25 30
 Met Glu Leu Ala Ser Lys Gly Ser Leu Asp Arg Leu Leu Gln Gln Asp
 35 40 45
 Lys Ala Ser Leu Thr Arg Thr Leu Gln His Arg Ile Ala Leu His Val
 50 55 60
 Ala Asp Gly Leu Arg Tyr Leu His Ser Ala Met Ile Ile Tyr Arg Asp
 65 70 75 80
 Leu Lys Pro His Asn Val Leu Leu Phe Thr Leu Tyr Pro Asn Ala Ala
 85 90 95
 Ile Ile Ala Lys Ile Ala Asp Tyr Gly Ile Ala Gln Tyr Cys Cys Arg
 100 105 110
 Met Gly Ile Lys Thr Ser Glu Gly Thr Pro Gly Phe Arg Ala Pro Glu
 115 120 125
 Val Ala Arg Gly Asn Val Ile Tyr Asn Gln Gln Ala Asp Val Tyr Ser
 130 135 140
 Phe Gly Leu Leu Leu Tyr Asp Ile Leu Thr Thr Gly Gly Arg Ile Val
 145 150 155 160
 Glu Gly Leu Lys Phe Pro Asn Glu Phe Asp Glu Leu Glu Ile Gln Gly
 165 170 175
 Lys Leu Pro Asp Pro Val Lys Glu
 180 184

<210> 993
 <211> 144
 <212> Amino acid
 <213> Homo sapiens

<400> 993
 Lys Ala Ser Asn Ser Thr His Glu Phe Arg Ile Gly Leu Pro Glu Gly
 1 5 10 15
 Trp Glu Ser Glu Lys Lys Ala Val Ile Pro Leu Gly Ile Gly Pro Pro
 20 25 30
 Leu Thr Leu Ile Cys Leu Gly Val Leu Gly Gly Ile Leu Ile Tyr Gly
 35 40 45
 Arg Lys Gly Phe Gln Thr Ala His Phe Tyr Leu Lys Asp Ser Pro Ser
 50 55 60

```

Pro Lys Val Ile Ser Thr Pro Pro Pro Pro Ile Phe Pro Ile Ser Lys
 65          70          75          80
Glu Val Gly Pro Ile Pro Ile Lys His Phe Pro Lys His Val Ala Asn
          85          90          95
Leu His Ala Ser Arg Gly Phe Thr Glu Lys Phe Glu Thr Leu Lys Lys
 100          105          110
Phe Tyr Gln Glu Gly Gln Ser Cys Thr Val Asp Leu Gly Ile Thr Ala
 115          120          125
Asn Ser Ser Asn His Pro Asp Asn Arg His Arg Asn Arg Ser Leu Ile
 130          135          140          144

```

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<210> 994
<211> 147
<212>Amino acid
<213> Homo sapiens

```

```

<400> 994
Ser Phe Pro Asp Arg Thr Ala Ser Leu Val Leu Leu Ser Val Pro Val
 1          5          10          15
Gly Gln Ala Gly Met Gln Gln Arg Gly Leu Ala Ile Val Ala Leu Ala
          20          25          30
Val Cys Ala Ala Leu His Ala Ser Pro Ala Ile Leu Pro Ile Ala Ser
          35          40          45
Ser Cys Cys Thr Glu Val Ser His His Ile Ser Arg Arg Leu Leu Glu
 50          55          60
Arg Val Asn Met Cys Arg Ile Gln Arg Ala Asp Gly Asp Cys Asp Leu
 65          70          75          80
Ala Ala Val Ile Leu His Val Lys Arg Arg Arg Ile Cys Val Ser Pro
          85          90          95
His Asn His Thr Val Lys Gln Trp Met Lys Val Gln Ala Ala Lys Lys
          100          105          110
Asn Gly Lys Gly Asn Val Cys His Arg Lys Lys His His Gly Lys Arg
          115          120          125
Asn Ser Asn Arg Ala His Gln Gly Lys His Glu Thr Tyr Gly His Lys
 130          135          140
Thr Pro Tyr
145          147

```

```

<210> 995
<211> 245
<212>Amino acid
<213> Homo sapiens

```

```

<400> 995
Phe Glu Gln Pro Gly Asn Pro Gly Asp Pro Arg Val Arg Thr Pro Pro
 1          5          10          15
Pro Trp Gly Pro His Phe Phe Ala Leu Ile Pro Ser Ser Pro Lys Glu
          20          25          30
Val Pro Ala Thr Pro Ser Ser Arg Arg Asp Pro Ile Ala Pro Thr Ala
          35          40          45
Thr Leu Leu Ser Lys Lys Thr Pro Ala Thr Leu Ala Pro Lys Glu Ala
 50          55          60

```

Leu Ile Pro Pro Ala Met Thr Val Pro Ser Pro Lys Lys Thr Pro Ala
 65 70 75 80
 Ile Pro Thr Pro Lys Glu Ala Pro Ala Thr Pro Ser Ser Lys Glu Ala
 85 90 95
 Ser Ser Pro Pro Ala Val Thr Pro Ser Thr Tyr Lys Gly Ala Pro Ser
 100 105 110
 Pro Lys Glu Leu Leu Ile Pro Pro Ala Val Thr Ser Pro Ser Pro Lys
 115 120 125
 Glu Ala Pro Thr Pro Pro Ala Val Thr Pro Pro Ser Pro Glu Lys Gly
 130 135 140
 Pro Ala Thr Pro Ala Pro Lys Gly Thr Pro Thr Ser Pro Pro Val Thr
 145 150 155 160
 Pro Ser Ser Leu Lys Asp Ser Pro Thr Ser Pro Ala Ser Val Thr Cys
 165 170 175
 Lys Met Gly Ala Thr Val Pro Gln Ala Ser Lys Gly Leu Pro Ala Lys
 180 185 190
 Lys Gly Pro Thr Ala Leu Lys Glu Val Leu Val Ala Pro Ala Pro Glu
 195 200 205
 Ser Thr Pro Ile Ile Thr Ala Pro Thr Arg Lys Gly Pro Gln Thr Lys
 210 215 220
 Lys Ser Ser Ala Thr Ser Pro Pro Ile Cys Pro Asp Pro Ser Ala Lys
 225 230 235 240
 Asn Gly Ser Lys Gly
 245

<210> 996
 <211> 25
 <212> Amino acid
 <213> Homo sapiens

<400> 996
 Phe Phe Leu Lys Ile Gln Gly Leu Gly Trp Ala Arg Trp Leu Thr Pro
 1 5 10 15
 Val Ile Pro Val Leu Trp Glu Ala Glu
 20 25

<210> 997
 <211> 56
 <212> Amino acid
 <213> Homo sapiens

<400> 997
 Ala Gly Phe Gly Tyr Gly Leu Pro Ile Ser Arg Leu Tyr Ala Lys Tyr
 1 5 10 15
 Phe Gln Gly Asp Leu Asn Leu Tyr Ser Leu Ser Gly Tyr Gly Thr Asp
 20 25 30
 Ala Ile Ile Tyr Leu Lys Val Ser Leu Glu Phe Asn Ser Lys Ile Leu
 35 40 45
 Phe Leu Lys Pro Leu Leu Leu Leu
 50 55 56

<210> 998
 <211> 198

<212>Amino acid

<213> Homo sapiens

<400> 998

```

Trp Met Arg Ala Pro Met Leu Gln Lys Gln Gln Ala Pro Arg Met Asp
 1           5           10           15
Thr Pro Pro Pro Glu Glu Arg Leu Glu Lys Gln Asn Glu Lys Leu Asn
      20           25           30
Asn Gln Glu Glu Glu Thr Glu Phe Lys Glu Leu Asp Gly Leu Arg Glu
      35           40           45
Ala Leu Ala Asn Leu Arg Gly Leu Ser Glu Glu Glu Arg Ser Glu Lys
      50           55           60
Ala Met Leu Arg Ser Arg Ile Glu Glu Gln Ser Gln Leu Ile Cys Ile
      65           70           75           80
Leu Lys Arg Arg Ser Asp Glu Ala Leu Glu Arg Cys Gln Ile Leu Glu
      85           90           95
Leu Leu Asn Ala Glu Leu Glu Glu Lys Met Met Gln Glu Ala Glu Lys
      100          105          110
Leu Lys Ala Gln Gly Glu Tyr Ser Arg Lys Leu Glu Glu Arg Phe Met
      115          120          125
Thr Leu Ala Ala Asn His Glu Leu Met Leu Arg Phe Lys Asp Glu Tyr
      130          135          140
Lys Ser Glu Asn Ile Lys Leu Arg Glu Glu Asn Glu Lys Leu Arg Leu
      145          150          155          160
Glu Asn Asn Ser Leu Phe Ser Gln Ala Leu Lys Asp Glu Glu Ala Lys
      165          170          175
Val Leu Gln Leu Thr Val Arg Cys Glu Ala Leu Thr Gly Glu Leu Glu
      180          185          190
Thr Leu Lys Glu Arg Cys
      195          198

```

<210> 999

<211> 79

<212>Amino acid

<213> Homo sapiens

<400> 999

```

Asp Pro Gly Ala Ser His Ala Ser Val Gln Val Gln Val Leu Lys Glu
 1           5           10           15
Gln Leu Phe Ala Gly Arg Met Pro Ser Pro Phe Arg Ser Cys Ala Leu
      20           25           30
Met Gly Met Cys Gly Ser Arg Ser Ala Asp Asn Leu Ser Cys Pro Ser
      35           40           45
Pro Leu Asn Val Met Glu Pro Val Ser Phe Phe Pro Leu Lys Ser Leu
      50           55           60
Gly Lys Gly Met Ile Gln His Phe Arg His Ile Val Ser Leu Val
      65           70           75           79

```

<210> 1000

<211> 206

<212>Amino acid

<213> Homo sapiens

<400> 1000

Val	Thr	Thr	Thr	Thr	His	Ser	Val	Gly	Arg	Gly	His	Glu	Leu	Gln	Leu
1				5					10					15	
Leu	Asn	Glu	Glu	Leu	Arg	Asn	Ile	Glu	Leu	Glu	Cys	Gln	Asn	Ile	Met
			20					25					30		
Gln	Ala	His	Arg	Leu	Gln	Lys	Val	Thr	Asp	Gln	Tyr	Gly	Asp	Ile	Trp
		35					40					45			
Thr	Leu	His	Asp	Gly	Gly	Phe	Arg	Asn	Tyr	Asn	Thr	Ser	Ile	Asp	Met
	50					55					60				
Gln	Arg	Gly	Lys	Leu	Asp	Asp	Ile	Met	Glu	His	Pro	Glu	Lys	Ser	Asp
65					70					75					80
Lys	Asp	Ser	Ser	Ser	Ala	Tyr	Asn	Thr	Ala	Glu	Ser	Cys	Arg	Ser	Thr
			85						90					95	
Pro	Leu	Thr	Val	Asp	Arg	Ser	Pro	Asp	Ser	Ser	Leu	Pro	Arg	Val	Ile
			100					105					110		
Asn	Leu	Thr	Asn	Lys	Lys	Asn	Leu	Arg	Ser	Thr	Met	Ala	Ala	Thr	Gln
	115						120					125			
Ser	Ser	Ser	Gly	Gln	Ser	Ser	Lys	Glu	Ser	Thr	Ser	Thr	Lys	Ala	Lys
	130					135					140				
Thr	Thr	Glu	Gln	Gly	Cys	Ser	Ala	Glu	Ser	Lys	Glu	Lys	Val	Leu	Glu
145					150					155					160
Gly	Ser	Lys	Leu	Pro	Asp	Gln	Glu	Lys	Ala	Val	Ser	Glu	His	Ile	Pro
			165					170						175	
Tyr	Leu	Ser	Pro	Tyr	His	Ser	Ser	Ser	Tyr	Arg	Tyr	Ala	Asn	Ile	Pro
		180						185					190		
Ala	His	Ala	Arg	His	Tyr	Gln	Ser	Tyr	Met	Gln	Leu	Ile	Gln		
	195						200					205	206		

<210> 1001

<211> 138

<212> Amino acid

<213> Homo sapiens

<400> 1001

Val	Trp	Gly	Cys	Leu	Ala	Thr	Val	Ser	Thr	His	Lys	Lys	Ile	Gln	Gly
1				5					10					15	
Leu	Pro	Phe	Gly	Asn	Cys	Leu	Pro	Val	Ser	Asp	Gly	Pro	Phe	Asn	Asn
			20					25					30		
Ser	Thr	Gly	Ile	Pro	Phe	Phe	Tyr	Met	Thr	Ala	Lys	Asp	Pro	Val	Val
	35					40						45			
Ala	Asp	Leu	Met	Lys	Asn	Pro	Met	Ala	Ser	Leu	Met	Leu	Pro	Glu	Ser
	50					55					60				
Glu	Gly	Glu	Phe	Cys	Arg	Lys	Asn	Ile	Val	Asp	Pro	Glu	Asp	Pro	Arg
65					70					75					80
Cys	Val	Gln	Leu	Thr	Leu	Thr	Gly	Gln	Met	Ile	Ala	Val	Ser	Pro	Glu
			85						90					95	
Glu	Val	Glu	Phe	Ala	Lys	Gln	Ala	Met	Phe	Ser	Arg	His	Pro	Gly	Met
		100					105						110		
Arg	Lys	Trp	Pro	Arg	Gln	Tyr	Glu	Trp	Phe	Phe	Met	Lys	Met	Arg	Ile
	115					120						125			
Glu	His	Ile	Trp	Leu	Gln	Lys	Trp	Tyr	Gly						
	130					135			138						

<210> 1002

<211> 133

<212>Amino acid
<213> Homo sapiens

<400> 1002
Gln Ala Ala Asn Met Ala Val Ala Arg Val Asp Ala Ala Leu Pro Pro
1 5 10 15
Gly Glu Gly Ser Val Val Asn Trp Ser Gly Gln Gly Leu Gln Lys Leu
20 25 30
Gly Pro Asn Leu Pro Cys Glu Ala Asp Ile His Thr Leu Ile Leu Asp
35 40 45
Lys Asn Gln Ile Ile Lys Leu Glu Asn Leu Glu Lys Cys Lys Arg Leu
50 55 60
Ile Gln Leu Ser Val Ala Asn Asn Arg Leu Val Arg Met Met Gly Val
65 70 75 80
Ala Lys Leu Thr Leu Leu Arg Val Leu Asn Leu Pro His Asn Ser Ile
85 90 95
Gly Cys Val Glu Gly Leu Lys Glu Leu Val His Leu Glu Trp Leu Asn
100 105 110
Leu Ala Gly Asn Asn Leu Ile Ala Met Glu Gln Ile Asn Ser Cys Thr
115 120 125
Ala Leu Gln His Leu
130 133

<210> 1003
<211> 276
<212>Amino acid
<213> Homo sapiens

<400> 1003
Phe Arg Ala Ala Val Gly Ala Val Pro Glu Gly Ala Trp Lys Asp Thr
1 5 10 15
Ala Gln Leu His Lys Ser Glu Glu Ala Lys Arg Val Leu Arg Tyr Tyr
20 25 30
Leu Phe Gln Gly Gln Arg Tyr Ile Trp Ile Glu Thr Gln Gln Ala Phe
35 40 45
Tyr Gln Val Ser Leu Leu Asp His Gly Arg Ser Cys Asp Asp Val His
50 55 60
Arg Ser Arg His Gly Leu Ser Leu Gln Asp Gln Met Glu Arg Lys Ala
65 70 75 80
Ile Tyr Gly Pro Asn Val Ile Ser Ile Pro Val Lys Ser Tyr Pro Gln
85 90 95
Leu Leu Val Asp Glu Ala Phe Ser Ile Ala Leu Trp Leu Ala Asp His
100 105 110
Tyr Tyr Trp Tyr Ala Leu Cys Ile Phe Leu Ile Ser Ser Ile Ser Ile
115 120 125
Cys Leu Ser Leu Tyr Lys Thr Arg Lys Gln Ser Gln Thr Leu Arg Asp
130 135 140
Met Val Lys Leu Ser Met Arg Val Cys Val Cys Arg Pro Gly Gly Glu
145 150 155 160
Glu Glu Trp Val Asp Ser Ser Glu Leu Val Pro Gly Asp Cys Leu Val
165 170 175
Leu Ser Gln Glu Gly Gly Leu Met Pro Cys Asp Ala Ala Leu Val Ala
180 185 190
Gly Glu Cys Met Val Asn Asp Ser Ser Leu Thr Gly Glu Ser Ile Pro
195 200 205

Val Leu Lys Thr Ala Leu Pro Glu Gly Leu Gly Pro Tyr Cys Ala Glu
 210 215 220
 Thr His Arg Arg His Thr Leu Phe Cys Gly Thr Leu Ile Leu His Ala
 225 230 235 240
 Arg Ala Tyr Val Gly Pro His Val Leu Ala Val Val Thr Arg Thr Gly
 245 250 255
 Met Ser Arg Glu Ala Gly Leu Glu Arg Asp Pro Gly Ser Ala Pro Leu
 260 265 270
 Lys Arg Trp Ser
 275 276

<210> 1004
 <211> 222
 <212> Amino acid
 <213> Homo sapiens

<400> 1004
 Phe Val Gly Gly Gly Leu His Leu His Leu Cys Leu Leu Leu Cys Phe
 1 5 10 15
 Met Leu Pro Glu Asp Ala Ala Met Ala Val Leu Thr Ala Ser Asn His
 20 25 30
 Val Ser Asn Val Thr Val Asn Tyr Asn Ile Thr Val Glu Arg Met Asn
 35 40 45
 Arg Met Gln Gly Leu Arg Val Ser Thr Val Pro Ala Val Leu Ser Pro
 50 55 60
 Asn Ala Thr Leu Ala Leu Thr Ala Gly Val Leu Val Asp Ser Ala Val
 65 70 75 80
 Glu Val Ala Phe Leu Trp Thr Phe Gly Asp Gly Glu Gln Ala Leu His
 85 90 95
 Gln Phe Gln Pro Pro Tyr Asn Glu Ser Phe Pro Val Pro Asp Pro Ser
 100 105 110
 Val Ala Gln Val Leu Val Glu His Asn Val Thr His Thr Tyr Ala Ala
 115 120 125
 Pro Gly Glu Tyr Val Leu Thr Val Leu Ala Ser Asn Ala Phe Glu Asn
 130 135 140
 Arg Thr Gln Gln Val Leu Ile Arg Ser Gly Arg Val Pro Ile Val Ser
 145 150 155 160
 Leu Glu Cys Val Ser Cys Lys Ala Gln Ala Val Tyr Glu Val Ser Arg
 165 170 175
 Ser Ser Tyr Val Tyr Leu Glu Gly Arg Cys Leu Asn Cys Ser Ser Gly
 180 185 190
 Ser Lys Arg Gly Arg Trp Ala Ala Arg Thr Phe Ser Asn Lys Thr Leu
 195 200 205
 Val Leu Asp Glu Thr Thr Thr Ser Thr Gly Ser Ala Ser Met
 210 215 220 222

<210> 1005
 <211> 363
 <212> Amino acid
 <213> Homo sapiens

<400> 1005
 Pro Glu Phe Leu Gly Arg Leu Phe Arg Gly Lys Ala Ala Thr Leu His
 1 5 10 15

```

Val His Ser Asp Gln Lys Pro Leu His Asp Gly Ala Leu Gly Ser Gln
      20              25              30
Gln Asn Leu Val Arg Met Lys Glu Ala Leu Arg Ala Ser Thr Met Asp
      35              40              45
Val Thr Val Val Leu Pro Ser Gly Leu Glu Lys Arg Ser Val Leu Asn
      50              55              60
Gly Ser His Ala Met Met Asp Leu Leu Val Glu Leu Cys Leu Gln Asn
      65              70              75              80
His Leu Asn Pro Ser His His Ala Leu Glu Ile Arg Ser Ser Glu Thr
      85              90              95
Gln Gln Pro Leu Ser Phe Lys Pro Asn Thr Leu Ile Gly Thr Leu Asn
      100             105             110
Val His Thr Val Phe Leu Lys Glu Lys Val Pro Glu Glu Lys Val Lys
      115             120             125
Pro Gly Pro Pro Lys Val Pro Glu Lys Ser Val Arg Leu Val Val Asn
      130             135             140
Tyr Leu Arg Thr Gln Lys Ala Val Val Arg Val Ser Pro Glu Val Pro
      145             150             155             160
Leu Gln Asn Ile Leu Pro Val Ile Cys Ala Lys Cys Glu Val Ser Pro
      165             170             175
Glu His Val Val Leu Leu Arg Asp Asn Ile Ala Gly Glu Glu Leu Glu
      180             185             190
Leu Ser Lys Ser Leu Asn Glu Leu Gly Ile Lys Glu Leu Tyr Ala Trp
      195             200             205
Asp Asn Arg Arg Glu Thr Phe Arg Lys Ser Ser Leu Gly Asn Asp Glu
      210             215             220
Thr Asp Lys Glu Lys Lys Phe Leu Gly Phe Phe Lys Val Asn Lys
      225             230             235             240
Arg Ser Asn Ser Lys Gly Cys Leu Thr Thr Pro Asn Ser Pro Ser Met
      245             250             255
His Ser Arg Ser Leu Thr Leu Gly Pro Ser Leu Ser Leu Gly Ser Ile
      260             265             270
Ser Gly Val Ser Val Lys Ser Glu Met Lys Lys Arg Arg Ala Pro Pro
      275             280             285
Pro Pro Gly Ser Gly Pro Pro Val Gln Asp Lys Ala Ser Glu Lys Val
      290             295             300
Ser Leu Gly Ser Gln Ile Asp Leu Gln Lys Lys Lys Arg Arg Ala Pro
      305             310             315             320
Ala Pro Pro Pro Pro Gln Pro Pro Pro Pro Ser Pro Leu Ile Pro Asn
      325             330             335
Arg Thr Glu Asp Lys Glu Glu Asn Arg Lys Ser Thr Met Val Tyr Cys
      340             345             350
Cys Ala Ser Phe Pro Thr Gln Ala Lys Arg Phe
      355             360             363

```

<210> 1006

<211> 95

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(95)

<223> X = any amino acid or stop code

<400> 1006

```

Val Gln Trp His Asn Leu His Ser Leu Gln Pro Leu Pro Ala Gly Phe
  1              5              10              15
Lys Xaa Phe Leu Cys Phe Ser Leu Pro Ser Ser Trp Asp Tyr Arg Cys

```

```

      20      25      30
Ala Pro Pro Leu Pro Ala Pro Phe Phe Phe Tyr Phe Leu Phe Leu Val
      35      40      45
Glu Leu Gly Phe His His Ile Gly Xaa Ala Gly Leu Glu Leu Thr Ser
      50      55      60
Thr Asp Leu Pro Ala Ser Ala Ser Glu Ser Ala Gly Ile Thr Gly Met
      65      70      75      80
Ser His Arg Ala Arg Pro Met Asp Phe Phe Leu Leu Lys Ile Leu
      85      90      95

```

<210> 1007
 <211> 151
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 1007
Gly Arg Arg Phe Arg Pro Pro Ser Asp Glu Glu Arg Glu Pro Trp Glu
  1      5      10      15
Pro Trp Thr Gln Leu Arg Leu Ser Gly His Leu Lys Pro Leu His Tyr
      20      25      30
Asn Leu Met Leu Thr Ala Phe Met Glu Asn Phe Thr Phe Ser Gly Glu
      35      40      45
Val Asn Val Glu Ile Ala Cys Arg Asn Ala Thr Arg Tyr Val Val Leu
      50      55      60
His Ala Ser Arg Val Ala Val Glu Lys Val Gln Leu Ala Glu Asp Arg
      65      70      75      80
Ala Phe Gly Ala Val Pro Val Ala Gly Phe Phe Leu Tyr Pro Gln Thr
      85      90      95
Gln Val Leu Val Val Val Leu Asn Arg Thr Leu Asp Ala Gln Arg Asn
      100      105      110
Tyr Asn Leu Lys Ile Ile Tyr Asn Ala Leu Ile Glu Asn Glu Leu Leu
      115      120      125
Gly Phe Phe Arg Ser Ser Tyr Val Leu His Gly Glu Arg Arg Phe Leu
      130      135      140
Gly Val Thr Gln Phe Ser Pro
      145      150 151

```

<210> 1008
 <211> 64
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(64)
 <223> X = any amino acid or stop code

```

      <400> 1008
Lys Glu Leu Asp Pro Phe Tyr Asn Ser Xaa Arg Lys Ile Lys Tyr Leu
  1      5      10      15
Arg Ile Tyr Leu Thr Lys Glu Val Lys Asp Leu Tyr Lys Glu Asn Tyr
      20      25      30
Lys Thr Leu Leu Lys Glu Ile Thr Asp Asp Thr Asn Lys Lys His Ile
      35      40      45

```

Pro Ser Ser Trp Thr Gly Arg Ile Asn Thr Val Lys Met Thr Ile Leu
 50 55 60 64

<210> 1009
 <211> 60
 <212> Amino acid
 <213> Homo sapiens

<400> 1009
 Val Pro His Pro Leu Gln Ala Ile His Glu Gln Met Asn Cys Lys Glu
 1 5 10 15
 Tyr Gln Glu Asp Leu Ala Leu Arg Ala Gln Asn Asp Ala Ala Arg
 20 25 30
 Arg Pro Ser Glu Met Phe Lys Val Arg Leu Ala Gln Gly Arg Gly Leu
 35 40 45
 Ala Ser Leu Ser Ser Gly Ile Gln Ser Gly Val Gly
 50 55 60

<210> 1010
 <211> 44
 <212> Amino acid
 <213> Homo sapiens

<400> 1010
 Arg Trp Asn Ser Leu Thr Cys Val Val Leu Thr Phe Leu Gly His Arg
 1 5 10 15
 Leu Leu Lys Arg Phe Leu Val Pro Lys Leu Arg Arg Phe Leu Lys Pro
 20 25 30
 Gln Gly His Pro Arg Leu Leu Leu Trp Phe Lys Arg
 35 40 44

<210> 1011
 <211> 219
 <212> Amino acid
 <213> Homo sapiens

<400> 1011
 Tyr Gly Glu Phe Val Thr Tyr Gln Gly Val Ala Val Thr Arg Ser Arg
 1 5 10 15
 Lys Glu Gly Ile Ala His Asn Tyr Lys Asn Glu Thr Glu Trp Arg Ala
 20 25 30
 Asn Ile Asp Thr Val Met Ala Trp Phe Thr Glu Glu Asp Leu Asp Leu
 35 40 45
 Val Thr Leu Tyr Phe Gly Glu Pro Asp Ser Thr Gly His Arg Tyr Gly
 50 55 60
 Pro Glu Ser Pro Glu Arg Arg Glu Met Val Arg Gln Val Asp Arg Thr
 65 70 75 80

```

Val Gly Tyr Leu Arg Glu Ser Ile Ala Arg Asn His Leu Thr Asp Arg
      85                      90                      95
Leu Asn Leu Ile Ile Thr Ser Asp His Gly Met Thr Thr Val Asp Lys
      100                      105                      110
Arg Ala Gly Asp Leu Val Glu Phe His Lys Phe Pro Asn Phe Thr Phe
      115                      120                      125
Arg Asp Ile Glu Phe Glu Leu Leu Asp Tyr Gly Pro Asn Gly Met Leu
      130                      135                      140
Leu Pro Lys Glu Gly Arg Leu Glu Lys Val Tyr Asp Ala Leu Lys Asp
      145                      150                      155                      160
Ala His Pro Lys Leu His Val Tyr Lys Lys Glu Ala Phe Pro Glu Ala
      165                      170                      175
Phe His Tyr Ala Asn Asn Pro Arg Val Thr Pro Leu Leu Met Tyr Ser
      180                      185                      190
Asp Leu Gly Tyr Val Ile His Gly Val Ser Arg Leu Leu Glu Ala Pro
      195                      200                      205
Pro Pro Gly Ala Pro Ser Pro Gly Ser Gly Ser
      210                      215                      219

```

<210> 1012

<211> 89

<212> Amino acid

<213> Homo sapiens

<400> 1012

```

Arg Ile Pro Leu Leu Arg Leu Arg Ser Ser Thr Tyr Arg Ser Lys Gly
  1                      5                      10                      15
Phe Asp Val Thr Val Lys His Ser His Gly Ser Trp Thr Gly Phe Gly
      20                      25                      30
Gly Glu Asp Leu Ala Thr Ile Pro Lys Gly Leu Asn Thr Tyr Phe Leu
      35                      40                      45
Val Asn Ile Ala Thr Ile Phe Glu Ser Lys Asn Phe Phe Leu Pro Gly
      50                      55                      60
Ile Lys Trp Asn Gly Ile Leu Gly Leu Ser Tyr Ala Thr Leu Ala Lys
      65                      70                      75                      80
Pro Ser Ser Ser Leu Glu Thr Phe Phe
      85                      89

```

<210> 1013

<211> 82

<212> Amino acid

<213> Homo sapiens

<400> 1013

```

Ile Lys Ser Tyr Ser Gly Pro Asn Gly Arg Ser Cys Gln Ile Trp Gln
  1                      5                      10                      15
Arg Leu Arg Trp Gly Ser Arg Glu Leu Leu Leu Gly Trp Lys Leu Ser
      20                      25                      30
His Ser Phe Ser Thr Cys Pro Phe Gln Phe Pro Asp Ile Val Glu Phe
      35                      40                      45
Cys Glu Ala Met Ala Asn Ala Gly Lys Thr Val Ile Val Ala Ala Leu
      50                      55                      60
Asp Gly Thr Phe Gln Arg Lys Val Arg Arg Leu Ile Gln Val Trp Ser
      65                      70                      75                      80

```

Trp Asp
82

<210> 1014
<211> 107
<212> Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(107)
<223> X = any amino acid or stop code

<400> 1014
Tyr Cys Phe Cys Phe Asp Leu Leu His Xaa Cys Ile His Arg Asp Val
1 5 10 15
Lys Pro Glu Asn Ile Leu Ile Thr Lys His Ser Val Ile Lys Leu Cys
20 25 30
Asp Phe Gly Phe Ala Arg Leu Leu Thr Gly Pro Ser Asp Tyr Tyr Thr
35 40 45
Asp Tyr Val Ala Thr Arg Trp Tyr Arg Ser Pro Glu Leu Pro Val Gly
50 55 60
Asp Thr Gln Tyr Gly Pro Pro Val Asp Val Trp Ala Ile Gly Cys Val
65 70 75 80
Ser Ala Glu Leu Leu Ser Gly Lys Cys Leu Trp Trp Pro Gly Lys Ser
85 90 95
Asp Met Leu Asp Gln Leu Tyr Leu Ile Arg Lys
100 105 107

<210> 1015
<211> 70
<212> Amino acid
<213> Homo sapiens

<400> 1015
Arg Gly Trp Ala Leu Asp Trp Ile Gly Ala Asp Leu Ser Leu His Leu
1 5 10 15
Gln Glu Glu Val Glu Thr Glu Val Ala Trp Glu Glu Cys Gly His Val
20 25 30
Leu Leu Ser Leu Cys Tyr Ser Ser Gln Gln Gly Gly Leu Leu Val Gly
35 40 45
Val Leu Arg Cys Ala His Leu Ala Pro Met Asp Ala Asn Gly Tyr Ser
50 55 60
Asp Pro Phe Val Arg Leu
65 70

<210> 1016
<211> 142
<212> Amino acid
<213> Homo sapiens

<400> 1016
 Gly Gly Ile Leu Ala Met Glu Tyr Ala Pro Gly Gly Thr Leu Ala Glu
 1 5 10 15
 Phe Ile Gln Lys Arg Cys Asn Ser Leu Leu Glu Glu Glu Thr Ile Leu
 20 25 30
 His Phe Phe Val Gln Ile Leu Leu Ala Leu His His Val His Thr His
 35 40 45
 Leu Ile Leu His Arg Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Lys
 50 55 60
 His Arg Met Val Val Lys Ile Gly Asp Phe Gly Ile Ser Lys Ile Leu
 65 70 75 80
 Ser Ser Lys Ser Lys Ala Tyr Thr Val Val Gly Thr Pro Cys Tyr Ile
 85 90 95
 Ser Pro Glu Leu Cys Glu Gly Lys Pro Tyr Asn Gln Lys Ser Asp Ile
 100 105 110
 Trp Ala Leu Gly Cys Val Leu Tyr Glu Leu Ala Ser Leu Lys Arg Ala
 115 120 125
 Phe Glu Ala Ala Asn Leu Pro Ala Leu Val Leu Lys Ile Met
 130 135 140 142

<210> 1017
 <211> 87
 <212>Amino acid
 <213> Homo sapiens

<400> 1017
 Val Gln Cys Gly Gly Ile His Gln Val Ser Gly Ala Val Val Val Ser
 1 5 10 15
 Gly Leu Leu Gln Gly Met Met Gly Leu Leu Gly Ser Pro Gly His Val
 20 25 30
 Phe Pro His Cys Gly Pro Leu Val Leu Ala Pro Ser Leu Val Val Ala
 35 40 45
 Gly Leu Ser Ala His Arg Glu Val Ala Gln Phe Cys Phe Thr His Trp
 50 55 60
 Gly Leu Ala Leu Leu Tyr Val Ser Pro Glu Arg Arg Gly Met Val Pro
 65 70 75 80
 Ser Gly Gly Val Trp Gly Asp
 85 87

<210> 1018
 <211> 160
 <212>Amino acid
 <213> Homo sapiens

<400> 1018
 Pro Arg Met Thr Gly Ser Thr His Ala Ser Ala Pro Ser Tyr Gly Gly
 1 5 10 15
 Ser Cys Arg Asn Asn Leu Phe Tyr Arg Glu Glu Thr Tyr Thr Pro Lys
 20 25 30
 Ala Glu Thr Asp Glu Met Asn Glu Val Glu Thr Ala Pro Ile Pro Glu
 35 40 45
 Glu Asn His Val Trp Leu Gln Pro Arg Val Met Arg Pro Thr Lys Pro

50	55	60																	
Lys	Lys	Thr	Ser	Ala	Val	Asn	Tyr	Met	Thr	Gln	Val	Val	Arg	Cys	Asp				
65					70					75					80				
Thr	Lys	Met	Lys	Asp	Arg	Cys	Ile	Gly	Ser	Thr	Cys	Asn	Arg	Tyr	Gln				
			85						90					95					
Cys	Pro	Ala	Gly	Cys	Leu	Asn	His	Lys	Ala	Lys	Ile	Phe	Gly	Ser	Leu				
		100						105					110						
Phe	Tyr	Glu	Ser	Phe	Ala	Ser	Ile	Cys	Arg	Ala	Ala	Ile	His	Tyr	Gly				
	115						120					125							
Ile	Leu	Asp	Asp	Lys	Gly	Gly	Leu	Val	Asp	Ile	Thr	Arg	Asn	Gly	Lys				
130						135					140								
Val	Pro	Phe	Phe	Val	Lys	Ser	Glu	Arg	His	Gly	Val	Gln	Ser	Leu	Arg				
145					150					155					160				

<210> 1019

<211> 174

<212>Amino acid

<213> Homo sapiens

<400> 1019

Val	Pro	Gln	Asn	Ile	Ile	Cys	Ala	Phe	Phe	Cys	Val	Pro	Cys	Arg	Phe				
1				5					10					15					
Ala	Ser	Thr	Ile	Pro	Phe	Trp	Gly	Leu	Thr	Leu	His	Leu	Gln	His	Leu				
		20					25						30						
Gly	Asn	Asn	Val	Phe	Leu	Leu	Gln	Thr	Leu	Phe	Gly	Ala	Val	Thr	Leu				
	35					40					45								
Leu	Ala	Asn	Cys	Val	Ala	Pro	Trp	Ala	Leu	Asn	His	Met	Ser	Arg	Arg				
	50					55					60								
Leu	Ser	Gln	Met	Leu	Leu	Met	Phe	Leu	Leu	Ala	Thr	Cys	Leu	Leu	Ala				
65				70						75					80				
Ile	Ile	Phe	Val	Pro	Gln	Glu	Met	Gln	Thr	Leu	Arg	Val	Val	Leu	Ala				
			85						90					95					
Thr	Leu	Gly	Val	Gly	Ala	Ala	Ser	Leu	Gly	Ile	Thr	Cys	Ser	Thr	Ala				
		100					105						110						
Gln	Glu	Asn	Glu	Leu	Ile	Pro	Ser	Ile	Ile	Arg	Gly	Arg	Ala	Thr	Gly				
	115					120					125								
Ile	Thr	Gly	Asn	Phe	Ala	Asn	Ile	Gly	Gly	Ala	Leu	Ala	Ser	Leu	Val				
130						135				140									
Met	Ile	Leu	Ser	Ile	Tyr	Ser	Arg	Pro	Leu	Pro	Trp	Ile	Ile	Tyr	Gly				
145				150						155					160				
Val	Phe	Ala	Ile	Leu	Ser	Gly	Leu	Val	Val	Leu	Leu	Leu	Pro						
			165					170				174							

<210> 1020

<211> 225

<212>Amino acid

<213> Homo sapiens

<400> 1020

Val	Leu	Val	Ser	Arg	Asp	His	Met	Lys	Ser	Ala	Gln	Gln	Phe	Phe	Gln				
1			5					10					15						
Leu	Val	Gly	Gly	Ser	Ala	Ser	Glu	Cys	Asp	Thr	Ile	Pro	Gly	Arg	Gln				

[illegible]

```
<210> 1021
<211> 118
<212> Amino acid
<213> Homo sapiens
```

[illegible]

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<210> 1022
<211> 178
<212>Amino acid
<213> Homo sapiens
```

<400> 1022

Gly Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr Leu Leu Leu Ser
 1 5 10 15
 Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu Ala Asn Leu Thr
 20 25 30
 Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg Arg Cys Asp His
 35 40 45
 Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe Pro Gln Leu His
 50 55 60
 Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly Leu Val Leu Lys
 65 70 75 80
 Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe Arg Gly Leu Gly
 85 90 95
 Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu Tyr Lys Cys Ile
 100 105 110
 Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu Arg Lys Leu Asn
 115 120 125
 Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala His Leu Val Ser
 130 135 140
 Gly Pro Pro Phe Leu Arg Gly Ser Leu Gly Arg Pro Leu Lys Gly Ala
 145 150 155 160
 Gly Thr Trp His Gly Asn Leu Ser Phe Pro Leu His Phe Glu Trp Gly
 165 170 175
 Lys Thr
 178

<210> 1023

<211> 146

<212>Amino acid

<213> Homo sapiens

<400> 1023

Ile Leu Phe Ala Ala Leu Ile Trp Ser Ser Phe Asp Glu Asn Ile Glu
 1 5 10 15
 Ala Ser Ala Gly Gly Gly Gly Gly Ser Ser Ile Asp Ala Val Met Val
 20 25 30
 Asp Ser Gly Ala Val Val Glu Gln Tyr Lys Arg Met Gln Ser Gln Glu
 35 40 45
 Ser Ser Ala Lys Arg Ser Asp Glu Gln Arg Lys Met Lys Glu Gln Gln
 50 55 60
 Ala Ala Glu Glu Leu Arg Glu Lys Gln Ala Ala Glu Gln Glu Arg Leu
 65 70 75 80
 Lys Gln Leu Glu Lys Glu Arg Leu Ala Ala Gln Glu Gln Lys Lys Gln
 85 90 95
 Ala Glu Glu Ala Ala Lys Gln Ala Glu Leu Lys Gln Lys Gln Ala Glu
 100 105 110
 Glu Ala Ala Ala Lys Ala Ala Ala Asp Ala Lys Ala Lys Ala Glu Ala
 115 120 125
 Asp Ala Lys Ala Ala Glu Glu Ala Ala Lys Lys Ala Ala Ala Asp Ala
 130 135 140
 Lys Lys
 145 146

<210> 1024

<211> 39

<212>Amino acid

<213> Homo sapiens

<400> 1024

Ala	Met	Glu	Ile	Val	His	Glu	Pro	Arg	Asp	Leu	Glu	Arg	Tyr	Met	Arg
1				5					10					15	
Glu	Ala	Val	Lys	Val	Ser	Asn	Asp	Ser	Pro	Val	Leu	Leu	Asp	Arg	Phe
		20					25						30		
Leu	Asn	Asp	Ala	Ile	Glu	Cys									
		35				39									

<210> 1025

<211> 53

<212>Amino acid

<213> Homo sapiens

<400> 1025

Met	Leu	Ser	Pro	Gly	Tyr	Asp	Tyr	Gly	Tyr	Val	Cys	Val	Glu	Phe	Ser
1				5				10						15	
Leu	Leu	Glu	Asp	Ala	Ile	Gly	Cys	Met	Glu	Ala	Asn	Gln	Val	Ala	Leu
		20					25						30		
Tyr	Phe	Gly	Gln	Met	Met	Leu	Glu	Gly	Tyr	Ile	Phe	Leu	Tyr	Met	Gly
		35					40					45			
Arg	Glu	Gly	Phe	Lys											
	50			53											

<210> 1026

<211> 365

<212>Amino acid

<213> Homo sapiens

<400> 1026

Pro	Arg	Val	Arg	Ser	Ser	Gly	Gly	Gln	Glu	Asp	Pro	Ala	Ser	Gln	Gln
1				5				10						15	
Trp	Ala	Arg	Pro	Arg	Phe	Thr	Gln	Pro	Ser	Lys	Met	Arg	Arg	Arg	Val
		20					25						30		
Ile	Ala	Arg	Pro	Val	Gly	Ser	Ser	Val	Arg	Leu	Lys	Cys	Val	Ala	Ser
		35					40					45			
Gly	His	Pro	Arg	Pro	Asp	Ile	Thr	Trp	Met	Lys	Asp	Asp	Gln	Ala	Leu
	50					55				60					
Thr	Arg	Pro	Glu	Ala	Ala	Glu	Pro	Arg	Lys	Lys	Lys	Trp	Thr	Leu	Ser
	65				70				75					80	
Leu	Lys	Asn	Leu	Arg	Pro	Glu	Asp	Ser	Gly	Lys	Tyr	Thr	Cys	Arg	Val
			85				90							95	
Ser	Asn	Arg	Ala	Gly	Ala	Ile	Asn	Ala	Thr	Tyr	Lys	Val	Asp	Val	Ile
		100					105						110		
Gln	Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
		115				120						125			
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	Arg
	130					135					140				
Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	Tyr	Gly

```

145              150              155              160
Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly Gln Lys Phe
              165              170              175
Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro Asp Gly Ser Tyr
              180              185              190
Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln Asp Asp Ala Gly Met
              195              200              205
Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly Tyr Ser Phe Arg Ser Ala
              210              215              220
Phe Leu Thr Val Leu Pro Asp Pro Lys Pro Pro Gly Pro Pro Val Ala
225              230              235              240
Ser Ser Ser Ser Ala Thr Ser Leu Pro Trp Pro Val Val Ile Gly Ile
              245              250              255
Pro Ala Gly Ala Val Phe Ile Leu Gly Thr Leu Leu Leu Trp Leu Cys
              260              265              270
Gln Ala Gln Lys Lys Pro Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro
275              280              285
Gly His Arg Pro Pro Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp
290              295              300
Leu Pro Ser Leu Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys
305              310              315              320
Glu Glu His Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly
              325              330              335
Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile Pro
              340              345              350
His His Thr His Thr His Thr Pro His Pro Pro Ala Asn
              355              360              365

```

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<210> 1027
<211> 30
<212>Amino acid
<213> Homo sapiens

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<400> 1027
Asn Phe His Phe Thr Gly Lys Cys Leu Phe Met Ser Gly Leu Ser Glu
 1              5              10              15
Val Gln Leu Thr His Met Asp Asp His Thr Leu Pro Gly Tyr
              20              25              30

```

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<210> 1028
<211> 104
<212>Amino acid
<213> Homo sapiens

```

```

<400> 1028
Ser Pro Arg Lys Arg Lys Thr Arg His Ser Thr Asn Pro Pro Leu Glu
 1              5              10              15
Cys His Val Gly Trp Val Met Asp Ser Arg Asp His Gly Pro Gly Thr
              20              25              30
Ser Ser Val Ser Thr Ser Asn Ala Ser Pro Ser Glu Gly Ala Pro Leu
              35              40              45
Ala Gly Ser Tyr Gly Cys Thr Pro His Ser Phe Pro Lys Phe Gln His
              50              55              60
Pro Ser His Glu Leu Leu Lys Glu Asn Gly Phe Thr Gln Gln Val Tyr

```

65					70					75				80
His	Lys	Tyr	Arg	Arg	Arg	Cys	Leu	Ser	Glu	Arg	Lys	Arg	Leu	Gly Ile
				85					90					95
Gly	Gln	Ser	Gln	Glu	Met	Asn	Thr							
			100				104							

<210> 1029

<211> 119

<212>Amino acid

<213> Homo sapiens

<400> 1029

Pro	Gly	Ser	Gly	Gly	Ser	Ala	Gly	Gly	Arg	Asp	Gly	Ser	Ala	Tyr	Gln
1				5					10					15	
Gly	Ala	Leu	Leu	Pro	Arg	Glu	Gln	Phe	Ala	Ala	Pro	Leu	Gly	Arg	Pro
			20					25					30		
Val	Gly	Thr	Ser	Tyr	Ser	Ala	Thr	Tyr	Pro	Ala	Tyr	Val	Ser	Pro	Asp
		35					40					45			
Val	Ala	Gln	Ser	Trp	Thr	Ala	Gly	Pro	Phe	Asp	Gly	Ser	Val	Leu	His
	50					55					60				
Gly	Leu	Pro	Gly	Arg	Arg	Pro	Thr	Phe	Val	Ser	Asp	Phe	Leu	Glu	Glu
65					70					75				80	
Phe	Pro	Gly	Glu	Gly	Arg	Glu	Cys	Val	Asn	Cys	Gly	Ala	Leu	Ser	Thr
				85					90					95	
Pro	Leu	Trp	Arg	Arg	Asp	Gly	Thr	Gly	His	Tyr	Leu	Cys	Asn	Ala	Cys
			100					105					110		
Gly	Leu	Tyr	His	Lys	Met	Asn									
			115			119									

<210> 1030

<211> 171

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(171)

<223> X = any amino acid or stop code

<400> 1030

Pro	Asp	His	Arg	His	Gly	Ala	Leu	Trp	Trp	Trp	Tyr	Ser	Cys	Gly	Val
1				5					10					15	
Leu	Pro	Val	Thr	Val	Ser	Arg	Asn	Glu	Gly	Asp	Glu	Arg	Asn	Gln	Val
			20					25					30		
Leu	Thr	Leu	Tyr	Leu	Trp	Ile	Arg	Gln	Glu	Trp	Thr	Asp	Ala	Tyr	Leu
		35				40						45			
Arg	Trp	Asp	Pro	Asn	Ala	Tyr	Gly	Gly	Leu	Asp	Ala	Ile	Arg	Ile	Pro
	50				55						60				
Ser	Ser	Leu	Val	Trp	Arg	Pro	Asp	Ile	Val	Leu	Tyr	Asn	Lys	Tyr	Cys
65					70					75				80	
Leu	Ser	Ala	Ala	Pro	Pro	Leu	Ser	Tyr	Pro	Ser	Leu	Asp	Leu	Pro	Leu
				85					90					95	
Ala	Val	Gly	Val	Xaa	Xaa	Ser	Pro	Leu	Pro	Thr	Thr	Xaa	Pro	Gly	Cys
			100					105					110		

His Ala Ala Leu Glu Ala Phe Pro Gln Asp Pro Ser Lys Leu Pro Ser
 115 120 125
 Thr Gln Pro Leu His Gly Thr Pro Thr Leu Gly Tyr Pro Arg Pro Ala
 130 135 140
 Gln Ala Glu Arg Leu Leu Gly Thr Tyr Cys Val Val Gln Gly Arg Cys
 145 150 155 160
 Leu Asn His Lys Gly Leu Ser Arg Ala His Phe
 165 170 171

<210> 1031
 <211> 198
 <212> Amino acid
 <213> Homo sapiens

<400> 1031
 Tyr Ala Leu Thr Gly Ala Leu Val Ile Val Thr Gly Met Val Met Gly
 1 5 10 15
 Asn Ile Ala Asp Tyr Phe Asn Leu Pro Val Ser Ser Met Ser Asn Thr
 20 25 30
 Phe Thr Phe Leu Asn Ala Gly Ile Leu Ile Ser Ile Phe Leu Asn Ala
 35 40 45
 Trp Leu Met Glu Ile Val Pro Leu Lys Thr Gln Leu Arg Phe Gly Phe
 50 55 60
 Leu Leu Met Val Leu Ala Val Ala Gly Leu Met Phe Ser His Ser Leu
 65 70 75 80
 Ala Leu Phe Ser Ala Ala Met Phe Ile Leu Gly Val Val Ser Gly Ile
 85 90 95
 Thr Met Ser Ile Gly Thr Phe Leu Val Thr Gln Met Tyr Glu Gly Arg
 100 105 110
 Gln Arg Gly Ser Arg Leu Leu Phe Thr Asp Ser Phe Phe Ser Met Ala
 115 120 125
 Gly Met Ile Phe Pro Met Ile Ala Ala Phe Leu Leu Ala Arg Ser Ile
 130 135 140
 Glu Trp Tyr Trp Val Tyr Ala Cys Ile Gly Leu Val Tyr Val Ala Ile
 145 150 155 160
 Phe Ile Leu Thr Phe Gly Cys Glu Phe Pro Ala Leu Cys Ser His Ala
 165 170 175
 Thr Lys Leu Gly Thr Ala Ser Ser Tyr Pro Ser Leu Asp Val Val Gln
 180 185 190
 Leu Arg Thr Leu Asn Ala
 195 198

<210> 1032
 <211> 138
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(138)
 <223> X = any amino acid or stop code

<400> 1032
 Met Ala Lys Val Gly Leu Lys Thr Glu His Tyr Asp Arg Tyr Pro His

1	5	10	15
Met Phe Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Gly Leu			
20	25	30	
Met Leu Asp Pro Asp Val Val Ile Ala Asp Glu Pro Val Ser Ala Leu			
35	40	45	
Asp Val Ser Val Arg Ala Gln Val Leu Asn Leu Met Met Asp Leu Gln			
50	55	60	
Gln Glu Leu Gly Leu Ser Tyr Val Phe Ile Ser His Asp Leu Ser Val			
65	70	75	80
Val Glu His Ile Ala Asp Glu Val Met Val Met Tyr Leu Gly Arg Cys			
85	90	95	
Val Glu Lys Gly Thr Lys Asp Gln Ile Phe Asn Asn Pro Arg His Pro			
100	105	110	
Tyr Thr Gln Ala Leu Leu Ser Ala Thr Pro Arg Leu Asn Pro Asp Asp			
115	120	125	
Arg Arg Glu Arg Ile Lys Leu Ser Xaa *			
130	135	137	

<210> 1033

<211> 141

<212>Amino acid

<213> Homo sapiens

<400> 1033

Ser Ala Thr Leu Glu Arg Val Leu Asn His Pro Asp Glu Thr Gln Ala			
1	5	10	15
Arg Arg Leu Met Thr Leu Glu Asp Ile Val Ser Gly Tyr Ser Asn Val			
20	25	30	
Leu Ile Ser Leu Ala Asp Ser Gln Gly Lys Thr Val Tyr His Ser Pro			
35	40	45	
Gly Ala Pro Asp Ile Arg Glu Phe Thr Arg Asp Ala Ile Pro Asp Lys			
50	55	60	
Asp Ala Gln Gly Gly Glu Val Tyr Leu Leu Ser Gly Pro Thr Met Met			
65	70	75	80
Met Pro Gly His Gly His Gly His Met Glu His Ser Asn Trp Arg Met			
85	90	95	
Ile Asn Leu Pro Val Gly Pro Leu Val Asp Gly Lys Pro Ile Tyr Thr			
100	105	110	
Leu Tyr Ile Ala Leu Ser Ile Asp Phe His Leu His Tyr Ile Asn Asp			
115	120	125	
Leu Met Asn Lys Leu Ile Met Thr Ala Ser Val Ile Ile			
130	135	140	141

<210> 1034

<211> 112

<212>Amino acid

<213> Homo sapiens

<400> 1034

Val Leu Ala Tyr Pro Gly Ile Lys Val Ser Thr Ala Glu Ala Arg Ala			
1	5	10	15
Ile Leu Pro Ala Gln Tyr Arg Arg Gln Asp Cys Ile Ala His Gly Arg			
20	25	30	
His Leu Ala Gly Phe Ile His Ala Cys Tyr Ser Arg Gln Pro Glu Leu			

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<210> 1035
<211> 92
<212> Amino acid
<213> Homo sapiens
```

```
<210> 1036
<211> 51
<212> Amino acid
<213> Homo sapiens
```

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<210> 1037
<211> 72
<212> Amino acid
<213> Homo sapiens
```

<400> 1037

Ala Pro Tyr Asp Ala Glu Asn Tyr Phe Asp Tyr Asp Asn Leu Asn Asn
 1 5 10 15
 Gly Pro Ser Leu Gln His Trp Phe Gly Val Asp Ser Leu Gly Arg Asp
 20 25 30
 Ile Phe Ser Arg Val Leu Val Gly Ala Gln Ile Ser Leu Ala Ala Gly
 35 40 45
 Val Phe Ala Val Phe Ile Gly Ala Ala Ile Gly Thr Leu Leu Gly Leu
 50 55 60
 Leu Ala Gly Tyr Tyr Glu Gly Trp
 65 70 72

<210> 1038

<211> 188

<212>Amino acid

<213> Homo sapiens

<400> 1038

Val Phe Cys Leu Ile Ala Asp Leu Asp Pro Ile Asp Glu Leu Val Asp
 1 5 10 15
 Phe Pro Ile Val Tyr Ala Ser Ala Leu Asn Gly Ile Ala Gly Leu Asp
 20 25 30
 His Glu Asp Met Ala Glu Asp Met Thr Pro Leu Tyr Gln Ala Ile Val
 35 40 45
 Asp His Val Pro Ala Pro Asp Val Asp Leu Asp Gly Pro Phe Gln Met
 50 55 60
 Gln Ile Ser Gln Leu Asp Tyr Asn Ser Tyr Val Gly Val Ile Gly Ile
 65 70 75 80
 Gly Arg Ile Lys Arg Gly Lys Val Lys Pro Asn Gln Gln Val Thr Ile
 85 90 95
 Ile Asp Ser Glu Gly Lys Thr Arg Asn Ala Lys Val Gly Lys Val Leu
 100 105 110
 Gly His Leu Gly Leu Glu Arg Ile Glu Thr Asp Leu Ala Glu Ala Gly
 115 120 125
 Asp Ile Val Ala Ile Thr Gly Leu Gly Glu Leu Asn Ile Ser Asp Thr
 130 135 140
 Val Cys Asp Thr Gln Asn Val Glu Ala Leu Pro Ala Leu Ser Val Asp
 145 150 155 160
 Glu Pro Thr Val Ser Met Phe Phe Cys Val Asn Thr Ser Pro Phe Cys
 165 170 175
 Gly Lys Glu Gly Lys Phe Val Thr Ser Arg Gln Ile
 180 185 188

<210> 1039

<211> 122

<212>Amino acid

<213> Homo sapiens

<400> 1039

Gln Gly Thr Arg Ala Glu Ser Gln Gly Ser Ser Lys Asp Lys Thr Arg
 1 5 10 15
 Leu Ala Phe Ala Gly Leu Lys Phe Gly Asp Tyr Gly Ser Ile Asp Tyr

```

      20      25      30
Gly Arg Asn Tyr Gly Val Ala Tyr Asp Ile Gly Ala Trp Thr Asp Val
      35      40      45
Leu Pro Glu Phe Gly Gly Asp Thr Trp Thr Gln Thr Asp Val Phe Met
      50      55      60
Thr Gln Arg Ala Thr Gly Val Ala Thr Tyr Arg Asn Asn Asp Phe Phe
      65      70      75      80
Gly Leu Val Asp Gly Leu Asn Phe Ala Ala Gln Tyr Gln Gly Lys Asn
      85      90      95
Asp Arg Ser Asp Phe Asp Asn Tyr Thr Glu Gly Asn Gly His Gly Phe
      100      105      110
Gly Phe Ser Ala Thr Tyr Glu Tyr Glu Gly
      115      120      122

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<210> 1040
 <211> 65
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 1040
Asp Thr Tyr Ser Val Ser Ile Pro Leu Gly Ala Thr Ile Asn Met Ala
  1      5      10      15
Gly Ala Ala Ile Thr Ile Thr Val Leu Thr Leu Ala Ala Val Asn Thr
      20      25      30
Leu Gly Ile Pro Val Asp Leu Pro Thr Ala Leu Leu Leu Ser Val Val
      35      40      45
Ala Ser Leu Cys Ala Cys Gly Ala Ser Gly Val Ala Gly Gly Ser Leu
      50      55      60
Leu
  65

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<210> 1041
 <211> 46
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 1041
Ala Asn Ala Gln Gln Gly Leu Pro Ser Gly Ile Thr Leu Lys Leu Asn
  1      5      10      15
Asn Leu Val Asp Lys Gly Leu Val Asp Arg Leu Tyr Ala Ala Ser Ser
      20      25      30
Ser Gly Val Pro Val Asn Leu Leu Val Arg Gly Thr Cys Ser
      35      40      45      46

```

<210> 1042
 <211> 146
 <212>Amino acid
 <213> Homo sapiens

<400> 1042

Ala Arg Met Thr Leu Ile Pro Gly Thr His Leu Leu Glu Asn Ile His
 1 5 10 15
 Asn Ile Trp Val Asn Gly Val Gly Thr Asn Ser Ala Pro Phe Trp Arg
 20 25 30
 Met Leu Leu Asn Ser Phe Val Met Ala Phe Ser Ile Thr Leu Gly Lys
 35 40 45
 Ile Thr Val Ser Met Leu Ser Ala Phe Ala Ile Val Trp Phe Arg Phe
 50 55 60
 Pro Leu Arg Asn Leu Phe Phe Trp Met Ile Phe Ile Thr Leu Met Leu
 65 70 75 80
 Pro Val Glu Val Arg Ile Phe Pro Thr Val Glu Val Ile Ala Asn Leu
 85 90 95
 Gln Met Leu Asp Ser Tyr Ala Gly Leu Thr Leu Pro Leu Met Ala Ser
 100 105 110
 Ala Thr Ala Thr Phe Leu Phe Arg Lys Leu Asn Met Ser Gly Pro Asp
 115 120 125
 Lys Val Val Pro Ala Ala Arg Ile Ser Gly Tyr Gly Pro Arg Val Arg
 130 135 140
 Lys Gln
 145 146

<210> 1043

<211> 133

<212>Amino acid

<213> Homo sapiens

<400> 1043

Cys Ala Lys Cys Leu Arg Asp Ala Asp Glu Cys Pro Ser Gly Ala Phe
 1 5 10 15
 Glu Arg Ile Gly Arg Asp Ile Ser Leu Asp Ala Leu Glu Arg Glu Val
 20 25 30
 Met Lys Asp Asp Ile Phe Phe Arg Thr Ser Gly Gly Gly Val Thr Leu
 35 40 45
 Ser Gly Gly Glu Val Leu Met Gln Ala Glu Phe Ala Thr Arg Phe Leu
 50 55 60
 Gln Arg Leu Arg Leu Trp Gly Val Ser Cys Ala Ile Glu Thr Ala Gly
 65 70 75 80
 Asp Ala Pro Ala Ser Lys Leu Leu Pro Leu Ala Lys Leu Cys Asp Glu
 85 90 95
 Val Leu Phe Asp Leu Lys Ile Met Asp Ala Thr Gln Ala Arg Asp Val
 100 105 110
 Val Lys Met Asn Leu Pro Arg Val Leu Glu Asn Leu Arg Leu Leu Val
 115 120 125
 Ser Glu Gly Val Asn
 130 133

<210> 1044

<211> 115

<212>Amino acid

<213> Homo sapiens

<400> 1044

Tyr Leu Leu Leu Phe Val Cys Phe Leu Val Met Ser Leu Leu Val Gly

```

      1             5             10             15
Leu Val Tyr Lys Phe Thr Ala Glu Arg Ala Gly Lys Gln Ser Leu Asp
      20             25             30
Asp Leu Met Asn Ser Ser Leu Tyr Leu Met Arg Ser Glu Leu Arg Glu
      35             40             45
Ile Pro Pro His Asp Trp Gly Lys Thr Leu Lys Glu Met Asp Leu Asn
      50             55             60
Leu Ser Phe Asp Leu Arg Val Glu Pro Leu Ser Lys Tyr His Leu Asp
      65             70             75             80
Asp Ile Ser Met His Arg Leu Arg Gly Gly Glu Ile Val Ala Leu Asp
      85             90             95
Asp Gln Tyr Thr Phe Leu Gln Arg Ile Pro Arg Ser His Tyr Val Leu
      100             105             110
Ala Val Gly
      115

```

```

<210> 1045
<211> 69
<212>Amino acid
<213> Homo sapiens

```

```

      <400> 1045
Val Glu Leu Phe Leu Ser Asp Glu Gly Asp Asp Val Val Ile Glu Val
      1             5             10             15
Ala Asp Gln Gly Cys Gly Val Pro Glu Ser Leu Arg Asp Lys Ile Phe
      20             25             30
Glu Gln Gly Val Ser Thr Arg Ala Asp Glu Pro Gly Glu His Gly Ile
      35             40             45
Gly Leu Tyr Leu Ile Ala Ser Tyr Val Thr Arg Cys Gly Gly Val Ile
      50             55             60
Thr Leu Glu Asp Asn
      65             69

```

```

<210> 1046
<211> 69
<212>Amino acid
<213> Homo sapiens

```

```

      <400> 1046
Asp Ala Ile Ile Ala Pro Asp Ala Asn Ala Leu Pro Ala Ala Ala Gln
      1             5             10             15
Ala Ala Glu Asn Leu Lys Asn Asp Lys Val Ala Ile Val Gly Phe Ser
      20             25             30
Thr Pro Asn Val Met Arg Pro Tyr Val Glu Arg Gly Thr Val Lys Glu
      35             40             45
Phe Gly Leu Trp Asp Val Val Gln Gln Gly Lys Ile Ser Val Tyr Val
      50             55             60
Ala Asp Ala Leu Gln
      65             69

```

```

<210> 1047
<211> 43
<212>Amino acid

```

<213> Homo sapiens

<400> 1047

```

Tyr Ile Val Val Thr Gly Lys Thr His Cys Gly Thr Pro Leu Thr Thr
 1           5           10           15
Val Thr Gly Asp Ala Thr Gln Ser Gly Tyr Leu Thr Leu Asn Leu Pro
          20           25           30
Glu Met Trp Glu Val Ser Gly Tyr Asn Arg Val
          35           40           43

```

<210> 1048

<211> 77

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(77)

<223> X = any amino acid or stop code

<400> 1048

```

Xaa Glu Gly Val Glu Pro Asp Ile Asn Ala Ser Lys Thr Arg Gln Gln
 1           5           10           15
Leu Asn Asp Val Ala Gly Lys Met Lys Ile Ile Glu Ala Arg Leu Ser
          20           25           30
Ala Leu Thr Asn Asn Gln Thr Lys Ser Leu Lys Leu Asn Pro Val Ala
          35           40           45
Leu Pro Lys Val Ala Ser Gln Leu Leu Asp Glu Leu Gly Tyr Ser Leu
          50           55           60
Leu Ala Arg Arg Ala Asp Leu Gln Ser Ala His Xaa *
65           70           75 76

```

<210> 1049

<211> 79

<212>Amino acid

<213> Homo sapiens

<400> 1049

```

Glu Asn Ile Ala Glu Glu Tyr Ala Thr Lys Arg Tyr Arg Ser Asn Val
 1           5           10           15
Ile Asn Trp Gly Met Leu Pro Leu Gln Met Ala Glu Val Pro Thr Phe
          20           25           30
Glu Val Gly Asp Tyr Ile Tyr Ile Pro Gly Ile Lys Ala Ala Leu Asp
          35           40           45
Asn Pro Gly Thr Thr Phe Lys Gly Tyr Val Ile His Glu Asp Ala Pro
          50           55           60
Val Thr Glu Ile Thr Leu Tyr Met Glu Ser Gln Glu Ala Arg Thr
65           70           75 79

```

<210> 1050
 <211> 99
 <212>Amino acid
 <213> Homo sapiens

<400> 1050
 Leu Gln Thr Glu Ile Gly Ser Met Val Tyr Ala Val Lys Pro Gly Asp
 1 5 10 15
 Gly Ser Ala Arg Glu Gln Ala Ala Ser Cys Gln Arg Val Ile Gly Gly
 20 25 30
 Leu Ala Asn Ile Ala Glu Glu Tyr Ala Thr Lys Arg Tyr Arg Ser Asn
 35 40 45
 Val Ile Asn Trp Gly Met Leu Pro Leu Gln Met Ala Glu Val Pro Thr
 50 55 60
 Phe Glu Val Gly Asp Tyr Ile Tyr Ile Leu Gly Phe Lys Ala Ala Lys
 65 70 75 80
 Tyr Ser Pro Gly Thr Ala Phe Thr Val Tyr Ala Ile Ser Gly Tyr Gly
 85 90 95
 Pro Arg Ile
 99

<210> 1051
 <211> 114
 <212>Amino acid
 <213> Homo sapiens

<400> 1051
 Thr Leu Glu Asp Leu Leu Met Ala Leu Asp Gly Glu Gln His Leu Gln
 1 5 10 15
 Gln Gln Val Ser Glu Lys Val Leu Ala Asp Asn Val Leu Ile Ala Pro
 20 25 30
 Gly Ser Val Lys Pro Asp Ala Thr Phe Trp Ser Ala Leu Ile Gln Asp
 35 40 45
 Arg Tyr Asn Val Met Thr Cys Ile Glu Lys Asp Ala Cys Val Leu Val
 50 55 60
 Glu Gln Asp Leu Asn Ser Asp Gly Gln Ala Glu Arg Ile Leu Phe Ala
 65 70 75 80
 Phe Asn Asp Asp Arg Val Ile Val Tyr Gly Phe Asp Ser Asp Arg Lys
 85 90 95
 Glu Trp Asp Ala Leu Asp Met Ser Leu Leu Pro Asn Glu Ile Thr Lys
 100 105 110
 Glu Lys
 114

<210> 1052
 <211> 210
 <212>Amino acid
 <213> Homo sapiens

<400> 1052

Glu Ser Asn Ser Arg Cys Arg Lys Met Pro Gly Glu Arg Cys Arg Gly
 1 5 10 15
 Gly Pro Ala Arg Leu Ser Leu Leu Leu Asp Leu Pro Thr Arg Pro Leu
 20 25 30
 Pro His Pro Arg Gln Val Ile Asp Phe Gly Ser Ala Ser Ile Phe Ser
 35 40 45
 Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile Gln Ser Arg Phe Tyr Arg
 50 55 60
 Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe Cys Glu Lys Val Asp Val
 65 70 75 80
 Trp Ser Leu Gly Cys Val Met Asp Glu Leu His Leu Gly Trp Pro Leu
 85 90 95
 Tyr Pro Gly Asn Asn Glu Tyr Asp Gln Val Arg Tyr Ile Cys Glu Thr
 100 105 110
 Gln Gly Leu Pro Lys Pro His Leu Leu His Ala Ala Cys Lys Ala His
 115 120 125
 His Phe Phe Lys Arg Asn Pro His Pro Asp Ala Ala Asn Pro Trp Gln
 130 135 140
 Leu Lys Ser Ser Ala Asp Tyr Leu Ala Glu Thr Lys Val Arg Pro Leu
 145 150 155 160
 Glu Arg Arg Lys Tyr Met Leu Lys Ser Leu Asp Gln Ile Glu Thr Val
 165 170 175
 Asn Gly Gly Ser Val Ala Ser Arg Leu Thr Phe Pro Asp Arg Glu Ala
 180 185 190
 Leu Ala Glu His Ala Asp Leu Lys Ser Met Val Glu Leu Met Lys Arg
 195 200 205
 Leu Leu
 210

<210> 1053

<211> 100

<212> Amino acid

<213> Homo sapiens

<400> 1053

Arg Leu Val Lys Lys Arg Val Glu Cys Arg Gln Cys Gly Lys Ala Gly
 1 5 10 15
 Arg Asn Gln Ser Thr Leu Lys Thr His Met Arg Ser His Thr Gly Glu
 20 25 30
 Lys Pro Tyr Glu Cys Asp His Cys Gly Lys Ala Phe Ser Ile Gly Ser
 35 40 45
 Asn Leu Asn Val His Arg Arg Ile His Thr Gly Glu Lys Pro Tyr Glu
 50 55 60
 Cys Leu Val Cys Gly Glu Ala Phe Ser Asp His Ser Ser Leu Arg Ser
 65 70 75 80
 His Val Lys Thr His Arg Gly Glu Lys Leu Phe Val Ser Ser Val Trp
 85 90 95
 Lys Arg Leu Gln
 100

<210> 1054

<211> 194

<212> Amino acid

<213> Homo sapiens

<400> 1054

```

Cys Gly Pro Gly Phe Ser Leu Ser Phe Phe Phe Leu Arg Trp Ser Phe
 1           5           10           15
Ala Leu Val Ala Gln Ala Gly Val Gln Trp His Asp Leu Gly Ser Leu
      20           25           30
Gln Pro Pro Ala Pro Gly Phe Lys Arg Phe Ser Ser Leu Ser Leu Leu
      35           40           45
Ser Arg Trp Asp Tyr Arg His Ala His Ala Arg Leu Ile Phe Val Phe
      50           55           60
Leu Val Glu Met Gly Phe Leu His Val Gly Gln Ala Gly Leu Glu Leu
      65           70           75           80
Pro Thr Ser Gly Asp Pro Pro Thr Ser Ala Ser Gln Ser Ala Arg Ile
      85           90           95
Thr Gly Val Thr Thr Pro Leu Gly Thr Phe Phe Phe Phe Leu Arg Trp
      100           105           110
Ser Phe Ala Leu Val Ala Gln Ala Gly Gly Gln Cys Leu Asp Leu Gly
      115           120           125
Ser Leu Gln Leu Pro Pro Pro Gly Phe Lys Arg Leu Val Cys His Phe
      130           135           140
Gln Thr Pro Gln Lys His Arg Cys Ser Cys Gln Ala Pro Gly Asp Cys
      145           150           155           160
Leu Gln Glu Ser Phe Val Met Thr Gly Cys Val Leu Arg Thr Val Ser
      165           170           175
Glu Ser Val Gln Arg Ala Asn Ala Gly Ala Gly Ala Glu Thr Val Gln
      180           185           190
Gly Leu
      194

```

<210> 1055

<211> 351

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(351)

<223> X = any amino acid or stop code

<400> 1055

```

Met Gly Asn Ala Ala Ala Lys Lys Gly Ser Glu Gln Glu Ser Val
 1           5           10           15
Lys Glu Phe Leu Ala Lys Ala Lys Glu Asp Phe Leu Lys Lys Trp Glu
      20           25           30
Ser Pro Ala Gln Asn Thr Ala His Leu Asp Gln Phe Glu Arg Ile Lys
      35           40           45
Thr Leu Gly Thr Gly Ser Phe Gly Arg Val Met Leu Val Lys His Lys
      50           55           60
Glu Thr Gly Asn His Tyr Ala Met Lys Ile Leu Asp Xaa Gln Lys Val
      65           70           75           80
Gly Lys Leu Lys Gln Ile Glu His Thr Leu Asn Glu Lys Arg Ile Leu
      85           90           95
Gln Ala Val Asn Phe Pro Phe Leu Val Lys Leu Glu Phe Ser Phe Lys
      100           105           110
Asp Asn Ser Asn Leu Tyr Met Val Met Glu Tyr Val Pro Gly Gly Glu
      115           120           125
Met Phe Ser His Leu Arg Arg Ile Gly Arg Phe Ser Glu Pro His Ala
      130           135           140
Arg Phe Tyr Ala Ala Gln Ile Val Leu Thr Phe Glu Tyr Leu His Ser

```

```

145          150          155          160
Leu Asp Leu Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu Leu Ile Asp
          165          170          175
Gln Gln Gly Tyr Ile Gln Val Thr Asp Phe Gly Phe Ala Lys Arg Val
          180          185          190
Lys Gly Arg Thr Trp Thr Leu Cys Gly Thr Pro Glu Tyr Leu Ala Pro
          195          200          205
Glu Ile Ile Leu Ser Lys Gly Tyr Asn Lys Ala Val Asp Trp Trp Ala
          210          215          220
Leu Gly Val Leu Ile Tyr Glu Met Ala Ala Gly Tyr Pro Pro Phe Phe
225          230          235          240
Ala Asp Gln Pro Ile Gln Ile Tyr Glu Lys Ile Val Ser Gly Lys Val
          245          250          255
Arg Phe Pro Ser His Phe Ser Ser Asp Leu Lys Asp Leu Leu Arg Asn
          260          265          270
Leu Leu Gln Val Asp Leu Thr Lys Arg Phe Gly Asn Leu Lys Asn Gly
          275          280          285
Val Asn Asp Ile Lys Asn His Lys Lys Trp Phe Ala Thr Thr Asp Trp Ile
          290          295          300
Ala Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Lys
305          310          315          320
Gly Pro Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Glu Ile
          325          330          335
Arg Val Ser Ile Asn Glu Lys Phe Gly Lys Glu Phe Ser Glu Phe
          340          345          350 351

```

<210> 1056

<211> 136

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (136)

<223> X = any amino acid or stop code

<400> 1056

```

Ser Ser Ser Arg Ser Ser His Gly Asp Ser Pro Pro His Ser Gln Thr
 1          5          10          15
Pro Cys Asp Thr Asn Arg Gly Leu Asp Thr Lys His Xaa Asp Ser Gln
          20          25          30
Ser Ile Glu Glu Lys Asp Ser Ser Gln Ser Glu Xaa Asn Arg Ile Glu
          35          40          45
Arg Arg Lys Glu Val Glu Arg Ile Leu Gln Thr Asn Ser Asp Tyr Met
          50          55          60
Xaa His Trp Ser Asn Xaa Pro Glu Asn Ile Leu Pro Lys Lys Phe Phe
          65          70          75          80
Ser Lys His Gln Lys Cys Thr Ala Thr Leu Ser Met Arg Asn Thr Ser
          85          90          95
Ile Met Lys Lys Glu Gly Leu Phe Xaa Ala Gln Phe Pro Ser Leu Leu
          100          105          110
Leu Ser His Leu Pro Ala Val Gly Leu Gly Ile Tyr Thr Gly Thr His
          115          120          125
Leu Thr Thr Ser Thr Ser Thr Phe
          130          135 136

```

<210> 1057

<211> 79

<212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(79)
 <223> X = any amino acid or stop code

<400> 1057

```

Thr Phe His Ser Ser Leu Glu Lys Asn Ile Leu Gln Pro Cys Arg Xaa
 1           5           10           15
Arg Arg Ala Ile Cys Leu Pro Leu Leu Leu Xaa Pro Ser Val Pro Leu
          20           25           30
Leu Ala Pro Gln Tyr Phe Ser Asp Leu Arg Asn Ser Ile Val Asn Ser
          35           40           45
Gln Pro Pro Glu Lys Gln Gln Ala Met His Leu Cys Phe Glu Asn Leu
          50           55           60
Met Glu Gly Ile Glu Arg Asn Leu Leu Thr Lys Asn Arg Asp Arg
 65           70           75           79

```

<210> 1058
 <211> 458
 <212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(458)
 <223> X = any amino acid or stop code

<400> 1058

```

Gly Thr Ser Gly Val Gln Gln Glu Ile Ser Arg Leu Thr Asn Glu Asn
 1           5           10           15
Leu Asp Leu Lys Glu Leu Val Glu Lys Leu Glu Lys Asn Glu Arg Lys
          20           25           30
Leu Lys Lys Gln Leu Lys Ile Tyr Met Lys Lys Ala Gln Asp Leu Glu
          35           40           45
Ala Ala Gln Ala Leu Ala Gln Ser Glu Arg Lys Arg His Glu Leu Asn
          50           55           60
Arg Gln Val Thr Val Gln Arg Lys Glu Lys Asp Phe Gln Gly Met Leu
 65           70           75           80
Glu Tyr His Lys Glu Asp Glu Ala Leu Leu Ile Arg Asn Leu Val Thr
          85           90           95
Asp Leu Lys Pro Gln Met Leu Ser Gly Thr Val Pro Cys Leu Pro Ala
          100          105          110
Tyr Ile Leu Tyr Met Cys Ile Arg His Ala Asp Tyr Thr Asn Asp Asp
          115          120          125
Leu Lys Val His Ser Leu Leu Thr Ser Thr Ile Asn Gly Ile Lys Lys
          130          135          140
Val Leu Lys Lys His Asn Asp Asp Phe Glu Met Thr Ser Phe Trp Leu
 145          150          155          160
Ser Asn Thr Cys Arg Leu Leu His Cys Leu Lys Gln Tyr Ser Gly Asp
          165          170          175
Glu Gly Phe Met Thr Gln Asn Thr Ala Lys Gln Asn Glu His Cys Leu
          180          185          190

```

```

Lys Asn Phe Asp Leu Thr Glu Tyr Arg Gln Val Leu Ser Asp Leu Ser
    195                200                205
Ile Gln Ile Tyr Gln Gln Leu Ile Lys Ile Ala Glu Gly Val Leu Gln
    210                215                220
Pro Met Ile Val Ser Ala Met Leu Glu Asn Xaa Ser Ile Gln Gly Leu
    225                230                235                240
Ser Gly Val Lys Pro Thr Gly Ser Gln Lys His Ser Ser Ser Met Ala
    245                250                255
Asp Glu Asp Asn Ser Tyr Arg Leu Glu Ala Ile Ile Arg Gln Met Asn
    260                265                270
Ala Phe His Thr Val Met Cys Asp Gln Gly Leu Asp Pro Glu Ile Ile
    275                280                285
Leu Gln Val Phe Lys Gln Leu Phe Tyr Met Ile Asn Ala Val Thr Leu
    290                295                300
Asn Asp Leu Leu Leu Arg Lys Asp Val Cys Ser Trp Ser Thr Gly Met
    305                310                315                320
Gln Leu Arg Tyr Asn Ile Ser Gln Leu Glu Glu Trp Leu Arg Gly Arg
    325                330                335
Asn Leu His Gln Ser Gly Ala Val Gln Thr Met Glu Pro Leu Ile Gln
    340                345                350
Ala Ala Gln Leu Leu Gln Leu Lys Lys Lys Thr Gln Glu Asp Ala Glu
    355                360                365
Ala Ile Cys Ser Leu Cys Thr Ser Leu Ser Thr Gln Gln Ile Val Lys
    370                375                380
Ile Leu Asn Leu Tyr Thr Pro Leu Asn Glu Phe Glu Glu Arg Val Thr
    385                390                395                400
Val Ala Phe Ile Arg Thr Ile Gln Ala Gln Leu Gln Glu Arg Asn Asp
    405                410                415
Pro Gln Gln Leu Leu Asp Ala Lys His Met Phe Pro Val Leu Phe
    420                425                430
Pro Phe Asn Pro Ser Ser Leu Thr Met Asp Ser Ile His Ile Pro Ala
    435                440                445
Cys Leu Asn Leu Glu Phe Leu Asn Glu Val
    450                455                458

```

<210> 1059

<211> 82

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(82)

<223> X = any amino acid or stop code

<400> 1059

```

His Glu Glu Asn Thr Ile Leu Lys Ala Ala Glu Val Gln Val Pro Pro
  1          5          10          15
Lys Xaa Val Val Thr Pro Glu Ala Lys Ala Phe Ile Xaa Arg Cys Leu
    20          25          30
Ala Tyr Gln Lys Glu Asp Cys Ile Asp Ala Gln Gln Leu Ala Cys Asp
    35          40          45
Pro Tyr Leu Leu His Tyr Ile Gln Lys Leu Val Phe Val Ser Ser Pro
    50          55          60
Ala Gly Ala Ala Ile Ala Ser Thr Phe Gly Val Ser Asn Ser Cys Ser
    65          70          75          80
Ser Asn
    82

```

<210> 1060
 <211> 277
 <212> Amino acid
 <213> Homo sapiens

<400> 1060
 Gly Thr Thr Asp Glu Ile Met Thr Arg Trp Ala Arg Val Ser Thr Thr
 1 5 10 15
 Tyr Asn Lys Arg Pro Leu Pro Ala Thr Ser Trp Glu Asp Met Lys Lys
 20 25 30
 Gly Ser Phe Glu Gly Thr Ser Gln Asn Leu Pro Lys Arg Lys Gln Leu
 35 40 45
 Glu Ala Asn Arg Leu Ser Leu Lys Asn Asp Ala Pro Gln Ala Lys His
 50 55 60
 Lys Lys Asn Lys Lys Lys Lys Glu Tyr Leu Asn Glu Asp Val Asn Gly
 65 70 75 80
 Phe Met Glu Tyr Leu Arg Gln Asn Ser Gln Met Val His Asn Gly Gln
 85 90 95
 Ile Ile Ala Thr Asp Ser Glu Glu Val Arg Glu Glu Ile Ala Val Ala
 100 105 110
 Leu Lys Lys Asp Ser Arg Arg Glu Gly Arg Arg Leu Lys Arg Gln Ala
 115 120 125
 Ala Lys Lys Asn Ala Met Val Cys Phe His Cys Arg Lys Pro Gly His
 130 135 140
 Gly Ile Ala Asp Cys Pro Ala Ala Leu Glu Asn Gln Asp Met Gly Thr
 145 150 155 160
 Gly Ile Cys Tyr Arg Cys Gly Ser Thr Glu His Glu Ile Thr Lys Cys
 165 170 175
 Lys Ala Lys Val Asp Pro Ala Leu Gly Glu Phe Pro Phe Ala Lys Cys
 180 185 190
 Phe Val Cys Gly Glu Met Gly His Leu Ser Arg Ser Cys Pro Asp Asn
 195 200 205
 Pro Lys Gly Leu Tyr Ala Asp Gly Gly Gly Cys Lys Leu Cys Gly Ser
 210 215 220
 Val Glu His Leu Lys Lys Asp Cys Pro Glu Ser Gln Asn Ser Glu Arg
 225 230 235 240
 Met Val Thr Val Gly Arg Trp Ala Lys Gly Met Ser Ala Asp Tyr Glu
 245 250 255
 Glu Ile Leu Asp Val Pro Lys Pro Gln Lys Pro Lys Thr Lys Ile Pro
 260 265 270
 Lys Val Val Asn Phe
 275 277

<210> 1061
 <211> 95
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(95)
 <223> X = any amino acid or stop code

<400> 1061

```

Asp His Val Arg Lys Ser Leu Leu Lys Asn Arg Ala Glu Asn Ile Val
 1           5           10           15
Asn Ile Phe Lys Cys Asn Val Val Ser Leu Pro Asn Leu Pro Ala Phe
          20           25           30
Gly Gln Ala Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Glu Ala
          35           40           45
Glu Val Gly Gly Ser Xaa Gly Gln Glu Ile Glu Thr Ile Leu Ala Asn
 50           55           60
Ala Val Lys Ser Pro Phe Leu Leu Lys Ile Gln Lys Lys Lys Ile Ser
 65           70           75           80
Arg Ala Trp Trp Arg Ala Pro Val Ser Pro Arg Tyr Ser Gly Gly
          85           90           95

```

<210> 1062

<211> 259

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(259)

<223> X = any amino acid or stop code

<400> 1062

```

Ser Asp Ala Trp Ala Asp Ala Trp Ala Arg Ser Leu Ser Val Ser Pro
 1           5           10           15
Ser Ser Tyr Pro Glu Leu His Thr Glu Val Pro Leu Ser Val Leu Ile
          20           25           30
Leu Gly Leu Leu Val Val Phe Ile Leu Ser Val Cys Phe Gly Ala Gly
          35           40           45
Leu Phe Val Phe Val Leu Lys Arg Arg Lys Gly Val Pro Ser Val Pro
 50           55           60
Arg Asn Thr Asn Asn Leu Asp Val Ser Ser Phe Gln Leu Gln Tyr Gly
 65           70           75           80
Ser Tyr Asn Thr Glu Thr His Asp Lys Thr Asp Gly His Val Tyr Asn
          85           90           95
Tyr Ile Pro Pro Pro Val Val Gln Met Cys Gln Asn Pro Ile Tyr Met
          100          105          110
Ala Gly Arg Glu Gly Arg Pro Ser Ser Leu Leu Pro Lys Pro Gly Lys
          115          120          125
Glu Phe Gln Leu Leu Gly Asn Leu Glu Glu Lys Lys Glu Glu Pro Ala
          130          135          140
Thr Pro Ala Tyr Thr Ile Ser Ala Thr Glu Leu Leu Glu Lys Gln Ala
          145          150          155          160
Thr Pro Arg Glu Pro Glu Leu Leu Tyr Gln Asn Ile Ala Glu Pro Ser
          165          170          175
Gln Gly Thr Ser Thr Ala Gln Ala Xaa Ser Thr Ile Thr Phe Val Pro
          180          185          190
Tyr Leu Lys Gly Gln Phe Ala Pro Ser Tyr Glu Ser Arg Arg Gln Asn
          195          200          205
Gln Asp Arg Ile Asn Lys Thr Val Leu Tyr Gly Thr Pro Arg Lys Cys
          210          215          220
Phe Val Gly Gln Ser Lys Pro Asn His Pro Leu Leu Gln Ala Lys Pro
          225          230          235          240
Gln Ser Glu Pro Asp Tyr Leu Glu Val Leu Glu Lys Gln Thr Ala Ile
          245          250          255
Ser Gln Leu
          259

```

<210> 1063
 <211> 498
 <212> Amino acid
 <213> Homo sapiens

<400> 1063
 Ala Leu Cys His Ile Ala Val Gly Gln Gln Met Asn Leu His Trp Leu
 1 5 10 15
 His Lys Ile Gly Leu Val Val Ile Leu Ala Ser Thr Val Val Ala Met
 20 25 30
 Ser Ala Val Ala Gln Leu Trp Glu Asp Glu Trp Glu Val Leu Leu Ile
 35 40 45
 Ser Leu Gln Gly Thr Ala Pro Phe Leu His Val Gly Ala Val Ala Ala
 50 55 60
 Val Thr Met Leu Ser Trp Ile Val Ala Gly Gln Phe Ala Arg Ala Glu
 65 70 75 80
 Arg Thr Ser Ser Gln Val Thr Ile Leu Cys Thr Phe Phe Thr Val Val
 85 90 95
 Phe Ala Leu Tyr Leu Ala Pro Leu Thr Ile Ser Ser Pro Cys Ile Met
 100 105 110
 Glu Lys Lys Asp Leu Gly Pro Lys Pro Ala Leu Ile Gly His Arg Gly
 115 120 125
 Ala Pro Met Leu Ala Pro Glu His Thr Leu Met Ser Phe Arg Lys Ala
 130 135 140
 Leu Glu Gln Lys Leu Tyr Gly Leu Gln Ala Asp Ile Thr Ile Ser Leu
 145 150 155 160
 Asp Gly Val Pro Phe Leu Met His Asp Thr Thr Leu Arg Arg Thr Thr
 165 170 175
 Asn Val Glu Glu Glu Phe Pro Glu Leu Ala Arg Arg Pro Ala Ser Met
 180 185 190
 Leu Asn Trp Thr Thr Leu Gln Arg Leu Asn Ala Gly Gln Trp Phe Leu
 195 200 205
 Lys Thr Asp Pro Phe Trp Thr Ala Ser Ser Leu Ser Pro Ser Asp His
 210 215 220
 Arg Glu Ala Gln Asn Gln Ser Ile Cys Ser Leu Ala Glu Leu Leu Glu
 225 230 235 240
 Leu Ala Lys Gly Asn Ala Thr Leu Leu Leu Asn Leu Arg Asp Pro Pro
 245 250 255
 Arg Glu His Pro Tyr Arg Ser Ser Phe Ile Asn Val Thr Leu Glu Ala
 260 265 270
 Val Leu His Ser Gly Phe Pro Gln His Gln Val Met Trp Leu Pro Ser
 275 280 285
 Arg Gln Arg Pro Leu Val Arg Lys Val Ala Pro Gly Phe Gln Gln Thr
 290 295 300
 Ser Gly Ser Lys Glu Ala Val Ala Ser Leu Arg Arg Gly His Ile Gln
 305 310 315 320
 Arg Leu Asn Leu Arg Tyr Thr Gln Val Ser Arg Gln Glu Leu Arg Asp
 325 330 335
 Tyr Ala Ser Trp Asn Leu Ser Val Asn Leu Tyr Thr Val Asn Ala Pro
 340 345 350
 Trp Leu Phe Ser Leu Leu Trp Cys Ala Gly Val Pro Ser Val Thr Ser
 355 360 365
 Asp Asn Ser His Thr Leu Ser Gln Val Pro Ser Pro Leu Trp Ile Met
 370 375 380
 Pro Pro Asp Glu Tyr Cys Leu Met Trp Val Thr Ala Asp Leu Val Ser
 385 390 395 400
 Phe Thr Leu Ile Val Gly Ile Phe Val Leu Gln Lys Trp Arg Leu Gly
 405 410 415
 Gly Ile Arg Ser Tyr Asn Pro Glu Gln Ile Met Leu Ser Ala Ala Val

420 425 430
 Arg Arg Thr Ser Arg Asp Val Ser Ile Met Lys Glu Lys Leu Ile Phe
 435 440 445
 Ser Glu Ile Ser Asp Gly Val Glu Val Ser Asp Val Leu Ser Val Cys
 450 455 460
 Ser Asp Asn Ser Tyr Asp Thr Tyr Ala Asn Ser Thr Ala Thr Pro Val
 465 470 475 480
 Gly Pro Arg Gly Gly Gly Ser His Thr Lys Thr Leu Ile Glu Arg Ser
 485 490 495
 Gly Arg
 498

<210> 1064
 <211> 374
 <212> Amino acid
 <213> Homo sapiens

<400> 1064
 Asn Ser Ala Asp Tyr Gly Asp Gly Pro Asp Ser Ser Asp Ala Asp Pro
 1 5 10 15
 Asp Ser Gly Thr Glu Glu Gly Val Leu Asp Phe Ser Asp Pro Phe Ser
 20 25 30
 Thr Glu Val Lys Pro Arg Ile Leu Leu Met Gly Leu Arg Arg Ser Gly
 35 40 45
 Lys Ser Ser Ile Gln Lys Val Val Phe His Lys Met Ser Pro Asn Glu
 50 55 60
 Thr Leu Phe Leu Glu Ser Thr Asn Lys Ile Cys Arg Glu Asp Val Ser
 65 70 75 80
 Asn Ser Ser Phe Val Asn Phe Gln Ile Trp Asp Phe Pro Gly Gln Ile
 85 90 95
 Asp Phe Phe Asp Pro Thr Phe Asp Tyr Glu Met Ile Phe Arg Gly Thr
 100 105 110
 Gly Ala Leu Ile Phe Val Ile Asp Ser Gln Asp Asp Tyr Met Glu Ala
 115 120 125
 Leu Ala Arg Leu His Leu Thr Val Thr Arg Ala Tyr Lys Val Asn Thr
 130 135 140
 Asp Ile Asn Phe Glu Val Phe Ile His Lys Val Asp Gly Leu Ser Asp
 145 150 155 160
 Asp His Lys Ile Glu Thr Gln Arg Asp Ile His Gln Arg Ala Asn Asp
 165 170 175
 Asp Leu Ala Asp Ala Gly Leu Glu Lys Ile His Leu Ser Phe Tyr Leu
 180 185 190
 Thr Ser Ile Tyr Asp His Ser Ile Phe Glu Ala Phe Ser Lys Val Val
 195 200 205
 Gln Lys Leu Ile Pro Gln Leu Pro Thr Leu Glu Asn Leu Leu Asn Ile
 210 215 220
 Phe Ile Ser Asn Ser Gly Ile Glu Lys Ala Phe Leu Phe Asp Val Val
 225 230 235 240
 Ser Lys Ile Tyr Ile Ala Thr Asp Ser Thr Pro Val Asp Met Gln Thr
 245 250 255
 Tyr Glu Leu Cys Cys Asp Met Ile Asp Val Val Ile Asp Ile Ser Cys
 260 265 270
 Ile Tyr Gly Leu Lys Glu Asp Gly Ala Gly Thr Pro Tyr Asp Lys Glu
 275 280 285
 Ser Thr Ala Ile Ile Lys Leu Asn Asn Thr Thr Val Leu Tyr Leu Lys
 290 295 300
 Glu Val Thr Lys Phe Leu Ala Leu Val Cys Phe Val Arg Glu Glu Ser
 305 310 315 320
 Phe Glu Arg Lys Gly Leu Ile Asp Tyr Asn Phe His Cys Phe Arg Lys

325 330 335
 Ala Ile His Glu Val Phe Glu Val Arg Met Lys Val Val Lys Ser Arg
 340 345 350
 Lys Val Gln Asn Arg Leu Gln Lys Lys Lys Arg Ala Thr Pro Asn Gly
 355 360 365
 Thr Pro Arg Val Leu Leu
 370 374

<210> 1065
 <211> 278
 <212> Amino acid
 <213> Homo sapiens

<400> 1065
 Arg Thr Arg Gly Arg Asp Pro Gly Ala Gly Phe Arg Arg Thr Ala Asn
 1 5 10 15
 Lys Arg Cys Cys Arg Arg Arg Phe Leu Ile Gly Cys Gly Trp Leu Pro
 20 25 30
 Leu Arg Ser Asp Trp Pro Leu Val Ser Lys Met Leu Ser Lys Gly Leu
 35 40 45
 Lys Arg Lys Arg Glu Glu Glu Glu Lys Glu Pro Leu Ala Val Asp
 50 55 60
 Ser Trp Trp Leu Asp Pro Gly His Ala Ala Val Ala Gln Ala Pro Pro
 65 70 75 80
 Ala Val Ala Ser Ser Ser Leu Phe Asp Leu Ser Val Leu Lys Leu His
 85 90 95
 His Ser Leu Gln Gln Ser Glu Pro Asp Leu Arg His Leu Val Leu Val
 100 105 110
 Val Asn Thr Leu Arg Arg Ile Gln Ala Ser Met Ala Pro Ala Ala Ala
 115 120 125
 Leu Pro Pro Val Pro Ser Pro Pro Ala Ala Pro Ser Val Ala Asp Asn
 130 135 140
 Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser Ala Ser Met Ala Ser Leu
 145 150 155 160
 Leu Glu Asp Leu Ser His Ile Glu Gly Leu Ser Gln Ala Pro Gln Pro
 165 170 175
 Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser Ile Gly Gly Ala Ala Pro
 180 185 190
 Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro Ala Thr Gly Cys Leu Leu
 195 200 205
 Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp Ile Asp Thr Ser Met Tyr
 210 215 220
 Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu Gly Leu Lys Pro Gly Pro
 225 230 235 240
 Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro Glu Leu Asp Glu Ala Glu
 245 250 255
 Leu Asp Tyr Leu Met Asp Val Leu Val Gly Thr Gln Ala Leu Glu Arg
 260 265 270
 Pro Pro Gly Pro Gly Arg
 275 278

<210> 1066
 <211> 502
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1)...(502)

<223> X = any amino acid or stop code

<400> 1066

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Leu Gln Glu Val Lys Ala Arg Arg Asn Thr Leu His Lys Glu Lys Asp
 1          5          10          15
His Leu Val Asn Asp Tyr Glu Gln Asn Met Lys Leu Leu Gln Thr Lys
          20          25          30
Tyr Asp Ala Asp Ile Asn Leu Leu Lys Gln Glu His Ala Leu Ser Ala
          35          40          45
Ser Lys Ala Ser Ser Met Ile Glu Glu Leu Glu Gln Asn Val Cys Gln
          50          55          60
Leu Lys Gln Gln Leu Gln Glu Ser Glu Leu Gln Arg Lys Gln Gln Leu
          65          70          75          80
Arg Asp Gln Glu Asn Lys Phe Gln Met Glu Lys Ser His Leu Lys His
          85          90          95
Ile Tyr Glu Lys Lys Ala His Asp Leu Gln Ser Glu Leu Asp Lys Gly
          100          105          110
Lys Glu Asp Thr Gln Lys Lys Ile His Lys Phe Glu Glu Ala Leu Lys
          115          120          125
Trp Lys Lys Trp Arg Gln Ile Xaa Leu Asp Pro Asn Leu Leu Arg Glu
          130          135          140
Lys Gln Ser Lys Glu Phe Leu Trp Gln Leu Glu Asp Ile Arg Gln Arg
          145          150          155          160
Tyr Glu Gln Gln Ile Val Glu Leu Lys Leu Glu His Glu Gln Glu Lys
          165          170          175
Thr His Leu Leu Gln Gln His Asn Ala Glu Lys Asp Ser Leu Val Arg
          180          185          190
Asp His Glu Arg Glu Ile Glu Asn Leu Glu Lys Gln Leu Arg Ala Ala
          195          200          205
Asn Met Glu His Glu Asn Gln Ile Gln Glu Phe Lys Lys Arg Asp Ala
          210          215          220
Gln Val Ile Ala Asp Met Glu Ala Gln Val His Lys Leu Arg Glu Glu
          225          230          235          240
Leu Ile Asn Val Asn Ser Gln Arg Lys Gln Gln Leu Val Glu Leu Gly
          245          250          255
Leu Leu Arg Glu Glu Glu Lys Gln Arg Ala Thr Arg Glu His Glu Ile
          260          265          270
Val Val Asn Lys Leu Lys Ala Glu Ser Glu Lys Met Lys Ile Glu Leu
          275          280          285
Lys Lys Thr His Ala Ala Glu Thr Glu Met Thr Leu Glu Lys Ala Asn
          290          295          300
Ser Lys Leu Lys Gln Ile Glu Lys Glu Tyr Thr Gln Lys Leu Ala Lys
          305          310          315          320
Ser Ser Gln Ile Ile Ala Glu Leu Gln Thr Thr Ile Ser Ser Leu Lys
          325          330          335
Glu Glu Asn Ser Gln Gln Gln Leu Ala Ala Glu Arg Arg Leu Gln Asp
          340          345          350
Val Arg Gln Lys Phe Glu Asp Glu Lys Lys Gln Leu Ile Arg Asp Asn
          355          360          365
Asp Gln Ala Ile Lys Val Leu Gln Asp Glu Leu Glu Asn Arg Ser Asn
          370          375          380
Gln Val Arg Cys Ala Glu Lys Lys Leu Gln His Lys Glu Leu Glu Ser
          385          390          395          400
Gln Glu Gln Ile Thr Tyr Ile Arg Gln Glu Tyr Glu Thr Lys Leu Lys
          405          410          415
Gly Leu Met Pro Ala Ser Leu Arg Gln Glu Leu Glu Asp Thr Ile Ser
          420          425          430
Ser Leu Lys Ser Gln Val Asn Phe Leu Gln Lys Arg Ala Ser Ile Leu
          435          440          445

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Gln Glu Glu Arg Asp Tyr Ile Ser Arg Gln Lys Val Gln Pro Ile Ser
 450 455 460
 Arg Xaa Leu His Glu Arg Met Gln Arg Met Arg Ile Ser Arg Leu Cys
 465 470 475 480
 Cys Gly Thr Ser Ser Ser Arg Phe Glu Asp Leu Asp Ile Val Asn Cys
 485 490 495
 Glu Ile Ser Gly Ile Phe
 500 502

<210> 1067

<211> 301

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(301)

<223> X = any amino acid or stop code

<400> 1067

Val Ile Asn Leu Val Tyr Leu Ile Ser Ser Pro Arg Pro Glu Leu Lys
 1 5 10 15
 Pro Val Asp Lys Glu Ser Glu Val Val Met Lys Phe Pro Asp Gly Phe
 20 25 30
 Glu Lys Phe Ser Pro Pro Ile Leu Gln Leu Asp Glu Val Asp Phe Tyr
 35 40 45
 Tyr Asp Pro Lys His Val Ile Phe Ser Arg Leu Ser Val Ser Ala Asp
 50 55 60
 Leu Glu Ser Arg Ile Cys Val Val Gly Glu Asn Gly Ala Gly Lys Ser
 65 70 75 80
 Thr Met Leu Lys Leu Leu Gly Asp Leu Ala Pro Val Arg Gly Ile
 85 90 95
 Arg His Ala His Arg Asn Leu Lys Ile Gly Tyr Phe Ser Gln His His
 100 105 110
 Val Glu Gln Leu Asp Leu Asn Val Gln Cys Leu Trp Glu Leu Ala Gly
 115 120 125
 His Ala Ser Phe Pro Gly Arg Pro Glu Glu Glu Tyr Arg His Gln Leu
 130 135 140
 Gly Phe Gly Met Gly Ile Ser Gly Glu Leu Ala Met Arg Pro Leu Cys
 145 150 155 160
 Gln Pro Val Leu Gly Ala Arg Lys Lys Pro Lys Trp Pro Phe Ala Gln
 165 170 175
 Met Asp Tyr Cys Pro Ala Pro Thr Phe Tyr Ile Leu Asp Glu Pro Thr
 180 185 190
 Asn His Leu Gly His Gly Arg Ala Ile Glu Ala Leu Gly Pro Cys Leu
 195 200 205
 Gln Thr Ile Ser Gly Val Gly Val Ile Leu Val Ser His Glu Xaa Ser
 210 215 220
 Ala Leu Ser Arg Leu Val Cys Arg Glu Leu Trp Val Cys Xaa Gly Gly
 225 230 235 240
 Gly Val Thr Arg Val Glu Arg Lys Asp Phe Asp Gln Tyr Arg Ala Leu
 245 250 255
 Leu Gln Gly Thr Val Ser Ala Arg Glu Gly Phe Pro Leu Gly Pro Pro
 260 265 270
 Arg Leu Lys Asp Ser Pro Arg Asp Met Gly Leu Val Ser Gln Thr Pro
 275 280 285
 Trp Gly His His Val Gly Tyr Pro Leu Pro Gly Arg Gly
 290 295 300 301

<210> 1068
 <211> 215
 <212> Amino acid
 <213> Homo sapiens

<400> 1068
 Cys Ser Ala Val Glu Val Lys Met Ala Ala Arg Thr Ala Phe Gly Ala
 1 5 10 15
 Val Cys Arg Arg Leu Trp Gln Gly Leu Gly Asn Phe Ser Val Asn Thr
 20 25 30
 Ser Lys Gly Asn Thr Ala Lys Asn Gly Gly Leu Leu Leu Ser Thr Asn
 35 40 45
 Met Lys Trp Val Gln Phe Ser Asn Leu His Val Asp Val Pro Lys Asp
 50 55 60
 Leu Thr Lys Pro Val Val Thr Ile Ser Asp Glu Pro Asp Ile Leu Tyr
 65 70 75 80
 Lys Arg Leu Ser Val Leu Val Lys Gly His Asp Lys Ala Val Leu Asp
 85 90 95
 Ser Tyr Glu Tyr Phe Ala Val Leu Ala Ala Lys Glu Leu Gly Ile Ser
 100 105 110
 Ile Lys Val His Glu Pro Pro Arg Lys Ile Glu Arg Phe Thr Leu Leu
 115 120 125
 Gln Ser Val His Ile Tyr Lys Lys His Arg Val Gln Tyr Glu Met Arg
 130 135 140
 Thr Leu Tyr Arg Cys Leu Glu Leu Glu His Leu Thr Gly Ser Thr Ala
 145 150 155 160
 Asp Val Tyr Leu Glu Tyr Ile Gln Arg Asn Leu Pro Glu Gly Val Ala
 165 170 175
 Met Glu Val Thr Lys Phe Cys Phe Phe Ile Phe Leu Thr Gln Leu Glu
 180 185 190
 Gln Leu Pro Glu His Ile Lys Glu Pro Ile Trp Glu Thr Leu Ser Glu
 195 200 205
 Glu Lys Glu Glu Ser Lys Ser
 210 215

<210> 1069
 <211> 274
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(274)
 <223> X = any amino acid or stop code

<400> 1069
 Asp Phe Trp Asp Thr Ala Gly Gln Glu Arg Phe Gln Ser Met His Ala
 1 5 10 15
 Ser Tyr Tyr His Lys Thr His Ala Cys Ile Met Val Phe Asp Val Gln
 20 25 30
 Arg Lys Val Thr His Arg Asn Leu Ser Thr Trp Tyr Thr Glu Leu Arg
 35 40 45
 Glu Phe Arg Pro Glu Ile Pro Cys Ile Val Val Ala Asn Lys Ile Asp
 50 55 60

Gly Gly Ala Ile Pro Ala Pro Gly Cys Xaa Gln Phe Thr Gly Asp Leu
 65 70 75 80
 Pro Ser Tyr Ile Ser Ser Ser Ile Pro Arg Ala Gly Asn Leu Gln Xaa
 85 90 95
 Leu Val Leu Pro Thr Ile Arg Tyr Asn Pro Trp Leu Val Ala Cys
 100 105 110
 Ile Leu Pro Thr Leu Xaa Arg Ser Gln Leu Ser Arg Pro Ala Leu Phe
 115 120 125
 Pro Arg His Arg Ser Leu Leu Thr Glu Leu Phe Leu Gly Pro Val Ser
 130 135 140
 Gln Ser Ser Leu Pro Ile Pro Leu Ser Gly Met Lys Ala Ser Ser Gly
 145 150 155 160
 Pro Pro Leu Gln Thr Phe Phe Pro Ser Leu Asp Arg Gln Thr Asn Val
 165 170 175
 Leu Pro Ser Leu Tyr Ala Asp Ile Asn Val Thr Gln Lys Ser Phe Asn
 180 185 190
 Phe Ala Lys Lys Phe Ser Leu Pro Leu Tyr Phe Val Ser Ala Ala Asp
 195 200 205
 Gly Thr Asn Val Val Lys Leu Phe Asn Asp Ala Ile Arg Leu Ala Val
 210 215 220
 Ser Tyr Lys Gln Asn Ser Gln Asp Phe Met Asp Glu Ile Phe Gln Glu
 225 230 235 240
 Leu Glu Asn Phe Ser Leu Glu Gln Glu Glu Asp Val Pro Asp Gln
 245 250 255
 Glu Gln Ser Ser Ser Ile Glu Thr Pro Ser Glu Glu Val Ala Ser Pro
 260 265 270
 His Ser
 274

<210> 1070

<211> 368

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(368)

<223> X = any amino acid or stop code

<400> 1070

Gly Ala Thr Pro Leu Gly Ser Val Gly Gly Arg Thr Gly Lys Met Asp
 1 5 10 15
 Ala Ala Thr Leu Thr Tyr Asp Thr Leu Arg Phe Ala Glu Phe Glu Asp
 20 25 30
 Phe Pro Glu Thr Ser Glu Pro Val Trp Ile Leu Gly Arg Lys Tyr Ser
 35 40 45
 Ile Phe Thr Glu Lys Asp Glu Ile Leu Ser Asp Val Ala Ser Arg Leu
 50 55 60
 Trp Phe Thr Tyr Arg Lys Asn Phe Pro Ala Ile Gly Gly Thr Gly Pro
 65 70 75 80
 Thr Ser Asp Thr Gly Trp Gly Cys Met Leu Arg Cys Gly Gln Met Ile
 85 90 95
 Phe Ala Gln Ala Leu Val Cys Arg His Leu Gly Arg Asp Trp Arg Trp
 100 105 110
 Thr Gln Arg Lys Arg Gln Pro Asp Ser Tyr Phe Ser Val Leu Asn Ala
 115 120 125
 Phe Ile Asp Arg Lys Asp Ser Tyr Tyr Ser Ile His Gln Ile Ala Gln
 130 135 140
 Met Gly Val Gly Glu Gly Lys Ser Ile Gly Gln Trp Tyr Gly Pro Asn

145		150		155		160									
Thr	Val	Ala	Gln	Val	Leu	Lys	Lys	Leu	Ala	Val	Phe	Asp	Thr	Trp	Ser
		165						170							175
Ser	Leu	Ala	Val	His	Ile	Ala	Met	Asp	Asn	Thr	Val	Val	Met	Glu	Glu
		180						185						190	
Ile	Arg	Arg	Leu	Cys	Arg	Thr	Ser	Val	Pro	Cys	Ala	Gly	Ala	Thr	Ala
		195					200						205		
Phe	Pro	Ala	Asp	Ser	Asp	Arg	His	Cys	Asn	Gly	Phe	Pro	Ala	Gly	Ala
		210				215						220			
Glu	Val	Thr	Asn	Arg	Pro	Ser	Pro	Trp	Arg	Pro	Leu	Val	Leu	Leu	Ile
225					230					235					240
Pro	Leu	Arg	Leu	Gly	Leu	Thr	Asp	Ile	Asn	Glu	Ala	Tyr	Val	Glu	Thr
			245					250						255	
Leu	Lys	His	Cys	Phe	Met	Met	Pro	Gln	Ser	Leu	Gly	Val	Ile	Gly	Gly
		260					265						270		
Lys	Pro	Asn	Ser	Ala	His	Tyr	Phe	Ile	Gly	Xaa	Val	Gly	Glu	Glu	Leu
		275					280					285			
Ile	Tyr	Leu	Asp	Pro	His	Thr	Thr	Gln	Pro	Ala	Val	Glu	Pro	Thr	Asp
		290				295					300				
Gly	Cys	Phe	Ile	Pro	Asp	Glu	Ser	Phe	His	Cys	Gln	His	Pro	Pro	Cys
305				310						315					320
Arg	Met	Ser	Ile	Ala	Glu	Leu	Asp	Pro	Ser	Ile	Ala	Val	Val	Arg	Gly
			325					330						335	
Gly	His	Leu	Ser	Thr	Gln	Ala	Phe	Gly	Ala	Glu	Cys	Cys	Leu	Gly	Met
		340					345					350			
Thr	Arg	Lys	Thr	Phe	Gly	Phe	Leu	Arg	Phe	Phe	Phe	Ser	Met	Leu	Gly
		355					360					365		368	

<210> 1071

<211> 81

<212> Amino acid

<213> Homo sapiens

<400> 1071

Ala	Leu	Cys	Val	Val	Pro	Phe	Asn	Thr	Phe	His	Asn	Asp	Phe	Leu	Leu
1				5					10					15	
Leu	Asp	Lys	Glu	Gly	Thr	Leu	Asp	Pro	Val	Met	Asp	Ser	Phe	Ser	Thr
			20					25					30		
His	Trp	Thr	Thr	Ile	Gly	Pro	Ala	Asp	Met	Phe	Phe	Ser	Phe	Arg	Gln
		35				40						45			
His	Tyr	Lys	Asn	Phe	Lys	Ser	His	Gly	Thr	Asn	Pro	Ser	Lys	Ser	Val
	50				55					60					
Trp	Ala	His	Ala	Thr	Cys	Gln	Ser	Cys	Ala	Phe	Pro	Asn	Leu	Leu	Gly
65					70					75					80
Trp															
81															

<210> 1072

<211> 494

<212> Amino acid

<213> Homo sapiens

<400> 1072

Thr Arg Leu Ala Glu Phe Gly Thr Arg Asp Pro Cys Ala Gln Ala Pro
 1 5 10 15
 Cys Glu Gln Gln Cys Glu Pro Gly Gly Pro Gln Gly Tyr Ser Cys His
 20 25 30
 Cys Arg Leu Gly Phe Arg Pro Ala Glu Asp Asp Pro His Arg Cys Val
 35 40 45
 Asp Thr Asp Glu Cys Gln Ile Ala Gly Val Cys Gln Gln Met Cys Val
 50 55 60
 Asn Tyr Val Gly Gly Phe Glu Cys Tyr Cys Ser Glu Gly His Glu Leu
 65 70 75 80
 Glu Ala Asp Gly Ile Ser Cys Ser Pro Ala Gly Ala Met Gly Ala Gln
 85 90 95
 Ala Ser Gln Asp Leu Gly Asp Glu Leu Leu Asp Asp Gly Glu Asp Glu
 100 105 110
 Glu Asp Glu Asp Glu Ala Trp Lys Ala Phe Asn Gly Gly Trp Thr Glu
 115 120 125
 Met Pro Gly Ile Leu Trp Met Glu Pro Thr Gln Pro Pro Asp Phe Ala
 130 135 140
 Leu Ala Tyr Arg Pro Ser Phe Pro Glu Asp Arg Glu Pro Gln Ile Pro
 145 150 155 160
 Tyr Pro Glu Pro Thr Trp Pro Pro Pro Leu Ser Ala Pro Arg Val Pro
 165 170 175
 Tyr His Ser Ser Val Leu Ser Val Thr Arg Pro Val Val Val Ser Ala
 180 185 190
 Thr His Pro Thr Leu Pro Ser Ala His Gln Pro Pro Val Ile Pro Ala
 195 200 205
 Thr His Pro Ala Leu Ser Arg Asp His Gln Ile Pro Val Ile Ala Ala
 210 215 220
 Asn Tyr Pro Asp Leu Pro Ser Ala Tyr Gln Pro Gly Ile Leu Ser Val
 225 230 235 240
 Ser His Ser Ala Gln Pro Pro Ala His Gln Pro Pro Met Ile Ser Thr
 245 250 255
 Lys Tyr Pro Glu Leu Phe Pro Ala His Gln Ser Pro Met Phe Pro Asp
 260 265 270
 Thr Arg Val Ala Gly Thr Gln Thr Thr His Leu Pro Gly Ile Pro
 275 280 285
 Pro Asn His Ala Pro Leu Val Thr Thr Leu Gly Ala Gln Leu Pro Pro
 290 295 300
 Gln Ala Pro Asp Ala Leu Val Leu Arg Thr Gln Ala Thr Gln Leu Pro
 305 310 315 320
 Ile Ile Pro Thr Ala Gln Pro Ser Leu Thr Thr Thr Ser Arg Ser Pro
 325 330 335
 Val Ser Pro Ala His Gln Ile Ser Val Pro Ala Ala Thr Gln Pro Ala
 340 345 350
 Ala Leu Pro Thr Leu Leu Pro Ser Gln Ser Pro Thr Asn Gln Thr Ser
 355 360 365
 Pro Ile Ser Pro Thr His Pro His Ser Lys Ala Pro Gln Ile Pro Arg
 370 375 380
 Glu Asp Gly Pro Ser Pro Lys Leu Ala Leu Trp Leu Pro Ser Pro Ala
 385 390 395 400
 Pro Thr Ala Ala Pro Thr Ala Leu Gly Glu Ala Gly Leu Ala Glu His
 405 410 415
 Ser Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu Leu Val Pro Thr
 420 425 430
 Cys Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile Val Tyr Cys Thr
 435 440 445
 Arg Cys Gly Pro His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr Arg
 450 455 460
 Trp Val Ile His Ala Gly Ser Lys Ser Pro Thr Glu Pro Met Pro Pro
 465 470 475 480
 Arg Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val
 485 490 494

<210> 1073
 <211> 468
 <212> Amino acid
 <213> Homo sapiens

<400> 1073
 Leu Arg Val Arg Arg Arg Pro His Leu Pro Ala Pro Pro Ala Leu Arg
 1 5 10 15
 Ala Arg Arg Ser Asp Arg Arg Ser Ser Arg Ala Pro Ala Ala Phe Pro
 20 25 30
 Pro Arg Pro Pro His Ala Ser Pro Ala Pro Gly Pro Ala Met Ala Gln
 35 40 45
 Ala Val Trp Ser Arg Leu Gly Arg Ile Leu Trp Leu Ala Cys Leu Leu
 50 55 60
 Pro Trp Ala Pro Ala Gly Val Ala Ala Gly Leu Tyr Glu Leu Asn Leu
 65 70 75 80
 Thr Thr Asp Ser Pro Ala Thr Thr Gly Ala Val Val Thr Ile Ser Ala
 85 90 95
 Ser Leu Val Ala Lys Asp Asn Gly Ser Leu Ala Leu Pro Ala Asp Ala
 100 105 110
 His Leu Tyr Arg Phe His Trp Ile His Thr Pro Leu Val Leu Thr Gly
 115 120 125
 Lys Met Glu Lys Gly Leu Ser Ser Thr Ile Arg Val Val Gly His Val
 130 135 140
 Pro Gly Glu Phe Pro Val Ser Val Trp Val Thr Ala Ala Asp Cys Trp
 145 150 155 160
 Met Cys Gln Pro Val Ala Arg Gly Phe Val Val Leu Pro Ile Thr Glu
 165 170 175
 Phe Leu Val Gly Asp Leu Val Val Thr Gln Asn Thr Ser Leu Pro Trp
 180 185 190
 Pro Ser Ser Tyr Leu Thr Lys Thr Val Leu Lys Val Ser Phe Leu Leu
 195 200 205
 His Asp Pro Ser Asn Phe Leu Lys Thr Ala Leu Phe Leu Tyr Ser Trp
 210 215 220
 Asp Phe Gly Asp Gly Thr Gln Met Val Thr Glu Asp Ser Val Val Tyr
 225 230 235 240
 Tyr Asn Tyr Ser Ile Ile Gly Thr Phe Thr Val Lys Leu Lys Val Val
 245 250 255
 Ala Glu Trp Glu Glu Val Glu Pro Asp Ala Thr Arg Ala Val Lys Gln
 260 265 270
 Lys Thr Gly Asp Phe Ser Ala Ser Leu Lys Leu Gln Glu Thr Leu Arg
 275 280 285
 Gly Ile Gln Val Leu Gly Pro Thr Leu Ile Gln Thr Phe Gln Lys Met
 290 295 300
 Thr Val Thr Leu Asn Phe Leu Gly Ser Pro Pro Leu Thr Val Cys Trp
 305 310 315 320
 Arg Leu Lys Pro Glu Cys Leu Pro Leu Glu Glu Gly Glu Cys His Pro
 325 330 335
 Val Ser Val Ala Ser Thr Ala Tyr Asn Leu Thr His Thr Phe Arg Asp
 340 345 350
 Pro Gly Asp Tyr Cys Phe Ser Ile Arg Ala Glu Asn Ile Ile Ser Lys
 355 360 365
 Thr His Gln Tyr His Lys Ile Gln Val Trp Pro Ser Arg Ile Gln Pro
 370 375 380
 Ala Val Phe Ala Phe Pro Cys Ala Thr Leu Ile Thr Val Met Leu Ala
 385 390 395 400
 Phe Ile Met Tyr Met Thr Leu Arg Asn Ala Thr Gln Gln Lys Asp Met
 405 410 415
 Val Glu Asn Pro Glu Pro Pro Ser Gly Val Arg Cys Cys Cys Gln Met

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<210> 1074
<211> 288
<212>Amino acid
<213> Homo sapiens
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```
<210> 1075
<211> 273
<212>Amino acid
<213> Homo sapiens
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<220>
 <221> misc_feature
 <222> (1)...(273)
 <223> X = any amino acid or stop code

<400> 1075
 Gly Ala Gly Ser Lys Ser Ser Met Met Gln Leu Met His Leu Glu Ser
 1 5 10 15
 Phe Tyr Glu Lys Pro Pro Pro Gly Leu Ile Lys Glu Asp Asp Thr Lys
 20 25 30
 Pro Glu Asp Cys Ile Pro Asp Val Pro Gly Asn Glu His Ala Arg Glu
 35 40 45
 Phe Leu Ala His Thr Pro Thr Lys Gly Leu Trp Met Pro Leu Glu Lys
 50 55 60
 Glu Val Lys Val Lys His Cys Thr Phe His Trp Ile Ala Ser Xaa Phe
 65 70 75 80
 Leu Gly Asp Gly Lys Phe Ile Pro Lys Ala Thr Arg Leu Lys Asp Val
 85 90 95
 Trp Val Ser Asn Xaa Phe Thr Cys Leu Phe Trp Asp Leu Thr Arg Phe
 100 105 110
 Ile His Asp Cys Ile Phe Phe Xaa Asn Trp Ser Leu Met Asn Lys Asn
 115 120 125
 Phe Asn Ile Ile Tyr Xaa Phe Phe Ile Ser Leu Arg Xaa Asn Thr Leu
 130 135 140
 Ile Leu Gln Lys Tyr Phe Pro Phe Ser Leu Leu Gly Trp His Cys
 145 150 155 160
 Lys Trp Tyr Gly His Arg Thr Gly Tyr Lys Glu Cys Pro Phe Phe Ile
 165 170 175
 Lys Asp Asn Gln Lys Leu Gln Gln Phe Arg Val Ala His Glu Asp Phe
 180 185 190
 Met Tyr Asp Ile Ile Arg Asp Asn Lys Gln His Glu Lys Asn Val Arg
 195 200 205
 Ile Gln Gln Leu Lys Gln Leu Leu Glu Asp Ser Thr Ser Gly Glu Asp
 210 215 220
 Arg Ser Ser Ser Ser Ser Glu Gly Lys Glu Lys His Lys Lys Lys
 225 230 235 240
 Lys Lys Lys Glu Lys His Lys Lys Arg Lys Lys Glu Lys Lys Lys Lys
 245 250 255
 Lys Lys Arg Lys His Lys Ser Ser Lys Ser Asn Glu Gly Ser Asp Ser
 260 265 270
 Glu
 273

<210> 1076
 <211> 815
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(815)
 <223> X = any amino acid or stop code

<400> 1076
 Glu Ile Ala Gly Ala Ala Ala Glu Asn Met Leu Gly Ser Leu Leu Cys

1	5	10	15
Leu Pro Gly Ser Gly Ser Val Leu Leu Asp Pro Cys Thr Gly Ser Thr			
	20	25	30
Ile Ser Glu Thr Thr Ser Glu Ala Trp Ser Val Glu Val Leu Pro Ser			
	35	40	45
Asp Ser Glu Ala Pro Asp Leu Lys Gln Glu Glu Arg Leu Gln Glu Leu			
	50	55	60
Glu Ser Cys Ser Gly Leu Gly Ser Thr Ser Asp Thr Asp Val Arg			
	65	70	75
Glu Val Ser Ser Arg Pro Ser Thr Pro Gly Leu Ser Val Val Ser Gly			
	85	90	95
Ile Ser Ala Thr Ser Glu Asp Ile Pro Asn Lys Ile Glu Asp Leu Arg			
	100	105	110
Ser Glu Cys Ser Ser Asp Phe Gly Gly Lys Asp Ser Val Thr Ser Pro			
	115	120	125
Asp Met Asp Glu Ile Thr His Asp Phe Leu Tyr Ile Leu Gln Pro Lys			
	130	135	140
Gln His Phe Gln His Ile Glu Ala Glu Ala Asp Met Arg Ile Gln Leu			
	145	150	155
Ser Ser Ser Ala His Gln Leu Thr Ser Pro Pro Ser Gln Ser Glu Ser			
	165	170	175
Leu Leu Ala Met Phe Asp Pro Leu Ser Ser His Glu Gly Ala Ser Ala			
	180	185	190
Val Val Arg Pro Lys Val His Tyr Ala Arg Pro Ser His Pro Pro Pro			
	195	200	205
Asp Pro Pro Ile Leu Glu Gly Ala Val Gly Gly Asn Glu Ala Arg Leu			
	210	215	220
Pro Asn Phe Gly Ser Pro Met Phe Xaa Leu Pro Ala Glu Met Glu Ala			
	225	230	235
Phe Lys Gln Arg His Ser Tyr Thr Pro Glu Arg Leu Val Arg Ser Arg			
	245	250	255
Ser Ser Asp Ile Val Ser Ser Val Arg Arg Pro Met Ser Asp Pro Ser			
	260	265	270
Trp Asn Arg Arg Pro Gly Asn Glu Glu Arg Glu Leu Pro Pro Ala Ala			
	275	280	285
Ala Ile Gly Ala Thr Ser Leu Val Ala Ala Pro His Ser Ser Ser Ser			
	290	295	300
Ser Pro Ser Lys Asp Ser Ser Arg Gly Glu Thr Glu Glu Arg Lys Asp			
	305	310	315
Ser Asp Asp Glu Lys Ser Asp Arg Asn Arg Pro Trp Trp Arg Lys Arg			
	325	330	335
Phe Val Ser Ala Met Pro Lys Ala Pro Ile Pro Phe Arg Lys Lys Glu			
	340	345	350
Lys Gln Glu Lys Asp Lys Asp Asp Leu Gly Pro Asp Arg Phe Ser Thr			
	355	360	365
Leu Thr Asp Asp Pro Ser Pro Arg Leu Ser Ala Gln Ala Gln Val Ala			
	370	375	380
Glu Asp Ile Leu Asp Lys Tyr Arg Asn Ala Ile Lys Arg Thr Ser Pro			
	385	390	395
Ser Asp Gly Ala Met Ala Asn Tyr Glu Ser Thr Glu Val Met Gly Asp			
	405	410	415
Gly Glu Ser Ala His Asp Ser Pro Arg Asp Glu Ala Leu Gln Asn Ile			
	420	425	430
Ser Ala Asp Asp Leu Pro Asp Ser Ala Ser Gln Ala Ala His Pro Gln			
	435	440	445
Asp Ser Ala Phe Ser Tyr Arg Asp Ala Lys Lys Lys Leu Arg Leu Ala			
	450	455	460
Leu Cys Ser Ala Asp Ser Val Ala Phe Pro Val Leu Thr His Ser Thr			
	465	470	475
Arg Asn Gly Leu Pro Asp His Thr Asp Pro Glu Asp Asn Glu Ile Val			
	485	490	495
Cys Phe Leu Lys Val Gln Ile Ala Glu Ala Ile Asn Leu Gln Asp Lys			
	500	505	510
Asn Leu Met Ala Gln Leu Gln Glu Thr Met Arg Cys Val Cys Arg Phe			

515	520	525
Asp Asn Arg Thr Cys Arg Lys Leu Leu Ala Ser Ile Ala Glu Asp Tyr		
530	535	540
Arg Lys Arg Ala Pro Tyr Ile Ala Tyr Leu Thr Arg Cys Arg Gln Gly		
545	550	555
Leu Gln Thr Thr Gln Ala His Leu Glu Arg Leu Leu Gln Arg Val Leu		
565	570	575
Arg Asp Lys Glu Val Ala Asn Arg Tyr Phe Thr Thr Val Cys Val Arg		
580	585	590
Leu Leu Leu Glu Ser Lys Glu Lys Lys Ile Arg Glu Phe Ile Gln Asp		
595	600	605
Phe Gln Lys Leu Thr Ala Ala Asp Asp Lys Thr Ala Gln Val Glu Asp		
610	615	620
Phe Leu Gln Phe Leu Tyr Gly Ala Met Ala Gln Asp Val Ile Trp Gln		
625	630	635
Asn Ala Ser Glu Glu Gln Leu Gln Asp Ala Gln Leu Ala Ile Glu Arg		
645	650	655
Ser Val Met Asn Arg Ile Phe Lys Leu Ala Phe Tyr Pro Asn Gln Asp		
660	665	670
Gly Asp Ile Leu Arg Asp Gln Val Leu His Glu His Ile Gln Arg Leu		
675	680	685
Ser Lys Val Val Thr Ala Asn His Arg Ala Leu Gln Ile Pro Glu Val		
690	695	700
Tyr Leu Arg Glu Ala Pro Trp Pro Ser Ala Gln Ser Glu Ile Arg Thr		
705	710	715
Ile Ser Ala Tyr Lys Thr Pro Arg Asp Lys Val Gln Cys Ile Leu Arg		
725	730	735
Met Cys Ser Thr Ile Met Asn Leu Leu Ser Leu Ala Asn Glu Asp Ser		
740	745	750
Val Pro Gly Ala Asp Asp Phe Val Pro Val Leu Val Phe Val Leu Ile		
755	760	765
Lys Ala Asn Pro Pro Cys Leu Leu Ser Thr Val Gln Tyr Ile Ser Ser		
770	775	780
Phe Tyr Ala Ser Cys Leu Ser Gly Glu Glu Ser Tyr Trp Trp Met Gln		
785	790	795
Phe Thr Ala Ala Val Glu Phe Ile Lys Thr Ile Asp Asp Arg Lys		
805	810	815

<210> 1077

<211> 256

<212> Amino acid

<213> Homo sapiens

<400> 1077

Trp Pro Met Ser Leu Ala Arg Gly His Gly Asp Thr Ala Ala Ser Thr	
1 5 10 15	
Ala Ala Pro Leu Ser Glu Glu Gly Glu Val Thr Ser Gly Leu Gln Ala	
20 25 30	
Leu Ala Val Glu Asp Thr Gly Gly Pro Ser Ala Ser Ala Gly Lys Ala	
35 40 45	
Glu Asp Glu Gly Glu Gly Gly Arg Glu Glu Thr Glu Arg Glu Gly Ser	
50 55 60	
Gly Gly Glu Glu Ala Gln Gly Glu Val Pro Ser Ala Gly Gly Glu Glu	
65 70 75 80	
Pro Ala Glu Glu Asp Ser Glu Asp Trp Cys Val Pro Cys Ser Asp Glu	
85 90 95	
Glu Val Glu Leu Pro Ala Asp Gly Gln Pro Trp Met Pro Pro Ser	
100 105 110	
Glu Ile Gln Arg Leu Tyr Glu Leu Leu Ala Ala His Gly Thr Leu Glu	

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      115      120      125
Leu Gln Ala Glu Ile Leu Pro Arg Arg Pro Pro Thr Pro Glu Ala Gln
      130      135      140
Ser Glu Glu Glu Arg Ser Asp Glu Glu Pro Glu Ala Lys Glu Glu Glu
145      150      155      160
Glu Glu Lys Pro His Met Pro Thr Glu Phe Asp Phe Asp Asp Glu Pro
      165      170      175
Val Thr Pro Lys Asp Ser Leu Ile Asp Arg Arg Arg Thr Pro Gly Ser
      180      185      190
Ser Ala Arg Ser Gln Lys Arg Glu Ala Arg Leu Asp Lys Val Leu Ser
      195      200      205
Asp Met Lys Arg His Lys Lys Leu Glu Glu Gln Ile Leu Arg Thr Gly
      210      215      220
Arg Asp Leu Phe Ser Leu Asp Ser Glu Asp Pro Ser Pro Ala Ser Pro
225      230      235      240
Pro Leu Arg Ser Ser Gly Ser Ser Leu Phe Pro Arg Gln Arg Lys Tyr
      245      250      255 256

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<210> 1078

<211> 590

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(590)

<223> X = any amino acid or stop code

<400> 1078

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      <400> 1078
Leu Gly Arg Gly Thr Phe Gly Gln Val Val Xaa Cys Trp Lys Arg Gly
  1      5      10      15
Thr Asn Glu Ile Val Ala Ile Lys Ile Leu Lys Asn His Pro Ser Tyr
      20      25      30
Ala Arg Gln Gly Gln Ile Glu Val Ser Ile Leu Ala Arg Leu Ser Thr
      35      40      45
Glu Ser Ala Asp Asp Tyr Asn Phe Val Arg Ala Tyr Glu Cys Phe Gln
      50      55      60
His Lys Asn His Thr Cys Leu Val Phe Glu Met Leu Glu Gln Asn Leu
      65      70      75      80
Tyr Asp Phe Leu Lys Gln Asn Lys Phe Ser Pro Leu Pro Leu Lys Tyr
      85      90      95
Ile Arg Pro Val Leu Gln Gln Val Ala Thr Ala Leu Met Lys Leu Lys
      100      105      110
Ser Leu Gly Leu Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu
      115      120      125
Val Asp Pro Ser Arg Gln Pro Tyr Arg Val Lys Val Ile Asp Phe Gly
      130      135      140
Ser Ala Ser His Val Ser Lys Ala Val Cys Ser Thr Tyr Leu Gln Ser
145      150      155      160
Arg Tyr Tyr Arg Ala Pro Glu Ile Ile Leu Gly Leu Pro Phe Cys Glu
      165      170      175
Ala Ile Asp Met Trp Ser Leu Gly Cys Val Ile Ala Glu Leu Phe Leu
      180      185      190
Gly Trp Pro Leu Tyr Pro Gly Ala Ser Glu Tyr Asp Gln Ile Arg Tyr
      195      200      205
Ile Ser Gln Thr Gln Gly Leu Pro Ala Glu Tyr Leu Leu Ser Ala Gly
      210      215      220

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Thr Lys Thr Thr Arg Phe Phe Asn Arg Asp Thr Asp Ser Pro Tyr Pro
225                230                235                240
Leu Trp Arg Leu Lys Thr Pro Asp Asp His Glu Ala Glu Thr Gly Ile
                245                250                255
Lys Ser Lys Glu Ala Arg Lys Tyr Ile Phe Asn Cys Leu Asp Asp Met
                260                265                270
Ala Gln Val Asn Met Thr Thr Asp Leu Glu Gly Ser Asp Met Leu Val
                275                280                285
Glu Lys Ala Val Arg Arg Glu Phe Ile Asp Leu Leu Lys Lys Met Leu
                290                295                300
Ser Ile Asp Ser Val Lys Arg Phe Ser Pro Val Gly Ser Leu Asn His
305                310                315                320
Pro Phe Val Thr Met Ser Leu Phe Leu Asp Phe Pro His Ser Thr His
                325                330                335
Val Lys Ser Cys Phe Gln Asn Met Glu Ile Cys Lys Arg Arg Val Asn
                340                345                350
Met Tyr Asp Thr Val Asn Gln Ser Lys Thr Pro Phe Ile Thr His Val
                355                360                365
Ala Pro Ser Thr Ser Thr Asn Leu Thr Met Thr Phe Asn Asn Gln Leu
                370                375                380
Thr Thr Val His Asn Gln Pro Ser Ala Ala Ser Met Ala Ala Val Ala
385                390                395                400
Gln Arg Ser Met Pro Leu Gln Thr Gly Thr Ala Gln Ile Cys Ala Arg
                405                410                415
Pro Asp Pro Phe Gln Gln Ala Leu Ile Val Cys Pro Pro Gly Phe Gln
                420                425                430
Gly Leu Gln Ala Ser Pro Ser Lys His Ala Gly Tyr Ser Val Arg Met
                435                440                445
Glu Asn Ala Val Pro Ile Val Thr Gln Ala Pro Gly Ala Gln Pro Leu
                450                455                460
Gln Ile Gln Pro Gly Leu Leu Ala Gln Gln Ala Trp Pro Ser Gly Thr
465                470                475                480
Gln Gln Ile Leu Leu Pro Pro Ala Trp Gln Gln Leu Thr Gly Val Ala
                485                490                495
Thr His Thr Ser Val Gln His Ala Ala Val Ile Pro Glu Thr Met Ala
                500                505                510
Gly Thr Gln Gln Leu Ala Asp Trp Arg Asn Thr His Ala His Gly Ser
                515                520                525
His Tyr Asn Pro Ile Met Gln Gln Pro Ala Leu Leu Thr Gly His Val
                530                535                540
Thr Leu Pro Ala Ala Gln Pro Leu Asn Val Gly Val Ala His Val Met
545                550                555                560
Arg Gln Gln Pro Thr Ser Thr Thr Ser Ser Arg Lys Ser Lys Gln His
                565                570                575
Leu Tyr Cys Gly Arg Ala Arg Val Ser Lys Ile Ala Ser Arg
                580                585                590

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<210> 1079

<211> 904

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(904)

<223> X = any amino acid or stop code

<400> 1079

Glu Phe Ala Ile Cys Arg Tyr Pro Leu Gly Met Ser Gly Gly Gln Ile

1	5	10	15
Pro Asp Glu Asp Ile Thr Ala Ser Ser Gln Trp Ser Glu Ser Thr Ala			
20	25	30	
Ala Lys Tyr Gly Arg Leu Asp Ser Glu Glu Gly Asp Gly Ala Trp Cys			
35	40	45	
Pro Glu Ile Pro Val Glu Pro Asp Asp Leu Lys Glu Phe Leu Gln Ile			
50	55	60	
Asp Leu His Thr Leu His Phe Ile Thr Leu Val Gly Thr Gln Gly Arg			
65	70	75	80
His Ala Gly Gly His Gly Ile Glu Phe Ala Pro Met Tyr Lys Ile Asn			
85	90	95	
Tyr Ser Arg Asp Gly Thr Arg Trp Ile Ser Trp Arg Asn Arg His Gly			
100	105	110	
Lys Gln Val Leu Asp Gly Asn Ser Asn Pro Tyr Asp Ile Phe Leu Lys			
115	120	125	
Asp Leu Glu Pro Pro Ile Val Ala Arg Phe Val Arg Phe Ile Pro Val			
130	135	140	
Thr Asp His Ser Met Asn Val Cys Met Arg Val Glu Leu Tyr Gly Cys			
145	150	155	160
Val Trp Leu Asp Gly Leu Val Ser Tyr Asn Ala Pro Ala Gly Gln Gln			
165	170	175	
Phe Val Leu Pro Gly Gly Ser Ile Ile Tyr Leu Asn Asp Ser Val Tyr			
180	185	190	
Asp Gly Ala Val Gly Tyr Ser Met Thr Glu Gly Leu Gly Gln Leu Thr			
195	200	205	
Asp Gly Val Ser Gly Leu Asp Asp Phe Thr Gln Thr His Glu Tyr His			
210	215	220	
Val Trp Pro Gly Tyr Asp Tyr Val Gly Trp Arg Asn Glu Ser Ala Thr			
225	230	235	240
Asn Gly Tyr Ile Glu Ile Met Phe Glu Phe Asp Arg Ile Arg Asn Phe			
245	250	255	
Thr Thr Met Lys Val His Cys Asn Asn Met Phe Ala Lys Gly Val Lys			
260	265	270	
Ile Phe Lys Glu Val Gln Cys Tyr Phe Arg Ser Glu Ala Ser Glu Trp			
275	280	285	
Glu Pro Asn Ala Ile Ser Phe Pro Leu Val Leu Asp Asp Val Asn Pro			
290	295	300	
Ser Ala Arg Phe Val Thr Val Pro Leu His His Arg Met Ala Ser Ala			
305	310	315	320
Ile Lys Cys Gln Tyr His Phe Ala Asp Thr Trp Met Met Phe Ser Glu			
325	330	335	
Ile Thr Phe Gln Ser Asp Ala Ala Met Tyr Asn Asn Ser Glu Ala Leu			
340	345	350	
Pro Thr Ser Pro Met Ala Pro Thr Thr Tyr Asp Pro Met Leu Lys Val			
355	360	365	
Asp Asp Ser Asn Thr Arg Ile Leu Ile Gly Cys Leu Val Ala Ile Ile			
370	375	380	
Phe Ile Leu Leu Ala Ile Ile Val Ile Ile Leu Trp Arg Gln Phe Trp			
385	390	395	400
Gln Lys Met Leu Glu Lys Ala Ser Arg Arg Met Leu Asp Asp Glu Met			
405	410	415	
Thr Val Ser Leu Ser Leu Pro Ser Asp Ser Ser Met Phe Asn Asn Asn			
420	425	430	
Arg Ser Ser Ser Pro Ser Glu Gln Gly Ser Asn Ser Thr Tyr Asp Arg			
435	440	445	
Ile Phe Pro Leu Arg Pro Asp Tyr Gln Glu Pro Ser Arg Leu Ile Arg			
450	455	460	
Lys Leu Pro Glu Phe Ala Pro Gly Glu Glu Glu Ser Gly Cys Ser Gly			
465	470	475	480
Val Val Lys Pro Val Gln Pro Ser Gly Pro Glu Gly Val Pro His Tyr			
485	490	495	
Ala Glu Ala Asp Ile Val Asn Leu Gln Gly Val Thr Gly Gly Asn Thr			
500	505	510	
Tyr Ser Val Pro Ala Val Thr Met Asp Leu Leu Ser Gly Lys Arg Cys			

515				520				525							
Gly	Cys	Gly	Arg	Glu	Phe	Pro	Pro	Gly	Lys	Leu	Leu	Thr	Phe	Lys	Glu
530				535				540							
Lys	Leu	Gly	Glu	Gly	Gln	Phe	Gly	Glu	Val	His	Leu	Cys	Glu	Val	Glu
545				550				555				560			
Gly	Met	Glu	Lys	Phe	Lys	Asp	Lys	Asp	Phe	Ala	Leu	Asp	Val	Ser	Ala
565				570				575							
Asn	Gln	Pro	Val	Leu	Val	Ala	Val	Lys	Met	Leu	Arg	Ala	Asp	Ala	Asn
580				585				590							
Lys	Asn	Ala	Arg	Asn	Asp	Phe	Leu	Lys	Glu	Ile	Lys	Ile	Met	Ser	Arg
595				600				605							
Leu	Lys	Asp	Pro	Asn	Ile	Ile	His	Leu	Leu	Ser	Val	Cys	Ile	Thr	Asp
610				615				620							
Asp	Pro	Leu	Cys	Met	Ile	Thr	Glu	Tyr	Met	Glu	Asn	Gly	Asp	Leu	Asn
625				630				635				640			
Gln	Phe	Leu	Ser	Arg	His	Glu	Pro	Pro	Asn	Ser	Ser	Ser	Ser	Asp	Val
645				650				655							
Arg	Thr	Val	Ser	Tyr	Thr	Asn	Leu	Lys	Phe	Met	Ala	Thr	Gln	Ile	Ala
660				665				670							
Ser	Gly	Met	Lys	Tyr	Leu	Ser	Ser	Leu	Asn	Phe	Val	His	Arg	Asp	Leu
675				680				685							
Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Lys	Asn	Tyr	Thr	Ile	Lys	Ile	Ala
690				695				700							
Asp	Phe	Gly	Met	Ser	Arg	Asn	Leu	Tyr	Ser	Gly	Asp	Tyr	Tyr	Arg	Ile
705				710				715				720			
Gln	Gly	Arg	Ala	Val	Leu	Pro	Ile	Arg	Trp	Met	Ser	Trp	Glu	Ser	Ile
725				730				735							
Leu	Leu	Gly	Lys	Phe	Thr	Thr	Ala	Ser	Asp	Val	Trp	Ala	Phe	Gly	Val
740				745				750							
Thr	Leu	Trp	Glu	Thr	Phe	Thr	Phe	Cys	Gln	Arg	Lys	Gly	Pro	Tyr	Ser
755				760				765							
Gln	Leu	Ser	Asp	Glu	Thr	Gly	Tyr	Xaa	Arg	Asn	Thr	Gly	Glu	Phe	Phe
770				775				780							
Pro	Arg	Pro	Lys	Gly	Gly	Gln	Thr	Tyr	Leu	Pro	Ser	Thr	Ser	Pro	Phe
785				790				795				800			
Val	Pro	Asp	Ser	Cys	Val	Ile	Lys	Leu	Met	Leu	Ser	Cys	Trp	Arg	Arg
805				810				815							
Asp	Thr	Lys	Asn	Arg	Pro	Ser	Phe	Gln	Glu	Ile	His	Leu	Leu	Leu	Leu
820				825				830							
Gln	Gln	Gly	Asp	Glu	Arg	Cys	Cys	Gln	Cys	Leu	Ala	Met	Phe	Leu	Arg
835				840				845							
Leu	Arg	Ser	Ser	Leu	Gln	Asp	Leu	Pro	Leu	Thr	His	Ala	Tyr	Ala	Thr
850				855				860							
Pro	Ser	Gly	His	Leu	Met	Lys	Leu	Arg	Asp	Arg	Gly	Leu	Phe	Ala	Leu
865				870				875				880			
Pro	Ser	Phe	Pro	Gly	His	Pro	His	Ser	Leu	Pro	Leu	Thr	His	Ile	Tyr
885				890				895							
Phe	Phe	Phe	Phe	Thr	Leu	Lys	Asn								
900				904											

<210> 1080

<211> 304

<212>Amino acid

<213> Homo sapiens

<400> 1080

Cys	Ser	Ala	Ser	Pro	Leu	Arg	Pro	Gly	Leu	Leu	Ala	Pro	Asp	Leu	Leu
1				5				10					15		
Tyr	Leu	Pro	Gly	Ala	Gly	Gln	Pro	Arg	Arg	Pro	Glu	Ala	Glu	Pro	Gly

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<210> 1081
<211> 139
<212> Amino acid
<213> Homo sapiens
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600

115 120 125
 Pro Gly Thr Ala Gly Glu Leu Ala Ala Pro Ser
 130 135 139

<210> 1082

<211> 1105

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(1105)

<223> X = any amino acid or stop code

<400> 1082

Glu	Lys	Asn	Ala	Leu	Glu	Pro	Thr	Val	Tyr	Phe	Gly	Met	Gly	Val	Xaa
1				5					10					15	
Ala	Pro	Gln	Val	Pro	Arg	Phe	Gln	Gln	Arg	Ile	Thr	Gly	Tyr	Gln	Tyr
			20					25					30		
Tyr	Leu	Gln	Leu	Arg	Lys	Asp	Ile	Trp	Glu	Glu	Gly	Ile	Pro	Cys	Thr
		35					40					45			
Leu	Glu	Gln	Pro	Ile	His	Leu	Ala	Gly	Leu	Ala	Val	Gln	Ala	Ile	Phe
	50					55					60				
Gly	Asp	Phe	Asp	Gln	Tyr	Glu	Ser	Gln	Asp	Phe	Leu	Gln	Lys	Phe	Ala
	65				70					75					80
Leu	Phe	Pro	Val	Gly	Trp	Leu	Gln	Asp	Glu	Lys	Val	Leu	Glu	Glu	Ala
				85					90					95	
Thr	Gln	Lys	Val	Ala	Leu	Leu	His	Gln	Lys	Tyr	Arg	Gly	Leu	Thr	Ala
			100					105					110		
Pro	Asp	Ala	Glu	Met	Leu	Tyr	Met	Gln	Glu	Val	Glu	Arg	Met	Asp	Gly
		115					120					125			
Tyr	Gly	Glu	Glu	Ser	Tyr	Pro	Ala	Lys	Asp	Ser	Gln	Gly	Ser	Asp	Ile
	130					135					140				
Ser	Ile	Gly	Ala	Cys	Leu	Glu	Gly	Ile	Phe	Val	Lys	His	Lys	Asn	Gly
	145				150					155					160
Arg	His	Pro	Val	Val	Phe	Arg	Trp	His	Asp	Ile	Ala	Asn	Met	Ser	His
				165					170					175	
Asn	Lys	Ser	Phe	Phe	Ala	Leu	Glu	Leu	Ala	Asn	Lys	Glu	Glu	Thr	Ile
			180					185					190		
Gln	Phe	Gln	Thr	Glu	Asp	Met	Glu	Thr	Ala	Lys	Tyr	Ile	Trp	Arg	Leu
		195					200					205			
Cys	Val	Ala	Arg	His	Lys	Phe	Tyr	Arg	Leu	Asn	Gln	Cys	Asn	Leu	Gln
	210					215					220				
Thr	Gln	Thr	Val	Thr	Val	Asn	Pro	Ile	Arg	Arg	Arg	Ser	Ser	Ser	Arg
	225				230					235					240
Met	Ser	Leu	Pro	Lys	Pro	Gln	Pro	Tyr	Val	Met	Pro	Pro	Pro	Pro	Gln
				245					250					255	
Leu	His	Tyr	Asn	Gly	His	Tyr	Thr	Glu	Pro	Tyr	Ala	Ser	Ser	Gln	Asp
			260					265					270		
Asn	Leu	Phe	Val	Pro	Asn	Gln	Glu	Gly	Tyr	Tyr	Gly	Gln	Phe	Gln	Thr
		275					280					285			
Ser	Leu	Asn	Arg	Ala	Gln	Ile	Asp	Phe	Asn	Gly	Arg	Ile	Arg	Asn	Ala
	290					295					300				
Ser	Val	Tyr	Ser	Ala	His	Ser	Thr	Asn	Ser	Leu	Asn	Asn	Pro	Gln	Pro
	305				310					315					320
Tyr	Leu	Gln	Pro	Ser	Pro	Met	Ser	Ser	Asn	Pro	Ser	Ile	Thr	Gly	Ser
				325					330					335	
Asp	Val	Met	Arg	Pro	Asp	Tyr	Leu	Pro	Ser	His	Arg	His	Ser	Ala	Val
			340					345						350	

Ile Pro Pro Ser Tyr Arg Pro Thr Pro Asp Tyr Glu Thr Val Met Lys
 355 360 365
 Gln Leu Asn Arg Gly Leu Val His Ala Glu Arg Gln Ser His Ser Leu
 370 375 380
 Arg Asn Leu Asn Ile Gly Ser Ser Tyr Ala Tyr Ser Arg Pro Ala Ala
 385 390 395 400
 Leu Val Tyr Ser Gln Pro Glu Ile Arg Glu His Ala Gln Leu Pro Ser
 405 410 415
 Pro Ala Ala Ala His Cys Pro Phe Ser Leu Ser Tyr Ser Phe His Ser
 420 425 430
 Pro Ser Pro Tyr Pro Tyr Pro Ala Glu Arg Arg Pro Val Val Gly Ala
 435 440 445
 Val Ser Val Pro Glu Leu Thr Asn Ala Gln Leu Gln Ala Gln Asp Tyr
 450 455 460
 Pro Ser Pro Asn Ile Met Arg Thr Gln Val Tyr Arg Pro Pro Pro Pro
 465 470 475 480
 Tyr Pro Pro Pro Arg Pro Ala Asn Ser Thr Pro Asp Leu Ser Arg His
 485 490 495
 Leu Tyr Ile Ser Ser Ser Asn Pro Asp Leu Ile Thr Arg Arg Val His
 500 505 510
 His Ser Val Gln Thr Phe Gln Glu Asp Ser Leu Pro Val Ala His Ser
 515 520 525
 Leu Gln Glu Val Ser Glu Pro Leu Thr Ala Ala Arg His Ala Gln Leu
 530 535 540
 His Lys Arg Asn Ser Ile Glu Val Ala Gly Leu Ser His Gly Leu Glu
 545 550 555 560
 Gly Leu Arg Leu Lys Glu Arg Thr Leu Ser Ala Ser Ala Ala Glu Val
 565 570 575
 Ala Pro Arg Ala Val Ser Val Gly Ser Gln Pro Ser Val Phe Thr Glu
 580 585 590
 Arg Thr Gln Arg Glu Gly Pro Glu Glu Ala Glu Gly Leu Arg Tyr Gly
 595 600 605
 His Lys Lys Ser Leu Ser Asp Ala Thr Met Leu Ile His Ser Ser Glu
 610 615 620
 Glu Glu Glu Asp Glu Asp Phe Glu Glu Glu Ser Gly Ala Arg Ala Pro
 625 630 635 640
 Pro Ala Arg Ala Arg Glu Pro Arg Pro Gly Leu Ala Gln Asp Pro Pro
 645 650 655
 Gly Cys Pro Arg Val Leu Leu Ala Gly Pro Leu His Ile Leu Glu Pro
 660 665 670
 Lys Ala His Val Pro Asp Ala Glu Lys Arg Met Met Asp Ser Ser Pro
 675 680 685
 Val Arg Thr Thr Ala Glu Ala Gln Arg Pro Trp Arg Asp Gly Leu Leu
 690 695 700
 Met Pro Ser Met Ser Glu Ser Asp Leu Thr Thr Ser Gly Arg Tyr Arg
 705 710 715 720
 Ala Arg Arg Asp Ser Leu Lys Lys Arg Pro Val Ser Asp Leu Leu Ser
 725 730 735
 Gly Lys Lys Asn Ile Val Glu Gly Leu Pro Pro Leu Gly Gly Met Lys
 740 745 750
 Lys Thr Arg Val Asp Ala Lys Lys Ile Gly Pro Leu Lys Leu Ala Ala
 755 760 765
 Leu Asn Gly Leu Ser Leu Ser Arg Val Pro Leu Pro Asp Glu Gly Lys
 770 775 780
 Glu Val Ala Thr Arg Ala Thr Asn Asp Glu Arg Cys Lys Ile Leu Glu
 785 790 795 800
 Gln Arg Leu Glu Gln Gly Met Val Phe Thr Glu Tyr Glu Arg Ile Leu
 805 810 815
 Lys Lys Arg Leu Val Asp Gly Glu Cys Ser Thr Ala Arg Leu Pro Glu
 820 825 830
 Asn Ala Glu Arg Asn Arg Phe Gln Asp Val Leu Pro Tyr Asp Asp Val
 835 840 845
 Arg Val Glu Leu Val Pro Thr Lys Glu Asn Asn Thr Gly Tyr Ile Asn
 850 855 860

Ala Ser His Ile Lys Val Ser Val Ser Gly Ile Glu Trp Asp Tyr Ile
 865 870 875 880
 Ala Thr Gln Gly Pro Leu Gln Asn Thr Cys Gln Asp Phe Trp Gln Met
 885 890 895
 Val Trp Glu Gln Gly Ile Ala Ile Ile Ala Met Val Thr Ala Glu Glu
 900 905 910
 Glu Gly Gly Arg Glu Lys Ser Phe Arg Tyr Trp Pro Arg Leu Gly Ser
 915 920 925
 Arg His Asn Thr Val Thr Tyr Gly Arg Phe Lys Ile Thr Thr Arg Phe
 930 935 940
 Arg Thr Asp Ser Gly Cys Tyr Ala Thr Thr Gly Leu Lys Met Lys His
 945 950 955 960
 Leu Leu Thr Gly Gln Glu Arg Thr Val Trp His Leu Gln Tyr Thr Asp
 965 970 975
 Trp Pro Glu His Gly Cys Pro Glu Asp Leu Lys Gly Phe Leu Ser Tyr
 980 985 990
 Leu Glu Glu Ile Gln Ser Val Arg Arg His Thr Asn Ser Thr Ser Asp
 995 1000 1005
 Pro Gln Ser Pro Asn Pro Pro Leu Leu Val His Cys Ser Ala Gly Val
 1010 1015 1020
 Gly Arg Thr Gly Val Val Ile Leu Ser Glu Ile Met Ile Ala Cys Leu
 1025 1030 1035 1040
 Glu His Asn Glu Val Leu Asp Ile Pro Arg Val Leu Asp Met Leu Arg
 1045 1050 1055
 Gln Gln Arg Met Met Leu Val Gln Thr Leu Cys Gln Tyr Thr Phe Val
 1060 1065 1070
 Tyr Arg Val Leu Ile Gln Val Pro Glu Lys Ala Pro Arg Leu Ile Leu
 1075 1080 1085
 Ser Ser Pro Gln Phe Pro Tyr Gly Ala Gln Ser Cys Glu Ala Phe Thr
 1090 1095 1100
 Ala
 1105

<210> 1083

<211> 99

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(99)

<223> X = any amino acid or stop code

<400> 1083

Arg Lys Lys Gln Lys Leu Ala Glu Glu Xaa Val Glu Leu Ser Lys Leu
 1 5 10 15
 Ala Asp Leu Lys Asp Ala Glu Ala Val Gln Lys Phe Phe Leu Glu Glu
 20 25 30
 Ile Xaa Leu Gly Glu Glu Ile Leu Ala Lys Gly Val Asp His Leu Thr
 35 40 45
 Asn Pro Ser Ala Val Cys Gly Gln Pro Gln Trp Leu Leu Gln Val Leu
 50 55 60
 Gln Gln Thr Leu Pro Leu Pro Val Ile Gln Met Leu Leu Thr Lys Pro
 65 70 75 80
 Leu Pro Val Asn Gln Arg Leu Val Ser Ala Gly Ser Leu Ala Lys Asp
 85 90 95
 Asp Val Glu
 99

<210> 1084
 <211> 206
 <212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(206)
 <223> X = any amino acid or stop code

<400> 1084
 Ser Phe Cys Leu His Glu Phe Gly Trp Leu Gly Ser Ser Pro Gln Ser
 1 5 10 15
 Asp His Pro Val Pro Ala Leu Leu Gly Leu Gly Ala Phe Val His His
 20 25 30
 Ser Leu Leu Gln Val His Ser Ser Pro Gly Ala Gly Pro Val Ser Phe
 35 40 45
 Leu Phe Leu Gly Glu Ser Cys Ser Pro Val Asp Glu Pro Arg Cys Val
 50 55 60
 Pro Ser Cys Ala Phe Gly Phe Leu Ser Cys Phe Pro Leu Leu Asn Ser
 65 70 75 80
 Ala Ala Leu Glu Arg Gly Leu Phe Phe Phe Val Val Phe Phe Phe Leu
 85 90 95
 Glu Ser Gly Ser Cys Gln Val Ala Arg Ala Gly Val Arg Asp Arg Asp
 100 105 110
 Arg Gly Ser Leu Gln Pro Pro Pro Pro Gly Leu Lys Gln Phe Cys Leu
 115 120 125
 Ser Leu Pro Ser Arg Trp Asp His Arg His Pro Pro Pro Leu Arg Val
 130 135 140
 Pro Xaa Phe Val Phe Val Phe Leu Val Glu Leu Gly Phe His His Val
 145 150 155 160
 Ala Gln Ala Gly Leu Lys Leu Leu Thr Leu Ser Asp Pro Pro Ala Pro
 165 170 175
 Ala Ser His Ser Ala Gly Ile Thr Gly Val Ser Gln Arg Asp Gln Pro
 180 185 190
 Val Leu Phe Leu Arg Trp Ala Ser Cys Ser Glu Leu Val Gly
 195 200 205 206

<210> 1085
 <211> 99
 <212>Amino acid
 <213> Homo sapiens

<400> 1085
 Glu Gly Phe Pro Gly Arg Ser Leu Ser Gly Gly Leu Cys Cys Arg Leu
 1 5 10 15
 Arg Arg Arg Phe Pro Ile Asp Gly Tyr Arg Pro Arg Arg Arg Arg
 20 25 30
 Trp Ser Cys Cys Pro Ser Gly Val Arg Pro Val Arg Arg Met Ser Gln
 35 40 45
 Lys Ser Trp Ile Glu Ser Thr Leu Thr Lys Arg Glu Cys Val Tyr Ile
 50 55 60
 Ile Pro Ser Ser Lys Asp Pro His Arg Cys Leu Pro Gly Cys Gln Ile
 65 70 75 80

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<210> 1086
<211> 53
<212> Amino acid
<213> Homo sapiens
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<210> 1087
<211> 250
<212> Amino acid
<213> Homo sapiens
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605

Lys Val Leu Glu Gln Gln Trp Ile Ser His Thr Phe Asp His Ile Asn
 225 230 235 240
 Lys Arg Trp Gly Pro His Tyr Asn Gly Leu
 245 250

<210> 1088
 <211> 455
 <212> Amino acid
 <213> Homo sapiens

<400> 1088
 Lys Gly Gln Leu Val Asn Leu Leu Pro Pro Glu Asn Phe Pro Trp Cys
 1 5 10 15
 Gly Gly Ser Gln Gly Pro Arg Met Leu Arg Thr Cys Tyr Val Leu Cys
 20 25 30
 Ser Gln Ala Gly Pro Arg Ser Arg Gly Trp Gln Ser Leu Ser Phe Asp
 35 40 45
 Gly Gly Ala Phe His Leu Lys Gly Thr Gly Glu Leu Thr Arg Ala Leu
 50 55 60
 Leu Val Leu Arg Leu Cys Ala Trp Pro Pro Leu Val Thr His Gly Leu
 65 70 75 80
 Leu Leu Gln Ala Trp Ser Arg Arg Leu Leu Gly Ser Arg Leu Ser Gly
 85 90 95
 Ala Phe Leu Arg Ala Ser Val Tyr Gly Gln Phe Val Ala Gly Glu Thr
 100 105 110
 Ala Glu Glu Val Lys Gly Cys Val Gln Gln Leu Arg Thr Leu Ser Leu
 115 120 125
 Arg Pro Leu Leu Ala Val Pro Thr Glu Glu Glu Pro Asp Ser Ala Ala
 130 135 140
 Lys Ser Gly Glu Ala Trp Tyr Glu Gly Asn Leu Gly Ala Met Leu Arg
 145 150 155 160
 Cys Val Asp Leu Ser Arg Gly Leu Leu Glu Pro Pro Ser Leu Ala Glu
 165 170 175
 Ala Ser Leu Met Gln Leu Lys Val Thr Ala Leu Thr Ser Thr Arg Leu
 180 185 190
 Cys Lys Glu Leu Ala Ser Trp Val Arg Arg Pro Gly Ala Ser Leu Glu
 195 200 205
 Leu Ser Pro Glu Arg Leu Ala Glu Ala Met Asp Ser Gly Gln Asn Leu
 210 215 220
 Gln Val Ser Cys Leu Asn Ala Glu Gln Asn Gln His Leu Arg Ala Ser
 225 230 235 240
 Leu Ser Arg Leu His Arg Val Ala Gln Tyr Ala Arg Ala Gln His Val
 245 250 255
 Arg Leu Leu Val Asp Ala Glu Tyr Thr Ser Leu Asn Pro Ala Leu Ser
 260 265 270
 Leu Leu Val Ala Ala Leu Ala Val Arg Trp Asn Ser Pro Gly Glu Gly
 275 280 285
 Gly Pro Trp Val Trp Asn Thr Tyr Gln Ala Cys Leu Lys Asp Thr Phe
 290 295 300
 Glu Arg Leu Gly Arg Asp Ala Glu Ala Ala His Arg Ala Gly Leu Ala
 305 310 315 320
 Phe Gly Val Lys Leu Val Arg Gly Ala Tyr Leu Asp Lys Glu Arg Ala
 325 330 335
 Val Ala Gln Leu His Gly Met Glu Asp Pro Pro Thr Gln Ala Asp Tyr
 340 345 350
 Glu Ala Thr Ser Gln Ser Tyr Ser Arg Cys Leu Glu Leu Met Leu Thr
 355 360 365
 His Val Ala Arg His Gly Pro Met Cys His Leu Met Val Ala Ser His
 370 375 380


```

Asn Glu Glu Ser Val Arg Gln Ala Thr Lys Gly Gln Ala Gly Tyr Val
385                               390                               395                               400
Val Tyr Lys Ser Ile Pro Tyr Gly Ser Leu Glu Glu Val Ile Pro Tyr
                               405                               410                               415
Leu Ile Arg Arg Ala Gln Glu Asn Arg Ser Val Leu Gln Gly Ala Arg
                               420                               425                               430
Arg Glu Gln Glu Leu Leu Ser Gln Lys Leu Trp Arg Arg Leu Leu Pro
                               435                               440                               445
Gly Cys Arg Arg Ile Pro His
                               450                               455

```

<210> 1089

<211> 243

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(243)

<223> X = any amino acid or stop code

<400> 1089

```

Val Val Glu Phe Gly Glu Met Ser Thr Ala Arg Ala Pro Glu Gly Leu
1                               5                               10                               15
Arg Trp Phe Gln Leu Tyr Val His Pro Asp Leu Gln Leu Asn Lys Gln
                               20                               25                               30
Leu Ile Gln Arg Val Glu Ser Leu Gly Phe Lys Ala Leu Val Ile Thr
                               35                               40                               45
Leu Asp Thr Pro Val Cys Gly Asn Arg Arg His Asp Ile Arg Asn Gln
                               50                               55                               60
Leu Arg Arg Asn Leu Thr Leu Thr Asp Leu Gln Ser Pro Lys Lys Gly
65                               70                               75                               80
Asn Ala Ile Pro Tyr Phe Gln Met Thr Pro Ile Ser Thr Ser Leu Cys
                               85                               90                               95
Trp Asn Asp Leu Ser Trp Phe Gln Ser Ile Thr Arg Leu Pro Ile Ile
                               100                              105                              110
Leu Lys Gly Ile Leu Thr Lys Glu Asp Ala Glu Leu Ala Val Lys His
                               115                              120                              125
Asn Val Gln Gly Ile Ile Val Ser Asn His Gly Gly Arg Gln Leu Asp
130                              135                              140
Glu Val Leu Ala Ser Ile Asp Ala Leu Thr Glu Val Gly Ala Ala Glu
145                              150                              155                              160
Xaa Gly Asn Met Lys Tyr Tyr Leu Asp Ala Gly Val Arg Thr Gly Asn
                               165                              170                              175
Asp Val Gln Lys Ala Leu Ala Leu Gly Ala Lys Cys Ile Phe Leu Gly
180                              185                              190
Arg Pro Ile Leu Trp Gly Leu Ala Cys Lys Gly Glu His Gly Val Lys
195                              200                              205
Glu Val Leu Asn Ile Leu Thr Asn Glu Phe His Thr Ser Met Ala Leu
210                              215                              220
Thr Gly Cys Arg Ser Val Ala Glu Ile Asn Arg Asn Leu Val Gln Phe
225                              230                              235                              240
Ser Arg Leu
                               243

```

<210> 1090

<211> 90

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(90)

<223> X = any amino acid or stop code

<400> 1090

```

Phe Phe Leu Arg Trp Ser Phe Thr Leu Leu Pro Arg Leu Glu Cys Gln
 1           5           10           15
Trp Leu Asn Leu Gly Ser Leu Gln Pro Pro Pro Gly Phe Lys Xaa
          20           25           30
Ser Ser Cys Leu Arg Leu Leu Ser Trp Gly Leu Gln Val Pro Thr
          35           40           45
Ser Met Leu Gly Xaa Phe Phe Cys Ile Phe Ser Arg Glu Gly Ile Ser
          50           55           60
Pro Cys Trp Pro Gly Trp Ser Gln Thr Pro Lys Val Ile His Leu Pro
          65           70           75           80
Arg Pro Pro Arg Val Leu Arg Leu Gln Ala
          85           90

```

<210> 1091

<211> 259

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(259)

<223> X = any amino acid or stop code

<400> 1091

```

Leu Leu Cys Phe Val His Thr Ala Leu Gln Ser Phe Gln Gly Glu Leu
 1           5           10           15
Tyr Glu Pro His Val Val Ile Ala Ile Val Val Phe Leu Val Lys Leu
          20           25           30
Gly Ile Cys Lys Xaa Arg Ala Ser Trp Arg Lys Lys Val Thr Leu Val
          35           40           45
Val Lys Xaa Ser Leu Lys Ile Cys Phe Thr Lys Tyr Gly Ser Cys Tyr
          50           55           60
His Pro Gly Glu Lys Ser Ser Ser Trp Leu Phe Asn Xaa Arg Met Val
          65           70           75           80
Asn Asp Cys Leu Ala Thr Ser Cys Ser Asn Arg Ser Phe Val Ile Gln
          85           90           95
Gln Ile Pro Ser Ser Asn Leu Phe Met Val Val Val Asp Ser Ser Cys
          100          105          110
Leu Cys Glu Ser Val Ala Pro Ile Thr Met Ala Pro Ile Glu Ile Arg
          115          120          125
Tyr Ile Leu Leu Cys Ala Gly Pro Leu Thr Thr Thr Glu Thr Ser Lys
          130          135          140
Gly Tyr Gln Trp Xaa Gly Asn Leu Gly Glu Lys Tyr Xaa Arg Arg Lys
          145          150          155          160
Ile Thr Ser Phe Pro Leu Leu Glu Arg Glu Ser Ser Xaa Glu Ser Cys
          165          170          175
His Cys Gln Ile Leu Thr Ser Glu Met Gln Ser Arg Lys Lys Gln Ser

```

```

      180      185      190
Leu Glu Thr Cys Leu Asn Tyr Ser Gln His Asn Glu Ser Leu Lys Cys
      195      200      205
Glu Arg Leu Lys Ala Gln Lys Ile Arg Arg Arg Pro Glu Ser Cys His
      210      215      220
Gly Phe His Pro Glu Glu Asn Ala Arg Glu Cys Gly Gly Ala Pro Ser
225      230      235      240
Leu Gln Ala Gln Thr Val Leu Leu Leu Leu Pro Leu Leu Leu Met Leu
      245      250      255
Phe Ser Arg
      259

```

```

<210> 1092
<211> 117
<212> Amino acid
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(117)
<223> X = any amino acid or stop code

```

```

      <400> 1092
Val Pro Ser Pro Thr His Asp Pro Lys Pro Ala Glu Ala Pro Met Pro
 1      5      10      15
Ala Xaa Pro Ala Pro Pro Gly Pro Ala Ser Pro Gly Gly Ala Leu Glu
      20      25      30
Pro Pro Ala Ala Ala Arg Ala Gly Gly Ser Pro Thr Ala Val Arg Ser
      35      40      45
Ile Leu Thr Lys Glu Arg Arg Pro Glu Gly Gly Tyr Lys Ala Val Trp
      50      55      60
Phe Gly Glu Asp Ile Gly Thr Glu Ala Asp Val Val Val Leu Asn Ala
      65      70      75      80
Pro Thr Leu Asp Val Asp Gly Ala Ser Asp Ser Gly Ser Gly Asp Glu
      85      90      95
Gly Glu Gly Ala Gly Arg Gly Gly Gly Pro Tyr Asp Ala Pro Gly Gly
      100      105      110
Asp Asp Ser Tyr Ile
      115      117

```

```

<210> 1093
<211> 763
<212> Amino acid
<213> Homo sapiens

```

```

      <400> 1093
Leu Ile Ser Leu Ala Gly Pro Thr Asp Asp Ile Gln Ser Thr Gly Pro
 1      5      10      15
Gln Val His Ala Leu Asn Ile Leu Arg Ala Leu Phe Arg Asp Thr Arg
      20      25      30
Leu Gly Glu Asn Ile Ile Pro Tyr Val Ala Asp Gly Ala Lys Ala Ala
      35      40      45
Ile Leu Gly Phe Thr Ser Pro Val Trp Ala Val Arg Asn Ser Ser Thr
      50      55      60

```

Leu Leu Phe Ser Ala Leu Ile Thr Arg Ile Phe Gly Val Lys Arg Ala
 65 70 75 80
 Lys Asp Glu His Ser Lys Thr Asn Arg Met Thr Gly Arg Glu Phe Phe
 85 90 95
 Ser Arg Phe Pro Glu Leu Tyr Pro Phe Leu Leu Lys Gln Leu Glu Thr
 100 105 110
 Val Ala Asn Thr Val Asp Ser Asp Met Gly Glu Pro Asn Arg His Pro
 115 120 125
 Ser Met Phe Leu Leu Leu Leu Val Leu Glu Arg Leu Tyr Ala Ser Pro
 130 135 140
 Met Asp Gly Thr Ser Ser Ala Leu Ser Met Gly Pro Phe Val Pro Phe
 145 150 155 160
 Ile Met Arg Cys Gly His Ser Pro Val Tyr His Ser Arg Glu Met Ala
 165 170 175
 Ala Arg Ala Leu Val Pro Phe Val Met Ile Asp His Ile Pro Asn Thr
 180 185 190
 Ile Arg Thr Leu Leu Ser Thr Leu Pro Ser Cys Thr Asp Gln Cys Phe
 195 200 205
 Arg Gln Asn His Ile His Gly Thr Leu Leu Gln Val Phe His Leu Val
 210 215 220
 Gln Ala Tyr Ser Asp Ser Lys His Gly Thr Asn Ser Asp Phe Gln His
 225 230 235 240
 Glu Leu Thr Asp Ile Thr Val Cys Thr Lys Ala Lys Leu Trp Leu Ala
 245 250 255
 Lys Arg Gln Asn Pro Cys Leu Val Thr Arg Ala Val Tyr Ile Asp Ile
 260 265 270
 Leu Phe Leu Leu Thr Cys Cys Leu Asn Arg Ser Ala Lys Asp Asn Gln
 275 280 285
 Pro Val Leu Glu Ser Leu Gly Phe Trp Glu Glu Val Arg Gly Ile Ile
 290 295 300
 Ser Gly Ser Glu Leu Ile Thr Gly Phe Pro Trp Ala Phe Lys Val Pro
 305 310 315 320
 Gly Leu Pro Gln Tyr Leu Gln Ser Leu Thr Arg Leu Ala Ile Ala Ala
 325 330 335
 Val Trp Ala Ala Ala Ala Lys Ser Gly Glu Arg Glu Thr Asn Val Pro
 340 345 350
 Ile Ser Phe Ser Gln Leu Leu Glu Ser Ala Phe Pro Glu Val Arg Ser
 355 360 365
 Leu Thr Leu Glu Ala Leu Leu Glu Lys Phe Leu Ala Ala Ala Ser Gly
 370 375 380
 Leu Gly Glu Lys Gly Val Pro Pro Leu Leu Cys Asn Met Gly Glu Lys
 385 390 395 400
 Phe Leu Leu Leu Ala Met Lys Glu Asn His Pro Glu Cys Phe Cys Lys
 405 410 415
 Ile Leu Lys Ile Leu His Cys Met Asp Pro Gly Glu Trp Leu Pro Gln
 420 425 430
 Thr Glu His Cys Val His Leu Thr Pro Lys Glu Phe Leu Ile Trp Thr
 435 440 445
 Met Asp Ile Ala Ser Asn Glu Arg Ser Glu Ile Gln Ser Val Ala Leu
 450 455 460
 Arg Leu Ala Ser Lys Val Ile Ser His His Met Gln Thr Cys Val Glu
 465 470 475 480
 Asn Arg Glu Leu Ile Ala Ala Glu Leu Lys Gln Trp Val Gln Leu Val
 485 490 495
 Ile Leu Ser Cys Glu Asp His Leu Pro Thr Glu Ser Arg Leu Ala Val
 500 505 510
 Val Glu Val Leu Thr Ser Thr Thr Pro Leu Phe Leu Thr Asn Pro His
 515 520 525
 Pro Ile Leu Glu Leu Gln Asp Thr Leu Ala Leu Trp Lys Cys Val Leu
 530 535 540
 Thr Leu Leu Gln Ser Glu Glu Gln Ala Val Arg Asp Ala Ala Thr Glu
 545 550 555 560
 Thr Val Thr Thr Ala Met Ser Gln Glu Asn Thr Cys Gln Ser Thr Glu
 565 570 575

Phe Ala Phe Cys Gln Val Asp Ala Ser Ile Ala Leu Ala Leu Ala Leu
 580 585 590
 Ala Val Leu Cys Asp Leu Leu Gln Gln Trp Asp Gln Leu Ala Pro Gly
 595 600 605
 Leu Pro Ile Leu Leu Gly Trp Leu Leu Gly Glu Ser Asp Asp Leu Val
 610 615 620
 Ala Cys Val Glu Ser Met His Gln Val Glu Glu Asp Tyr Leu Phe Glu
 625 630 635 640
 Lys Ala Glu Val Asn Phe Trp Ala Glu Thr Leu Ile Phe Val Lys Tyr
 645 650 655
 Leu Cys Lys His Leu Phe Cys Leu Leu Ser Lys Ser Gly Trp Arg Pro
 660 665 670
 Pro Ser Pro Glu Met Leu Cys His Leu Gln Arg Met Val Ser Glu Gln
 675 680 685
 Cys His Leu Leu Ser Gln Phe Phe Arg Glu Leu Pro Pro Ala Ala Glu
 690 695 700
 Phe Val Lys Thr Val Glu Phe Thr Arg Leu Arg Ile Gln Glu Glu Arg
 705 710 715 720
 Thr Leu Ala Cys Leu Arg Leu Leu Ala Phe Leu Glu Gly Lys Glu Gly
 725 730 735
 Glu Asp Thr Leu Val Leu Ser Val Trp Asp Ser Tyr Ala Glu Ser Arg
 740 745 750
 Gln Leu Thr Leu Pro Arg Thr Glu Ala Ala Cys
 755 760 763

<210> 1094

<211> 413

<212> Amino acid

<213> Homo sapiens

<400> 1094

His Ala Phe Arg Pro Ile Ala Leu Gln Arg Gly Val Ser Phe Arg Gly
 1 5 10 15
 Cys Ser Asn Gln Tyr Ala Glu Ser Arg Arg Leu Gln Gly Glu Ser Gly
 20 25 30
 Ser Arg Ala Phe Ala His Leu Met Glu Ser Leu Leu Gln His Leu Asp
 35 40 45
 Arg Phe Ser Glu Leu Leu Ala Val Ser Ser Thr Thr Tyr Val Ser Thr
 50 55 60
 Trp Asp Pro Ala Thr Val Arg Arg Ala Leu Gln Trp Ala Arg Tyr Leu
 65 70 75 80
 Arg His Ile His Arg Arg Phe Gly Arg His Gly Pro Ile Arg Thr Ala
 85 90 95
 Leu Glu Arg Arg Leu His Asn Gln Trp Arg Gln Glu Gly Gly Phe Gly
 100 105 110
 Arg Gly Pro Val Pro Gly Leu Ala Asn Phe Gln Ala Leu Gly His Cys
 115 120 125
 Asp Val Leu Leu Ser Leu Arg Leu Leu Glu Asn Arg Ala Leu Gly Asp
 130 135 140
 Ala Ala Arg Tyr His Leu Val Gln Gln Leu Phe Pro Gly Pro Gly Val
 145 150 155 160
 Arg Asp Ala Asp Glu Glu Thr Leu Gln Glu Ser Leu Ala Arg Leu Ala
 165 170 175
 Arg Arg Arg Ser Ala Val His Met Leu Arg Phe Asn Gly Tyr Arg Glu
 180 185 190
 Asn Pro Asn Leu Gln Glu Asp Ser Leu Met Lys Thr Gln Ala Glu Leu
 195 200 205
 Leu Leu Glu Arg Leu Gln Glu Val Gly Lys Ala Glu Ala Glu Arg Pro
 210 215 220

Ala Arg Phe Leu Ser Ser Leu Trp Glu Arg Leu Pro Gln Asn Asn Phe
 225 230 235 240
 Leu Lys Val Ile Ala Val Ala Leu Leu Gln Pro Pro Leu Ser Arg Arg
 245 250 255
 Pro Gln Glu Glu Leu Glu Pro Gly Ile His Lys Ser Pro Gly Glu Gly
 260 265 270
 Ser Gln Val Leu Val His Trp Leu Leu Gly Asn Ser Glu Val Phe Ala
 275 280 285
 Ala Phe Cys Arg Ala Leu Pro Ala Gly Leu Leu Thr Leu Val Thr Ser
 290 295 300
 Arg His Pro Ala Leu Ser Pro Val Tyr Leu Gly Leu Leu Thr Asp Trp
 305 310 315 320
 Gly Gln Arg Leu His Tyr Asp Leu Gln Lys Gly Ile Trp Val Gly Thr
 325 330 335
 Glu Ser Gln Asp Val Pro Trp Glu Glu Leu His Asn Arg Phe Gln Ser
 340 345 350
 Leu Cys Gln Ala Pro Pro Pro Leu Lys Asp Lys Val Leu Thr Ala Leu
 355 360 365
 Glu Thr Cys Lys Ala Gln Asp Gly Asp Phe Glu Glu Pro Gly Leu Ser
 370 375 380
 Ile Trp Thr Asp Leu Leu Leu Ala Leu Arg Ser Gly Ala Phe Arg Lys
 385 390 395 400
 Arg Gln Val Leu Gly Leu Ser Ala Gly Leu Ser Ser Val
 405 410 413

<210> 1095

<211> 344

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(344)

<223> X = any amino acid or stop code

<400> 1095

Ser His Leu Ile Gln His Gln Arg Ile His Thr Xaa Glu Xaa Ala His
 1 5 10 15
 Glu Cys Asn Glu Cys Gly Lys Ala Phe Ser Gln Thr Ser Cys Leu Ile
 20 25 30
 Gln His His Lys Met His Arg Lys Glu Lys Ser Tyr Glu Cys Asn Glu
 35 40 45
 Tyr Glu Gly Ser Phe Ser His Ser Ser Asp Leu Ile Leu Gln Gln Glu
 50 55 60
 Val Leu Thr Arg Gln Lys Ala Phe Asp Cys Asp Val Trp Glu Lys Asn
 65 70 75 80
 Ser Ser Gln Arg Ala His Leu Val Gln His Gln Ser Ile His Thr Lys
 85 90 95
 Glu Lys Pro His Glu Cys Asn Glu Asp Gly Lys Ile Phe Asn Gln Ile
 100 105 110
 Gln Ala Leu Ile Gln His Leu Arg Val His Thr Arg Glu Lys Tyr Val
 115 120 125
 Cys Thr Ala Cys Gly Lys Ala Phe Ser His Ser Ser Ala Ile Ala Gln
 130 135 140
 His Gln Ile Ile His Thr Arg Glu Lys Pro Ser Glu Cys Asp Glu Xaa
 145 150 155 160
 Arg Lys Gly Ile Ser Val Lys Leu Leu Ile Asp Ser Cys Arg Ile Tyr
 165 170 175
 Thr Ser Glu Lys Ser Tyr Lys Cys Ile Glu Cys Gly Lys Phe Phe Met

```

      180      185      190
Leu Leu Val Phe Ser Tyr Leu Ser His Ile Trp Arg Ile His Met Gly
      195      200      205
Ile Lys Phe His Cys Cys Asn Glu Cys Glu Lys Ala Ile Ser Gln Arg
      210      215      220
Asn Tyr Leu Val Xaa Tyr Gln Ile His Ala Met Gln Lys Asp Tyr Lys
225      230      235      240
Cys Asn Glu Ala Cys Met Cys Val Arg Arg Phe Ser His Asn Pro Thr
      245      250      255
Leu Ile Gln His Gln Arg Ile Tyr Thr Xaa Glu Asn Leu Phe Gly Cys
      260      265      270
Ser Lys Cys Gly Arg Ser Phe Asn Arg Ser Leu Thr Ser Leu Cys His
      275      280      285
Ile Arg Ile Ser Ile Arg Arg Gln Glu Phe Asp Val Thr Gln Met Glu
      290      295      300
Lys Leu Asp Thr Thr Phe Gln Ala Ser Thr Gln His Arg Asn Asn Gly
305      310      315      320
Glu Lys Ile Val Asp Tyr Leu Phe Met Lys Leu Leu Ile His Ser Pro
      325      330      335
Asn Leu Phe His Cys Thr Lys Ile
      340      344

```

```

<210> 1096
<211> 76
<212>Amino acid
<213> Homo sapiens

```

```

      <400> 1096
Ala Val Thr Leu Thr Ala Lys Ile Cys Ser Phe Thr Pro Glu Pro Ser
  1      5      10      15
Glu Thr Met Ser Pro Pro Ala Gly Thr Asn Asn Ser Arg His Ala Ala
      20      25      30
Leu Arg Ala Val Thr Leu Pro Val Lys Val Cys Ser Phe Thr Pro Glu
      35      40      45
Pro Ala Arg Ser Arg Thr His Gln Lys Glu Glu Thr Pro Asn Thr Ser
      50      55      60
Glu His Gln Lys Glu Gln Thr Pro Glu Ala Pro Pro
      65      70      75      76

```

```

<210> 1097
<211> 1462
<212>Amino acid
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(1462)
<223> X = any amino acid or stop code

```

```

      <400> 1097
Met Ala Tyr Ser Trp Gln Thr Asp Pro Asn Pro Asn Glu Ser His Glu
  1      5      10      15
Lys Gln Tyr Glu His Gln Glu Phe Leu Phe Val Asn Gln Pro His Ser
      20      25      30

```

Ser Ser Gln Val Ser Leu Gly Phe Asp Gln Ile Val Asp Glu Ile Ser
 35 40 45
 Gly Lys Ile Pro His Tyr Glu Ser Glu Ile Asp Glu Asn Thr Phe Phe
 50 55 60
 Val Pro Thr Ala Pro Lys Trp Asp Ser Thr Gly His Ser Leu Asn Glu
 65 70 75 80
 Ala His Gln Ile Ser Leu Asn Glu Phe Thr Ser Lys Ser Arg Glu Leu
 85 90 95
 Ser Trp His Gln Val Ser Lys Ala Pro Ala Ile Gly Phe Ser Pro Ser
 100 105 110
 Val Leu Pro Lys Pro Gln Asn Thr Asn Lys Glu Cys Ser Trp Gly Ser
 115 120 125
 Pro Ile Gly Lys His His Gly Ala Asp Asp Ser Arg Phe Ser Ile Leu
 130 135 140
 Ala Pro Ser Phe Thr Ser Leu Asp Lys Ile Asn Leu Glu Lys Glu Leu
 145 150 155 160
 Glu Asn Glu Asn His Asn Tyr His Ile Gly Phe Glu Ser Ser Ile Pro
 165 170 175
 Pro Thr Asn Ser Ser Phe Ser Ser Asp Phe Met Pro Lys Glu Glu Asn
 180 185 190
 Lys Arg Ser Gly His Val Asn Ile Val Glu Pro Ser Leu Met Leu Leu
 195 200 205
 Lys Gly Ser Leu Gln Pro Gly Met Trp Glu Ser Thr Trp Gln Lys Asn
 210 215 220
 Ile Glu Ser Ile Gly Cys Ser Ile Gln Leu Val Glu Val Pro Gln Ser
 225 230 235 240
 Ser Asn Thr Ser Leu Ala Ser Phe Cys Asn Lys Val Lys Lys Ile Arg
 245 250 255
 Glu Arg Tyr His Ala Ala Asp Val Asn Phe Asn Ser Gly Lys Ile Trp
 260 265 270
 Ser Thr Thr Thr Ala Phe Pro Tyr Gln Leu Phe Ser Lys Thr Lys Phe
 275 280 285
 Asn Ile His Ile Phe Ile Asp Asn Ser Thr Gln Pro Leu His Phe Met
 290 295 300
 Pro Cys Ala Asn Tyr Leu Val Lys Asp Leu Ile Ala Glu Ile Leu His
 305 310 315 320
 Phe Cys Thr Asn Asp Gln Leu Leu Pro Lys Asp His Ile Leu Ser Val
 325 330 335
 Trp Gly Ser Glu Glu Phe Leu Gln Asn Asp His Cys Leu Gly Ser His
 340 345 350
 Lys Met Phe Gln Lys Asp Lys Ser Val Ile Gln Leu His Leu Gln Lys
 355 360 365
 Ser Arg Glu Ala Pro Gly Lys Leu Ser Arg Lys His Glu Glu Asp His
 370 375 380
 Ser Gln Phe Tyr Leu Asn Gln Leu Leu Glu Phe Met His Ile Trp Lys
 385 390 395 400
 Val Ser Arg Gln Cys Leu Leu Thr Leu Ile Arg Lys Tyr Asp Phe His
 405 410 415
 Leu Lys Tyr Leu Leu Lys Thr Gln Glu Asn Val Tyr Asn Ile Ile Glu
 420 425 430
 Glu Val Lys Lys Ile Cys Ser Val Leu Gly Cys Val Glu Thr Lys Gln
 435 440 445
 Ile Thr Asp Ala Val Asn Glu Leu Ser Leu Ile Leu Gln Arg Lys Gly
 450 455 460
 Glu Asn Phe Tyr Gln Ser Ser Glu Thr Ser Ala Lys Gly Leu Ile Glu
 465 470 475 480
 Lys Val Thr Thr Glu Leu Ser Thr Ser Ile Tyr Gln Leu Ile Asn Val
 485 490 495
 Tyr Cys Asn Ser Phe Tyr Ala Asp Phe Gln Pro Val Asn Val Pro Arg
 500 505 510
 Cys Thr Ser Tyr Leu Asn Pro Gly Leu Pro Ser His Leu Ser Phe Thr
 515 520 525
 Val Tyr Ala Ala His Asn Ile Pro Glu Thr Trp Val His Arg Ile Asn
 530 535 540

Phe Pro Leu Glu Ile Lys Ser Leu Pro Arg Glu Ser Met Leu Thr Val
 545 550 555 560
 Lys Leu Phe Gly Ile Ala Cys Ala Thr Asn Asn Ala Asn Leu Leu Ala
 565 570 575
 Trp Thr Cys Leu Pro Leu Phe Pro Lys Glu Lys Ser Ile Leu Gly Ser
 580 585 590
 Met Leu Phe Ser Met Thr Leu Gln Ser Glu Pro Pro Val Glu Met Ile
 595 600 605
 Thr Pro Gly Val Trp Asp Val Ser Gln Pro Ser Pro Val Thr Leu Gln
 610 615 620
 Ile Asp Phe Pro Ala Thr Gly Trp Glu Tyr Met Lys Pro Asp Ser Glu
 625 630 635 640
 Glu Asn Arg Ser Asn Leu Glu Glu Pro Leu Lys Glu Cys Ile Lys His
 645 650 655
 Ile Ala Arg Leu Ser Gln Lys Gln Thr Pro Leu Leu Leu Ser Glu Glu
 660 665 670
 Lys Lys Arg Tyr Leu Trp Phe Tyr Arg Phe Tyr Cys Asn Asn Glu Asn
 675 680 685
 Cys Ser Leu Pro Leu Val Leu Gly Ser Ala Pro Gly Trp Asp Glu Arg
 690 695 700
 Thr Val Ser Glu Met His Thr Ile Leu Arg Arg Trp Thr Phe Ser Gln
 705 710 715 720
 Pro Leu Glu Ala Leu Gly Leu Leu Thr Ser Ser Phe Pro Asp Gln Glu
 725 730 735
 Ile Arg Lys Val Ala Val Gln Gln Leu Asp Asn Leu Leu Asn Asp Glu
 740 745 750
 Leu Leu Glu Tyr Leu Pro Gln Leu Val Gln Ala Val Lys Phe Glu Trp
 755 760 765
 Asn Leu Glu Ser Pro Leu Val Gln Leu Leu Leu His Arg Ser Leu Gln
 770 775 780
 Ser Ile Gln Val Ala His Arg Leu Tyr Trp Leu Leu Lys Asn Ala Glu
 785 790 795 800
 Asn Glu Ala Tyr Phe Lys Ser Trp Tyr Gln Lys Leu Leu Ala Ala Leu
 805 810 815
 Gln Phe Cys Ala Gly Lys Ala Leu Asn Asp Glu Phe Ser Lys Glu Gln
 820 825 830
 Lys Leu Ile Lys Ile Leu Gly Asp Ile Gly Glu Arg Val Lys Ser Ala
 835 840 845
 Ser Asp His Gln Arg Gln Glu Val Leu Lys Lys Glu Ile Gly Arg Leu
 850 855 860
 Glu Glu Phe Phe Gln Asp Val Asn Thr Cys His Leu Pro Leu Asn Pro
 865 870 875 880
 Ala Leu Cys Ile Lys Gly Ile Asp His Asp Ala Cys Ser Tyr Phe Thr
 885 890 895
 Ser Asn Ala Leu Pro Leu Lys Ile Thr Phe Ile Asn Ala Asn Leu Met
 900 905 910
 Gly Lys Asn Ile Ser Ile Ile Phe Lys Ala Gly Asp Asp Leu Arg Gln
 915 920 925
 Asp Met Leu Val Leu Gln Leu Ile Gln Val Met Asp Asn Ile Trp Leu
 930 935 940
 Gln Glu Gly Leu Asp Met Gln Met Ile Ile Tyr Arg Cys Leu Ser Thr
 945 950 955 960
 Gly Lys Asp Gln Arg Leu Val Gln Met Val Pro Asp Ala Val Thr Leu
 965 970 975
 Ala Lys Ile His Arg His Ser Gly Leu Ile Gly Pro Leu Lys Glu Asn
 980 985 990
 Thr Ile Lys Lys Trp Phe Ser Gln His Asn His Leu Lys Ala Asp Tyr
 995 1000 1005
 Glu Lys Ala Leu Arg Asn Phe Phe Tyr Ser Cys Ala Gly Trp Cys Val
 1010 1015 1020
 Val Thr Phe Ile Leu Gly Val Cys Asp Arg His Asn Asp Asn Ile Met
 1025 1030 1035 1040
 Leu Thr Lys Ser Gly His Met Phe His Ile Asp Phe Gly Lys Phe Leu
 1045 1050 1055

Gly His Ala Gln Thr Phe Gly Gly Ile Lys Arg Asp Arg Ala Pro Phe
 1060 1065 1070
 Ile Phe Thr Ser Glu Met Glu Tyr Phe Ile Thr Glu Gly Gly Lys Asn
 1075 1080 1085
 Pro Gln His Phe Gln Asp Phe Val Glu Leu Cys Cys Arg Ala Tyr Asn
 1090 1095 1100
 Ile Ile Arg Lys His Ser Gln Leu Leu Leu Asn Leu Leu Glu Met Met
 1105 1110 1115 1120
 Leu Tyr Ala Gly Leu Pro Glu Leu Ser Gly Ile Gln Asp Leu Lys Tyr
 1125 1130 1135
 Val Tyr Asn Asn Leu Arg Pro Gln Asp Thr Asp Leu Glu Ala Thr Ser
 1140 1145 1150
 His Phe Thr Lys Lys Ile Lys Glu Ser Leu Glu Cys Phe Pro Val Lys
 1155 1160 1165
 Leu Asn Asn Leu Ile His Thr Leu Ala Gln Met Ser Ala Ile Ser Pro
 1170 1175 1180
 Ala Lys Ser Thr Ser Gln Thr Phe Pro Gln Glu Ser Cys Leu Leu Ser
 1185 1190 1195 1200
 Thr Thr Arg Ser Ile Glu Arg Ala Thr Ile Leu Gly Phe Ser Lys Lys
 1205 1210 1215
 Ser Ser Asn Leu Tyr Leu Ile Gln Val Thr His Ser Asn Asn Glu Thr
 1220 1225 1230
 Ser Leu Thr Glu Lys Ser Phe Glu Gln Phe Ser Lys Leu His Ser Gln
 1235 1240 1245
 Leu Gln Lys Gln Phe Ala Ser Leu Thr Leu Pro Glu Phe Pro His Trp
 1250 1255 1260
 Trp His Leu Pro Phe Thr Asn Ser Asp His Arg Arg Phe Arg Asp Leu
 1265 1270 1275 1280
 Asn His Tyr Met Glu Gln Ile Leu Asn Val Ser His Glu Val Thr Asn
 1285 1290 1295
 Ser Asp Cys Val Leu Ser Phe Phe Leu Ser Glu Ala Gly Gln Gln Thr
 1300 1305 1310
 Val Glu Glu Ser Ser Pro Val Tyr Leu Gly Glu Lys Phe Pro Asp Lys
 1315 1320 1325
 Lys Pro Lys Val Gln Leu Val Ile Ser Tyr Glu Asp Val Lys Leu Thr
 1330 1335 1340
 Ile Leu Val Lys His Met Lys Asn Ile His Leu Pro Asp Gly Ser Ala
 1345 1350 1355 1360
 Pro Ser Ala His Val Glu Phe Tyr Leu Leu Pro Tyr Pro Ser Glu Val
 1365 1370 1375
 Arg Arg Arg Lys Thr Lys Ser Val Pro Lys Cys Thr Asp Pro Thr Tyr
 1380 1385 1390
 Asn Glu Ile Val Val Tyr Asp Glu Val Thr Glu Leu Gln Gly His Val
 1395 1400 1405
 Leu Met Leu Ile Val Lys Ser Lys Thr Val Phe Val Gly Ala Ile Asn
 1410 1415 1420
 Ile Arg Leu Cys Ser Val Pro Leu Asp Lys Glu Lys Trp Tyr Pro Leu
 1425 1430 1435 1440
 Gly Asn Ser Ile Ile Xaa Pro Leu Leu Leu Phe Tyr Thr Ser Asn Phe
 1445 1450 1455
 Met Gln Ser Val Leu His
 1460 1462

<210> 1098

<211> 111

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)... (111)

<223> X = any amino acid or stop code

<400> 1098

```

Phe Phe Leu Arg Trp Ser Leu Asp Ser Val Thr Gln Ala Gly Val Gln
 1           5           10           15
Ser His Asp Leu Ser Ser Leu Gln Pro Pro Pro Pro Gly Phe Lys Gln
           20           25           30
Ser Ser Leu Phe Gly Leu Pro Ser Ser Trp Glu Xaa Arg Trp Val Pro
           35           40           45
Pro Cys Pro Ala Asn Phe Phe Val Phe Leu Val Glu Thr Gly Phe Arg
           50           55           60
His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Asn Asp Leu Pro
           65           70           75           80
Val Ser Ala Cys Gln Ser Ala Gly Ile Thr Gly Val Thr Thr Val Pro
           85           90           95
Gln Arg Lys Ser Met Ile Leu Tyr Glu Val Thr Ile Cys Tyr Pro
           100           105           110 111

```

<210> 1099

<211> 1070

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (1070)

<223> X = any amino acid or stop code

<400> 1099

```

Phe Val Arg Glu Ile Arg Gly Pro Ala Val Pro Arg Leu Thr Ser Ala
 1           5           10           15
Glu Asp Arg His Arg His Gly Pro His Ala His Ser Pro Glu Leu Gln
           20           25           30
Arg Thr Gly Arg Asp Tyr Ser Leu Asp Tyr Leu Pro Phe Arg Leu Trp
           35           40           45
Val Gly Ile Trp Val Ala Thr Phe Cys Leu Val Leu Val Ala Thr Glu
           50           55           60
Ala Ser Val Leu Val Arg Tyr Phe Thr Arg Phe Thr Glu Glu Gly Phe
           65           70           75           80
Cys Ala Leu Ile Ser Leu Ile Phe Ile Tyr Asp Ala Val Gly Lys Met
           85           90           95
Leu Asn Leu Thr His Thr Tyr Pro Ile Gln Lys Pro Gly Ser Ser Ala
           100           105           110
Tyr Gly Cys Leu Cys Gln Tyr Pro Gly Pro Gly Gly Asn Glu Ser Gln
           115           120           125
Trp Ile Arg Thr Arg Pro Lys Asp Arg Asp Asp Ile Val Ser Met Asp
           130           135           140
Leu Gly Leu Ile Asn Ala Ser Leu Leu Pro Pro Pro Glu Cys Thr Arg
           145           150           155           160
Gln Gly Gly His Pro Arg Gly Pro Gly Cys His Thr Val Pro Asp Ile
           165           170           175
Ala Phe Phe Ser Leu Leu Leu Phe Leu Thr Ser Phe Phe Phe Ala Met
           180           185           190
Ala Leu Lys Cys Val Lys Thr Ser Arg Phe Phe Pro Ser Val Val Arg
           195           200           205
Lys Gly Leu Ser Asp Phe Ser Ser Val Leu Ala Ile Leu Leu Gly Cys
           210           215           220

```

Gly Leu Asp Ala Phe Leu Gly Leu Ala Thr Pro Lys Leu Met Val Pro
 225 230 235 240
 Arg Glu Phe Lys Pro Thr Leu Pro Gly Arg Gly Trp Leu Val Ser Pro
 245 250 255
 Phe Gly Ala Asn Pro Trp Trp Trp Ser Val Ala Ala Ala Leu Pro Ala
 260 265 270
 Leu Leu Leu Ser Ile Leu Ile Phe Met Asp Gln Gln Ile Thr Ala Val
 275 280 285
 Ile Leu Asn Arg Met Glu Tyr Arg Leu Gln Lys Gly Ala Gly Phe His
 290 295 300
 Leu Asp Leu Phe Trp Val Ala Val Leu Met Leu Leu Thr Ser Ala Leu
 305 310 315 320
 Gly Leu Pro Trp Tyr Val Ser Ala Thr Val Ile Ser Leu Ala His Met
 325 330 335
 Asp Ser Leu Arg Arg Glu Ser Arg Ala Cys Ala Pro Gly Glu Arg Pro
 340 345 350
 Asn Phe Leu Gly Ile Arg Glu Gln Arg Leu Thr Gly Leu Val Val Phe
 355 360 365
 Ile Leu Thr Gly Ala Ser Ile Phe Leu Ala Pro Val Leu Lys Phe Ile
 370 375 380
 Pro Met Pro Val Leu Tyr Gly Ile Phe Leu Tyr Met Gly Val Ala Ala
 385 390 395 400
 Leu Ser Ser Ile Gln Phe Thr Asn Arg Val Lys Leu Leu Leu Met Pro
 405 410 415
 Ala Lys His Gln Pro Asp Leu Leu Leu Arg His Val Pro Leu Thr
 420 425 430
 Arg Val His Leu Phe Thr Ala Ile Ser Phe Ala Cys Leu Gly Leu Leu
 435 440 445
 Trp Ile Ile Lys Ser Thr Pro Ala Ala Ile Ile Phe Pro Leu Met Leu
 450 455 460
 Leu Gly Leu Val Gly Val Arg Lys Ala Leu Glu Arg Val Phe Ser Pro
 465 470 475 480
 Gln Glu Leu Leu Trp Leu Asp Glu Leu Met Pro Glu Glu Glu Arg Ser
 485 490 495
 Ile Pro Glu Lys Gly Leu Glu Pro Glu His Ser Phe Ser Gly Ser Asp
 500 505 510
 Ser Glu Asp Ser Glu Leu Met Tyr Gln Pro Lys Ala Pro Glu Ile Asn
 515 520 525
 Ile Ser Val Asn Xaa Leu Glu Xaa Glu Phe Val Arg Glu Ile Arg Gly
 530 535 540
 Pro Ala Val Pro Arg Leu Thr Ser Ala Glu Asp Arg His Arg His Gly
 545 550 555 560
 Pro His Ala His Ser Pro Glu Leu Gln Arg Thr Gly Arg Asp Tyr Ser
 565 570 575
 Leu Asp Tyr Leu Pro Phe Arg Leu Trp Val Gly Ile Trp Val Ala Thr
 580 585 590
 Phe Cys Leu Val Leu Val Ala Thr Glu Ala Ser Val Leu Val Arg Tyr
 595 600 605
 Phe Thr Arg Phe Thr Glu Glu Gly Phe Cys Ala Leu Ile Ser Leu Ile
 610 615 620
 Phe Ile Tyr Asp Ala Val Gly Lys Met Leu Asn Leu Thr His Thr Tyr
 625 630 635 640
 Pro Ile Gln Lys Pro Gly Ser Ser Ala Tyr Gly Cys Leu Cys Gln Tyr
 645 650 655
 Pro Gly Pro Gly Gly Asn Glu Ser Gln Trp Ile Arg Thr Arg Pro Lys
 660 665 670
 Asp Arg Asp Asp Ile Val Ser Met Asp Leu Gly Leu Ile Asn Ala Ser
 675 680 685
 Leu Leu Pro Pro Pro Glu Cys Thr Arg Gln Gly Gly His Pro Arg Gly
 690 695 700
 Pro Gly Cys His Thr Val Pro Asp Ile Ala Phe Phe Ser Leu Leu Leu
 705 710 715 720
 Phe Leu Thr Ser Phe Phe Phe Ala Met Ala Leu Lys Cys Val Lys Thr
 725 730 735

Ser Arg Phe Phe Pro Ser Val Val Arg Lys Gly Leu Ser Asp Phe Ser
 740 745 750
 Ser Val Leu Ala Ile Leu Leu Gly Cys Gly Leu Asp Ala Phe Leu Gly
 755 760 765
 Leu Ala Thr Pro Lys Leu Met Val Pro Arg Glu Phe Lys Pro Thr Leu
 770 775 780
 Pro Gly Arg Gly Trp Leu Val Ser Pro Phe Gly Ala Asn Pro Trp Trp
 785 790 795 800
 Trp Ser Val Ala Ala Ala Leu Pro Ala Leu Leu Leu Ser Ile Leu Ile
 805 810 815
 Phe Met Asp Gln Gln Ile Thr Ala Val Ile Leu Asn Arg Met Glu Tyr
 820 825 830
 Arg Leu Gln Lys Gly Ala Gly Phe His Leu Asp Leu Phe Cys Val Ala
 835 840 845
 Val Leu Met Leu Leu Thr Ser Ala Leu Gly Leu Pro Trp Tyr Val Ser
 850 855 860
 Ala Thr Val Ile Ser Leu Ala His Met Asp Ser Leu Arg Arg Glu Ser
 865 870 875 880
 Arg Ala Cys Ala Pro Gly Glu Arg Pro Asn Phe Leu Gly Ile Arg Glu
 885 890 895
 Gln Arg Leu Thr Gly Leu Val Val Phe Ile Leu Thr Gly Ala Ser Ile
 900 905 910
 Phe Leu Ala Pro Val Leu Lys Phe Ile Pro Met Pro Val Leu Tyr Gly
 915 920 925
 Ile Phe Leu Tyr Met Gly Val Ala Ala Leu Ser Ser Ile Gln Phe Thr
 930 935 940
 Asn Arg Val Lys Leu Leu Asp Ala Ser Lys Thr Pro Ala Arg Pro
 945 950 955 960
 Ala Thr Leu Ala Ala Cys Ala Ser Asp Gln Gly Pro Pro Leu His Ser
 965 970 975
 His Gln Leu Cys Pro Val Trp Gly Cys Phe Gly Ile Ile Lys Ser Thr
 980 985 990
 Pro Ala Ala Ile Ile Phe Pro Leu Met Leu Leu Gly Leu Val Gly Val
 995 1000 1005
 Arg Lys Ala Leu Glu Arg Val Phe Ser Pro Gln Glu Leu Leu Trp Leu
 1010 1015 1020
 Asp Glu Leu Met Pro Glu Glu Glu Arg Ser Ile Pro Glu Lys Gly Leu
 1025 1030 1035 1040
 Glu Pro Glu His Ser Phe Ser Gly Ser Asp Ser Glu Asp Ser Glu Leu
 1045 1050 1055
 Met Tyr Gln Pro Lys Ala Pro Glu Ile Asn Ile Ser Val Asn
 1060 1065 1070

<210> 1100

<211> 875

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(875)

<223> X = any amino acid or stop code

<400> 1100

Met Gly Leu Lys Ala Arg Arg Ala Ala Gly Ala Ala Gly Gly Gly Gly
 1 5 10 15
 Asp Gly Gly Gly Gly Gly Gly Gly Ala Ala Asn Pro Ala Gly Gly Asp
 20 25 30
 Ala Ala Ala Ala Gly Asp Glu Glu Arg Lys Val Gly Leu Ala Pro Gly

620

```

545          550          555          560
Arg Ile Lys Tyr Leu Gln Thr Arg Ile Asp Met Ile Phe Thr Pro Gly
          565          570          575
Pro Pro Ser Thr Pro Lys His Lys Lys Ser Gln Lys Gly Ser Ala Phe
          580          585          590
Thr Phe Pro Ser Gln Gln Ser Pro Arg Asn Glu Pro Tyr Val Ala Arg
          595          600          605
Pro Ser Thr Ser Glu Ile Glu Asp Gln Arg His Xaa Trp Gly Lys Phe
          610          615          620
Val Lys Ser Leu Lys Gly Gln Val Gln Gly Leu Gly Arg Lys Leu Asp
625          630          635          640
Phe Leu Val Asp Met His Met Gln His Met Glu Arg Leu Gln Val Gln
          645          650          655
Val Thr Glu Tyr Tyr Pro Thr Lys Gly Thr Ser Ser Pro Ala Glu Ala
          660          665          670
Glu Lys Lys Glu Asp Asn Arg Tyr Ser Asp Leu Lys Thr Ile Ile Cys
          675          680          685
Asn Tyr Ser Glu Thr Gly Pro Pro Glu Pro Pro Tyr Ser Phe His Gln
          690          695          700
Val Thr Ile Asp Lys Val Ser Pro Tyr Gly Phe Phe Ala His Asp Pro
705          710          715          720
Val Asn Leu Pro Arg Gly Gly Pro Ser Ser Gly Lys Val Gln Ala Thr
          725          730          735
Pro Pro Ser Ser Ala Thr Thr Tyr Val Glu Arg Pro Thr Val Leu Pro
          740          745          750
Ile Leu Thr Leu Leu Asp Ser Arg Val Ser Cys His Ser Gln Ala Asp
          755          760          765
Leu Gln Gly Pro Tyr Ser Asp Arg Ile Ser Pro Arg Gln Arg Arg Ser
          770          775          780
Ile Thr Arg Asp Ser Asp Thr Pro Leu Ser Leu Met Ser Val Asn His
785          790          795          800
Glu Glu Leu Glu Arg Ser Pro Ser Gly Phe Ser Ile Ser Gln Asp Arg
          805          810          815
Asp Asp Tyr Val Phe Gly Pro Asn Gly Gly Ser Ser Trp Met Arg Glu
          820          825          830
Lys Arg Tyr Leu Ala Glu Gly Glu Thr Asp Thr Asp Thr Asp Pro Phe
          835          840          845
Thr Pro Ser Gly Ser Met Pro Leu Ser Ser Thr Gly Asp Gly Ile Ser
          850          855          860
Asp Ser Val Trp Thr Pro Ser Asn Lys Pro Ile
865          870          875

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<210> 1101

<211> 3530

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)... (3530)

<223> X = any amino acid or stop code

<400> 1101

```

Arg Thr Arg Gly Ile Ile Glu Phe Asp Pro Lys Tyr Thr Ala Phe Glu
1          5          10          15
Val Glu Glu Asp Val Gly Leu Ile Met Ile Pro Val Val Arg Leu His
          20          25          30
Gly Thr Tyr Gly Tyr Val Thr Ala Asp Phe Ile Ser Gln Ser Ser Ser
          35          40          45

```

Ala	Ser	Pro	Gly	Gly	Val	Asp	Tyr	Ile	Leu	His	Gly	Ser	Thr	Val	Thr
50						55					60				
Phe	Gln	His	Gly	Gln	Asn	Leu	Ser	Phe	Ile	Asn	Ile	Ser	Ile	Ile	Asp
65					70					75					80
Asp	Asn	Glu	Ser	Glu	Phe	Glu	Glu	Pro	Ile	Glu	Ile	Leu	Leu	Thr	Gly
				85					90					95	
Ala	Thr	Gly	Gly	Ala	Val	Leu	Gly	Arg	His	Leu	Val	Ser	Arg	Ile	Ile
			100					105						110	
Ile	Ala	Lys	Ser	Asp	Ser	Pro	Phe	Gly	Val	Ile	Arg	Phe	Leu	Asn	Gln
		115					120					125			
Ser	Lys	Ile	Ser	Ile	Ala	Asn	Pro	Asn	Ser	Thr	Met	Ile	Leu	Ser	Leu
		130				135					140				
Val	Leu	Glu	Arg	Thr	Gly	Gly	Leu	Leu	Gly	Glu	Ile	Gln	Val	Asn	Trp
145					150					155					160
Glu	Thr	Val	Gly	Pro	Asn	Ser	Gln	Glu	Ala	Leu	Leu	Pro	Gln	Asn	Arg
				165					170					175	
Asp	Ile	Ala	Asp	Pro	Val	Ser	Gly	Leu	Phe	Tyr	Phe	Gly	Glu	Gly	Glu
			180					185						190	
Gly	Gly	Val	Arg	Thr	Ile	Ile	Leu	Thr	Ile	Tyr	Pro	His	Glu	Glu	Ile
		195					200					205			
Glu	Val	Glu	Glu	Thr	Phe	Ile	Ile	Lys	Leu	His	Leu	Val	Lys	Gly	Glu
		210				215					220				
Ala	Lys	Leu	Asp	Ser	Arg	Ala	Lys	Asp	Val	Thr	Leu	Thr	Ile	Gln	Glu
225					230					235					240
Phe	Gly	Asp	Pro	Asn	Gly	Val	Val	Gln	Phe	Ala	Pro	Glu	Thr	Leu	Ser
				245					250					255	
Lys	Lys	Thr	Tyr	Ser	Glu	Pro	Leu	Ala	Leu	Glu	Gly	Pro	Leu	Leu	Ile
		260					265						270		
Thr	Phe	Phe	Val	Arg	Arg	Val	Lys	Gly	Thr	Phe	Gly	Glu	Ile	Met	Val
		275					280					285			
Tyr	Trp	Glu	Leu	Ser	Ser	Glu	Phe	Asp	Ile	Thr	Glu	Asp	Phe	Leu	Ser
		290				295					300				
Thr	Ser	Gly	Phe	Phe	Thr	Ile	Ala	Asp	Gly	Glu	Ser	Glu	Ala	Ser	Phe
305					310					315					320
Asp	Val	His	Leu	Leu	Pro	Asp	Glu	Val	Pro	Glu	Ile	Glu	Glu	Asp	Tyr
				325					330					335	
Val	Ile	Gln	Leu	Val	Ser	Val	Glu	Gly	Ala	Glu	Leu	Asp	Leu	Glu	
		340					345					350			
Lys	Ser	Ile	Thr	Trp	Phe	Ser	Val	Tyr	Ala	Asn	Asp	Asp	Pro	His	Gly
		355					360					365			
Val	Phe	Ala	Leu	Tyr	Ser	Asp	Arg	Gln	Ser	Ile	Leu	Ile	Gly	Gln	Asn
		370				375					380				
Leu	Ile	Arg	Ser	Ile	Gln	Ile	Asn	Ile	Thr	Arg	Leu	Ala	Gly	Thr	Phe
385					390					395					400
Gly	Asp	Val	Ala	Val	Gly	Leu	Arg	Ile	Ser	Ser	Asp	His	Lys	Glu	Gln
			405						410					415	
Pro	Ile	Val	Thr	Glu	Asn	Ala	Glu	Arg	Gln	Leu	Val	Val	Lys	Asp	Gly
			420					425					430		
Ala	Thr	Tyr	Lys	Val	Asp	Val	Val	Pro	Ile	Lys	Asn	Gln	Val	Phe	Leu
		435				440						445			
Ser	Leu	Gly	Ser	Asn	Phe	Thr	Leu	Gln	Leu	Val	Thr	Val	Met	Leu	Val
		450				455					460				
Gly	Gly	Arg	Phe	Tyr	Gly	Met	Pro	Thr	Ile	Leu	Gln	Glu	Ala	Lys	Ser
465					470					475					480
Ala	Val	Leu	Pro	Val	Ser	Glu	Lys	Ala	Ala	Asn	Ser	Gln	Val	Gly	Phe
			485					490						495	
Glu	Ser	Thr	Ala	Phe	Gln	Leu	Met	Asn	Ile	Thr	Ala	Gly	Thr	Ser	His
			500					505					510		
Val	Met	Ile	Ser	Arg	Arg	Gly	Thr	Tyr	Gly	Ala	Leu	Ser	Val	Ala	Trp
		515					520						525		
Thr	Thr	Gly	Tyr	Ala	Pro	Gly	Leu	Glu	Ile	Pro	Glu	Phe	Ile	Val	Val
		530				535					540				
Gly	Asn	Met	Thr	Pro	Thr	Leu	Gly	Ser	Leu	Ser	Phe	Ser	His	Gly	Glu
545					550					555					560

Gln Arg Lys Gly Val Phe Leu Trp Thr Phe Pro Ser Pro Gly Trp Pro
 565 570 575
 Glu Ala Phe Val Leu His Leu Ser Gly Val Gln Ser Ser Ala Pro Gly
 580 585 590
 Gly Ala Gln Leu Arg Ser Gly Phe Ile Val Ala Glu Ile Glu Pro Met
 595 600 605
 Gly Val Phe Gln Phe Ser Thr Ser Ser Arg Asn Ile Ile Val Ser Glu
 610 615 620
 Asp Thr Gln Met Ile Arg Leu His Val Gln Arg Leu Phe Gly Phe His
 625 630 635 640
 Ser Asp Leu Ile Lys Val Ser Tyr Gln Thr Thr Ala Gly Ser Ala Lys
 645 650 655
 Pro Leu Glu Asp Phe Glu Pro Val Gln Asn Gly Glu Leu Phe Phe Gln
 660 665 670
 Lys Phe Gln Thr Glu Val Asp Phe Glu Ile Thr Ile Ile Asn Asp Gln
 675 680 685
 Leu Ser Glu Ile Glu Glu Phe Phe Tyr Ile Asn Leu Thr Ser Val Glu
 690 695 700
 Ile Arg Gly Leu Gln Lys Phe Asp Val Asn Trp Ser Pro Arg Leu Asn
 705 710 715 720
 Leu Asp Phe Ser Val Ala Val Ile Thr Ile Leu Asp Asn Asp Asp Leu
 725 730 735
 Ala Gly Met Asp Ile Ser Phe Pro Glu Thr Thr Val Ala Val Ala Val
 740 745 750
 Asp Thr Thr Leu Ile Pro Val Glu Thr Glu Ser Thr Thr Tyr Leu Ser
 755 760 765
 Thr Ser Lys Thr Thr Thr Ile Leu Gln Pro Thr Asn Val Val Ala Ile
 770 775 780
 Val Thr Glu Ala Thr Gly Val Ser Ala Ile Pro Glu Lys Leu Val Thr
 785 790 795 800
 Leu His Gly Thr Pro Ala Val Ser Glu Lys Pro Asp Val Ala Thr Val
 805 810 815
 Thr Ala Asn Val Ser Ile His Gly Thr Phe Ser Leu Gly Pro Ser Ile
 820 825 830
 Val Tyr Ile Glu Glu Glu Met Lys Asn Gly Thr Phe Asn Thr Ala Glu
 835 840 845
 Val Leu Ile Arg Arg Thr Gly Gly Phe Thr Gly Asn Val Ser Ile Thr
 850 855 860
 Val Lys Thr Phe Gly Glu Arg Cys Ala Gln Met Glu Pro Asn Ala Leu
 865 870 875 880
 Pro Phe Arg Gly Ile Tyr Gly Ile Ser Asn Leu Thr Trp Ala Val Glu
 885 890 895
 Glu Glu Asp Phe Glu Glu Gln Thr Leu Thr Leu Ile Phe Leu Asp Gly
 900 905 910
 Glu Arg Glu Arg Lys Val Ser Val Gln Ile Leu Asp Asp Asp Glu Pro
 915 920 925
 Glu Gly Gln Glu Phe Phe Tyr Val Phe Leu Thr Asn Pro Gln Gly Gly
 930 935 940
 Ala Gln Ile Val Glu Gly Lys Asp Asp Thr Gly Phe Ala Ala Phe Ala
 945 950 955 960
 Met Val Ile Ile Thr Gly Ser Asp Leu His Asn Gly Ile Ile Gly Phe
 965 970 975
 Ser Glu Glu Ser Gln Ser Gly Leu Glu Leu Arg Glu Gly Ala Val Met
 980 985 990
 Arg Arg Leu His Leu Ile Val Thr Arg Gln Pro Asn Arg Ala Phe Glu
 995 1000 1005
 Asp Val Lys Val Phe Trp Arg Val Thr Leu Asn Lys Thr Val Val Val
 1010 1015 1020
 Leu Gln Lys Asp Gly Val Asn Leu Met Glu Glu Leu Gln Ser Val Ser
 1025 1030 1035 1040
 Gly Thr Thr Thr Cys Thr Met Gly Gln Thr Lys Cys Phe Ile Ser Ile
 1045 1050 1055
 Glu Leu Lys Pro Glu Lys Val Pro Gln Val Glu Val Tyr Phe Phe Val
 1060 1065 1070

Glu Leu Tyr Glu Ala Thr Ala Gly Ala Ala Ile Asn Asn Ser Ala Arg
 1075 1080 1085
 Phe Ala Gln Ile Lys Ile Leu Glu Ser Asp Glu Ser Gln Ser Leu Val
 1090 1095 1100
 Tyr Phe Ser Val Gly Ser Arg Leu Ala Val Ala His Lys Lys Ala Thr
 1105 1110 1115 1120
 Leu Ile Ser Leu Gln Val Ala Arg Asp Ser Gly Thr Gly Leu Met Met
 1125 1130 1135
 Ser Val Asn Phe Ser Thr Gln Glu Leu Arg Ser Ala Glu Thr Ile Gly
 1140 1145 1150
 Arg Thr Ile Ile Ser Pro Ala Ile Ser Gly Lys Asp Phe Val Ile Thr
 1155 1160 1165
 Glu Gly Thr Leu Val Phe Glu Pro Gly Gln Arg Ser Thr Val Leu Asp
 1170 1175 1180
 Val Ile Leu Thr Pro Glu Thr Gly Ser Leu Asn Ser Phe Pro Lys Arg
 1185 1190 1195 1200
 Phe Gln Ile Val Leu Phe Asp Pro Lys Gly Gly Ala Arg Ile Asp Lys
 1205 1210 1215
 Val Tyr Gly Thr Ala Asn Ile Thr Leu Val Ser Asp Ala Asp Ser Gln
 1220 1225 1230
 Ala Ile Trp Gly Leu Ala Asp Gln Leu His Gln Pro Val Asn Asp Asp
 1235 1240 1245
 Ile Leu Asn Arg Val Leu His Thr Ile Ser Met Lys Val Ala Thr Glu
 1250 1255 1260
 Asn Thr Asp Glu Gln Leu Ser Ala Met Met His Leu Ile Glu Lys Ile
 1265 1270 1275 1280
 Thr Thr Glu Gly Lys Ile Gln Ala Phe Ser Val Ala Ser Arg Thr Leu
 1285 1290 1295
 Phe Tyr Glu Ile Leu Cys Ser Leu Ile Asn Pro Lys Arg Lys Asp Thr
 1300 1305 1310
 Arg Gly Phe Ser His Phe Ala Glu Leu Thr Glu Asn Phe Ala Phe Ser
 1315 1320 1325
 Leu Leu Thr Asn Val Thr Cys Gly Ser Pro Gly Glu Lys Ser Lys Thr
 1330 1335 1340
 Ile Leu Asp Ser Cys Pro Tyr Leu Ser Ile Leu Ala Leu His Trp Tyr
 1345 1350 1355 1360
 Pro Gln Gln Ile Asn Gly His Lys Phe Glu Gly Lys Glu Gly Asp Tyr
 1365 1370 1375
 Ile Arg Ile Pro Glu Arg Leu Leu Asp Val Gln Asp Ala Glu Ile Met
 1380 1385 1390
 Ala Gly Lys Ser Thr Cys Lys Leu Val Gln Phe Thr Glu Tyr Ser Ser
 1395 1400 1405
 Gln Gln Trp Phe Ile Ser Gly Asn Asn Leu Pro Thr Leu Lys Asn Lys
 1410 1415 1420
 Val Leu Ser Leu Ser Val Lys Gly Gln Ser Ser Gln Leu Leu Thr Asn
 1425 1430 1435 1440
 Asp Asn Glu Val Leu Tyr Arg Ile Tyr Ala Ala Glu Pro Arg Ile Ile
 1445 1450 1455
 Pro Gln Thr Ser Leu Cys Leu Leu Trp Asn Gln Ala Ala Ala Ser Trp
 1460 1465 1470
 Leu Ser Asp Ser Gln Phe Cys Lys Val Ile Glu Glu Thr Ala Asp Tyr
 1475 1480 1485
 Val Glu Cys Ala Cys Leu His Met Ser Val Tyr Ala Val Tyr Ala Arg
 1490 1495 1500
 Thr Asp Asn Leu Ser Ser Tyr Asn Glu Ala Phe Phe Thr Ser Gly Phe
 1505 1510 1515 1520
 Ile Cys Ile Ser Gly Leu Cys Leu Ala Val Leu Ser His Ile Phe Cys
 1525 1530 1535
 Ala Arg Tyr Ser Met Phe Ala Ala Lys Leu Leu Thr His Met Met Ala
 1540 1545 1550
 Ala Ser Leu Gly Thr Gln Ile Leu Phe Leu Ala Ser Ala Tyr Ala Ser
 1555 1560 1565
 Pro Gln Leu Ala Glu Glu Ser Cys Ser Ala Met Ala Ala Val Thr His
 1570 1575 1580

Tyr Leu Tyr Leu Cys Gln Phe Ser Trp Met Leu Ile Gln Ser Val Asn
 1585 1590 1595 1600
 Phe Trp Tyr Val Leu Val Met Asn Asp Glu His Thr Glu Arg Arg Tyr
 1605 1610 1615
 Leu Leu Phe Phe Leu Leu Ser Trp Gly Leu Pro Ala Phe Val Val Ile
 1620 1625 1630
 Leu Leu Ile Val Ile Leu Lys Gly Ile Tyr His Gln Ser Met Ser Gln
 1635 1640 1645
 Ile Tyr Gly Leu Ile His Gly Asp Leu Cys Phe Ile Pro Asn Val Tyr
 1650 1655 1660
 Ala Ala Leu Phe Thr Ala Ala Leu Val Pro Leu Thr Cys Leu Val Val
 1665 1670 1675 1680
 Val Phe Val Val Phe Ile His Ala Tyr Gln Val Lys Pro Gln Trp Lys
 1685 1690 1695
 Ala Tyr Asp Asp Val Phe Arg Gly Arg Thr Asn Ala Ala Glu Ile Pro
 1700 1705 1710
 Leu Ile Leu Tyr Leu Phe Ala Leu Ile Ser Val Thr Trp Leu Trp Gly
 1715 1720 1725
 Gly Leu His Met Ala Tyr Arg His Phe Trp Met Leu Val Leu Phe Val
 1730 1735 1740
 Ile Phe Asn Ser Leu Gln Leu Leu Tyr Pro Leu Phe Tyr Phe Leu Leu
 1745 1750 1755 1760
 Leu Xaa Asp Gln Ser Ser Ser Ala Ser Pro Gly Gly Val Asp Tyr Ile
 1765 1770 1775
 Leu His Gly Ser Thr Val Thr Phe Gln His Gly Gln Asn Leu Ser Phe
 1780 1785 1790
 Ile Asn Ile Ser Ile Ile Asp Asp Asn Glu Ser Glu Phe Glu Glu Pro
 1795 1800 1805
 Ile Glu Ile Leu Leu Thr Gly Ala Thr Gly Gly Ala Val Leu Gly Arg
 1810 1815 1820
 His Leu Val Ser Arg Ile Ile Ile Ala Lys Ser Asp Ser Pro Phe Gly
 1825 1830 1835 1840
 Val Ile Arg Phe Leu Asn Gln Ser Lys Ile Ser Ile Ala Asn Pro Asn
 1845 1850 1855
 Ser Thr Met Ile Leu Ser Leu Val Leu Glu Arg Thr Gly Gly Leu Leu
 1860 1865 1870
 Gly Glu Ile Gln Val Asn Trp Glu Thr Val Gly Pro Asn Ser Gln Glu
 1875 1880 1885
 Ala Leu Leu Pro Gln Asn Arg Asp Ile Ala Asp Pro Val Ser Gly Leu
 1890 1895 1900
 Phe Tyr Phe Gly Glu Gly Glu Gly Gly Val Arg Thr Ile Ile Leu Thr
 1905 1910 1915 1920
 Ile Tyr Pro His Glu Glu Ile Glu Val Glu Glu Thr Phe Ile Ile Lys
 1925 1930 1935
 Leu His Leu Val Lys Gly Glu Ala Lys Leu Asp Ser Arg Ala Lys Asp
 1940 1945 1950
 Val Thr Leu Thr Ile Gln Glu Phe Gly Asp Pro Asn Gly Val Val Gln
 1955 1960 1965
 Phe Ala Pro Glu Thr Leu Ser Lys Lys Thr Tyr Ser Glu Pro Leu Ala
 1970 1975 1980
 Leu Glu Gly Pro Leu Leu Ile Thr Phe Phe Val Arg Arg Val Lys Gly
 1985 1990 1995 2000
 Thr Phe Gly Glu Ile Met Val Tyr Trp Glu Leu Ser Ser Glu Phe Asp
 2005 2010 2015
 Ile Thr Glu Asp Phe Leu Ser Thr Ser Gly Phe Phe Thr Ile Ala Asp
 2020 2025 2030
 Gly Glu Ser Glu Ala Ser Phe Asp Val His Leu Leu Pro Asp Glu Val
 2035 2040 2045
 Pro Glu Ile Glu Glu Asp Tyr Val Ile Gln Leu Val Ser Val Glu Gly
 2050 2055 2060
 Gly Ala Glu Leu Asp Leu Glu Lys Ser Ile Thr Trp Phe Ser Val Tyr
 2065 2070 2075 2080
 Ala Asn Asp Asp Pro His Gly Val Phe Ala Leu Tyr Ser Asp Arg Gln
 2085 2090 2095

Ser Ile Leu Ile Gly Gln Asn Leu Ile Arg Ser Ile Gln Ile Asn Ile
 2100 2105 2110
 Thr Arg Leu Ala Gly Thr Phe Gly Asp Val Ala Val Gly Leu Arg Ile
 2115 2120 2125
 Ser Ser Asp His Lys Glu Gln Pro Ile Val Thr Glu Asn Ala Glu Arg
 2130 2135 2140
 Gln Leu Val Val Lys Asp Gly Ala Thr Tyr Lys Val Asp Val Val Pro
 2145 2150 2155 2160
 Ile Lys Asn Gln Val Phe Leu Ser Leu Gly Ser Asn Phe Thr Leu Gln
 2165 2170 2175
 Leu Val Thr Val Met Leu Val Gly Gly Arg Phe Tyr Gly Met Pro Thr
 2180 2185 2190
 Ile Leu Gln Glu Ala Lys Ser Ala Val Leu Pro Val Ser Glu Lys Ala
 2195 2200 2205
 Ala Asn Ser Gln Val Gly Phe Glu Ser Thr Ala Phe Gln Leu Met Asn
 2210 2215 2220
 Ile Thr Ala Gly Thr Ser His Val Met Ile Ser Arg Arg Gly Thr Tyr
 2225 2230 2235 2240
 Gly Ala Leu Ser Val Ala Trp Thr Thr Gly Tyr Ala Pro Gly Leu Glu
 2245 2250 2255
 Ile Pro Glu Phe Ile Val Val Gly Asn Met Thr Pro Thr Leu Gly Ser
 2260 2265 2270
 Leu Ser Phe Ser His Gly Glu Gln Arg Lys Gly Val Phe Leu Trp Thr
 2275 2280 2285
 Phe Pro Ser Pro Gly Trp Pro Glu Ala Phe Val Leu His Leu Ser Gly
 2290 2295 2300
 Val Gln Ser Ser Ala Pro Gly Gly Ala Gln Leu Arg Ser Gly Phe Ile
 2305 2310 2315 2320
 Val Ala Glu Ile Glu Pro Met Gly Val Phe Gln Phe Ser Thr Ser Ser
 2325 2330 2335
 Arg Asn Ile Ile Val Ser Glu Asp Thr Gln Met Ile Arg Leu His Val
 2340 2345 2350
 Gln Arg Leu Phe Gly Phe His Ser Asp Leu Ile Lys Val Ser Tyr Gln
 2355 2360 2365
 Thr Thr Ala Gly Ser Ala Lys Pro Leu Glu Asp Phe Glu Pro Val Gln
 2370 2375 2380
 Asn Gly Glu Leu Phe Phe Gln Lys Phe Gln Thr Glu Val Asp Phe Glu
 2385 2390 2395 2400
 Ile Thr Ile Ile Asn Asp Gln Leu Ser Glu Ile Glu Glu Phe Phe Tyr
 2405 2410 2415
 Ile Asn Leu Thr Ser Val Glu Ile Arg Gly Leu Gln Lys Phe Asp Val
 2420 2425 2430
 Asn Trp Ser Pro Arg Leu Asn Leu Asp Phe Ser Val Ala Val Ile Thr
 2435 2440 2445
 Ile Leu Asp Asn Asp Asp Leu Ala Gly Met Asp Ile Ser Phe Pro Glu
 2450 2455 2460
 Thr Thr Val Ala Val Ala Val Asp Thr Thr Leu Ile Pro Val Glu Thr
 2465 2470 2475 2480
 Glu Ser Thr Thr Tyr Leu Ser Thr Ser Lys Thr Thr Thr Ile Leu Gln
 2485 2490 2495
 Pro Thr Asn Val Val Ala Ile Val Thr Glu Ala Thr Gly Val Ser Ala
 2500 2505 2510
 Ile Pro Glu Lys Leu Val Thr Leu His Gly Thr Pro Ala Val Ser Glu
 2515 2520 2525
 Lys Pro Asp Val Ala Thr Val Thr Ala Asn Val Ser Ile His Gly Thr
 2530 2535 2540
 Phe Ser Leu Gly Pro Ser Ile Val Tyr Ile Glu Glu Glu Met Lys Asn
 2545 2550 2555 2560
 Gly Thr Phe Asn Thr Ala Glu Val Leu Ile Arg Arg Thr Gly Gly Phe
 2565 2570 2575
 Thr Gly Asn Val Ser Ile Thr Val Lys Thr Phe Gly Glu Arg Cys Ala
 2580 2585 2590
 Gln Met Glu Pro Asn Ala Leu Pro Phe Arg Gly Ile Tyr Gly Ile Ser
 2595 2600 2605

Asn Leu Thr Trp Ala Val Glu Glu Glu Asp Phe Glu Glu Gln Thr Leu
 2610 2615 2620
 Thr Leu Ile Phe Leu Asp Gly Glu Arg Glu Arg Lys Val Ser Val Gln
 2625 2630 2635 2640
 Ile Leu Asp Asp Asp Glu Pro Glu Gly Gln Glu Phe Phe Tyr Val Phe
 2645 2650 2655
 Leu Thr Asn Pro Gln Gly Gly Ala Gln Ile Val Glu Gly Lys Asp Asp
 2660 2665 2670
 Thr Gly Phe Ala Ala Phe Ala Met Val Ile Ile Thr Gly Ser Asp Leu
 2675 2680 2685
 His Asn Gly Ile Ile Gly Phe Ser Glu Glu Ser Gln Ser Gly Leu Glu
 2690 2695 2700
 Leu Arg Glu Gly Ala Val Met Arg Arg Leu His Leu Ile Val Thr Arg
 2705 2710 2715 2720
 Gln Pro Asn Arg Ala Phe Glu Asp Val Lys Val Phe Trp Arg Val Thr
 2725 2730 2735
 Leu Asn Lys Thr Val Val Val Leu Gln Lys Asp Gly Val Asn Leu Met
 2740 2745 2750
 Glu Glu Leu Gln Ser Val Ser Gly Thr Thr Thr Cys Thr Met Gly Gln
 2755 2760 2765
 Thr Lys Cys Phe Ile Ser Ile Glu Leu Lys Pro Glu Lys Val Pro Gln
 2770 2775 2780
 Val Glu Val Tyr Phe Phe Val Glu Leu Tyr Glu Ala Thr Ala Gly Ala
 2785 2790 2795 2800
 Ala Ile Asn Asn Ser Ala Arg Phe Ala Gln Ile Lys Ile Leu Glu Ser
 2805 2810 2815
 Asp Glu Ser Gln Ser Leu Val Tyr Phe Ser Val Gly Ser Arg Leu Ala
 2820 2825 2830
 Val Ala His Lys Lys Ala Thr Leu Ile Ser Leu Gln Val Ala Arg Asp
 2835 2840 2845
 Ser Gly Thr Gly Leu Met Met Ser Val Asn Phe Ser Thr Gln Glu Leu
 2850 2855 2860
 Arg Ser Ala Glu Thr Ile Gly Arg Thr Ile Ile Ser Pro Ala Ile Ser
 2865 2870 2875 2880
 Gly Lys Asp Phe Val Ile Thr Glu Gly Thr Leu Val Phe Glu Pro Gly
 2885 2890 2895
 Gln Arg Ser Thr Val Leu Asp Val Ile Leu Thr Pro Glu Thr Gly Ser
 2900 2905 2910
 Leu Asn Ser Phe Pro Lys Arg Phe Gln Ile Val Leu Phe Asp Pro Lys
 2915 2920 2925
 Gly Gly Ala Arg Ile Asp Lys Val Tyr Gly Thr Ala Asn Ile Thr Leu
 2930 2935 2940
 Val Ser Asp Ala Asp Ser Gln Ala Ile Trp Gly Leu Ala Asp Gln Leu
 2945 2950 2955 2960
 His Gln Pro Val Asn Asp Asp Ile Leu Asn Arg Val Leu His Thr Ile
 2965 2970 2975
 Ser Met Lys Val Ala Thr Glu Asn Thr Asp Glu Gln Leu Ser Ala Met
 2980 2985 2990
 Met His Leu Ile Glu Lys Ile Thr Thr Glu Gly Lys Ile Gln Ala Phe
 2995 3000 3005
 Ser Val Ala Ser Arg Thr Leu Phe Tyr Glu Ile Leu Cys Ser Leu Ile
 3010 3015 3020
 Asn Pro Lys Arg Lys Asp Thr Arg Gly Phe Ser His Phe Ala Glu Leu
 3025 3030 3035 3040
 Thr Glu Asn Phe Ala Phe Ser Leu Leu Thr Asn Val Thr Cys Gly Ser
 3045 3050 3055
 Pro Gly Glu Lys Ser Lys Thr Ile Leu Asp Ser Cys Pro Tyr Leu Ser
 3060 3065 3070
 Ile Leu Ala Leu His Trp Tyr Pro Gln Gln Ile Asn Gly His Lys Phe
 3075 3080 3085
 Glu Gly Lys Glu Gly Asp Tyr Ile Arg Ile Pro Glu Arg Leu Leu Asp
 3090 3095 3100
 Val Gln Asp Ala Glu Ile Met Ala Gly Lys Ser Thr Cys Lys Leu Val
 3105 3110 3115 3120

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<210> 1102
<211> 945
<212> Amino acid
<213> Homo sapiens
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<220>
<221> misc_feature
<222> (1)...(945)
<223> X = any amino acid or stop code
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<400> 1102

Ala	Ala	Gly	Ala	Thr	Met	Glu	Arg	Asp	Gly	Cys	Ala	Gly	Gly	Gly	Ser
1				5					10					15	
Arg	Gly	Gly	Glu	Gly	Gly	Arg	Ala	Pro	Arg	Glu	Gly	Pro	Ala	Gly	Asn
			20					25					30		
Gly	Arg	Asp	Arg	Gly	Arg	Ser	His	Ala	Ala	Glu	Ala	Pro	Gly	Asp	Pro
		35					40					45			
Gln	Ala	Ala	Ala	Ser	Leu	Leu	Ala	Pro	Met	Asp	Val	Gly	Glu	Glu	Pro
	50					55				60					
Leu	Glu	Lys	Ala	Ala	Arg	Ala	Arg	Thr	Ala	Lys	Asp	Pro	Asn	Thr	Tyr
65					70					75				80	
Lys	Val	Leu	Ser	Leu	Val	Leu	Ser	Val	Cys	Val	Leu	Thr	Thr	Ile	Leu
				85					90					95	
Gly	Cys	Ile	Phe	Gly	Leu	Lys	Pro	Ser	Cys	Ala	Lys	Glu	Val	Lys	Ser
			100					105					110		
Cys	Lys	Gly	Arg	Cys	Phe	Glu	Arg	Thr	Phe	Gly	Asn	Cys	Arg	Cys	Asp
		115					120				125				
Ala	Ala	Cys	Val	Glu	Leu	Gly	Asn	Cys	Cys	Leu	Gly	Leu	Pro	Gly	Gly
	130					135					140				
Thr	Cys	Ile	Glu	Pro	Glu	His	Ile	Trp	Thr	Cys	Asn	Lys	Phe	Arg	Cys
145					150					155				160	
Gly	Glu	Lys	Arg	Leu	Thr	Arg	Ser	Leu	Cys	Ala	Cys	Ser	Asp	Asp	Cys
				165					170					175	
Lys	Asp	Arg	Gly	Asp	Cys	Leu	Pro	Ser	Asn	Leu	Gln	Phe	Leu	Cys	Val
		180						185					190		
Gln	Gly	Glu	Lys	Ser	Trp	Gly	Arg	Lys	Asn	Pro	Cys	Glu	Ser	His	Leu
	195					200						205			
Met	Glu	Pro	Gln	Cys	Pro	Ala	Gly	Phe	Glu	Thr	Pro	Ser	Leu	Pro	Leu
	210					215					220				
Leu	Ile	Phe	Ser	Leu	Asp	Gly	Phe	Arg	Ala	Glu	Tyr	Leu	His	Thr	Trp
225					230					235				240	
Gly	Gly	Leu	Leu	Pro	Val	Ile	Ser	Lys	Leu	Lys	Lys	Cys	Gly	Thr	Tyr
				245					250					255	
Thr	Lys	Asn	Met	Arg	Pro	Val	Tyr	Pro	Thr	Lys	Thr	Phe	Pro	Asn	His
		260						265					270		
Tyr	Ser	Ile	Val	Thr	Gly	Leu	Tyr	Pro	Glu	Ser	His	Gly	Ile	Ile	Asn
		275					280					285			
Asn	Lys	Met	Tyr	Asp	Pro	Lys	Met	Asn	Ala	Ser	Phe	Ser	Leu	Lys	Ser
	290					295				300					
Lys	Glu	Lys	Phe	Asn	Pro	Glu	Trp	Tyr	Lys	Gly	Glu	Pro	Ile	Trp	Val
305					310					315				320	
Thr	Ala	Lys	Tyr	Gln	Gly	Leu	Lys	Ser	Gly	Thr	Phe	Phe	Trp	Pro	Gly
				325					330					335	
Ser	Asp	Val	Glu	Ile	Asn	Gly	Ile	Phe	Pro	Asp	Ile	Tyr	Lys	Met	Tyr
		340						345					350		
Asn	Gly	Ser	Val	Pro	Phe	Glu	Glu	Arg	Ile	Leu	Ala	Val	Leu	Gln	Trp
	355					360						365			
Leu	Gln	Leu	Pro	Lys	Asp	Glu	Arg	Pro	His	Phe	Tyr	Thr	Leu	Tyr	Leu
	370					375					380				
Glu	Glu	Pro	Asp	Ser	Ser	Gly	His	Ser	Tyr	Gly	Pro	Val	Ser	Ser	Glu
385					390					395				400	
Val	Ile	Lys	Ala	Leu	Gln	Arg	Val	Asp	Gly	Met	Val	Gly	Met	Leu	Met
				405					410					415	
Asp	Gly	Leu	Lys	Glu	Leu	Asn	Leu	His	Arg	Cys	Leu	Asn	Leu	Ile	Leu
		420						425					430		
Ile	Ser	Asp	His	Gly	Met	Glu	Gln	Gly	Ser	Cys	Lys	Lys	Tyr	Ile	Tyr
		435					440					445			
Leu	Asn	Lys	Tyr	Leu	Gly	Asp	Val	Lys	Asn	Ile	Lys	Val	Ile	Tyr	Gly
	450					455					460				
Pro	Ala	Ala	Arg	Leu	Arg	Pro	Ser	Asp	Val	Pro	Asp	Lys	Tyr	Tyr	Ser

465 470 475 480
 Phe Asn Tyr Glu Gly Ile Ala Arg Asn Leu Ser Cys Arg Glu Pro Asn
 485 490 495
 Gln His Phe Lys Pro Tyr Leu Lys His Phe Leu Pro Lys Arg Leu His
 500 505 510
 Phe Ala Lys Ser Asp Arg Ile Glu Pro Leu Thr Phe Tyr Leu Asp Pro
 515 520 525
 Gln Trp Gln Leu Ala Leu Asn Pro Ser Glu Arg Lys Tyr Cys Gly Ser
 530 535 540
 Gly Phe His Gly Ser Asp Asn Val Phe Ser Asn Met Gln Ala Leu Phe
 545 550 555 560
 Val Gly Tyr Gly Pro Gly Phe Lys His Gly Ile Glu Ala Asp Thr Phe
 565 570 575
 Glu Asn Ile Glu Val Tyr Asn Leu Met Cys Asp Leu Leu Asn Leu Thr
 580 585 590
 Pro Ala Pro Asn Asn Gly Thr His Gly Ser Leu Asn His Leu Leu Lys
 595 600 605
 Asn Pro Val Tyr Thr Pro Lys His Pro Lys Glu Val His Pro Leu Val
 610 615 620
 Gln Cys Pro Phe Thr Arg Asn Pro Arg Asp Asn Leu Gly Cys Ser Cys
 625 630 635 640
 Asn Pro Ser Ile Leu Pro Ile Glu Asp Phe Gln Thr Gln Phe Asn Leu
 645 650 655
 Thr Val Ala Glu Glu Lys Ile Ile Lys His Glu Thr Leu Pro Tyr Gly
 660 665 670
 Arg Pro Arg Val Leu Gln Lys Glu Asn Thr Ile Cys Leu Leu Ser Gln
 675 680 685
 His Gln Phe Met Ser Gly Tyr Ser Gln Asp Ile Leu Met Pro Leu Trp
 690 695 700
 Thr Ser Tyr Thr Val Asp Arg Asn Asp Ser Phe Ser Thr Glu Asp Phe
 705 710 715 720
 Ser Asn Cys Leu Tyr Gln Asp Phe Arg Ile Pro Leu Ser Pro Val His
 725 730 735
 Lys Cys Ser Phe Tyr Lys Asn Asn Thr Lys Val Ser Tyr Gly Phe Leu
 740 745 750
 Ser Pro Pro Gln Leu Asn Lys Asn Ser Ser Gly Ile Tyr Ser Glu Ala
 755 760 765
 Leu Leu Thr Thr Asn Ile Val Pro Met Tyr Gln Ser Phe Gln Val Ile
 770 775 780
 Trp Arg Tyr Phe His Asp Thr Leu Leu Arg Lys Tyr Ala Glu Glu Arg
 785 790 795 800
 Asn Gly Val Asn Val Val Ser Gly Pro Val Phe Asp Phe Asp Tyr Asp
 805 810 815
 Gly Arg Cys Asp Ser Leu Glu Asn Leu Arg Gln Lys Arg Arg Val His
 820 825 830
 Pro Val Thr Gln Glu Asn Phe Trp Ile Pro Asn Ser Thr Ser Phe Tyr
 835 840 845
 Val Val Leu Thr Ser Cys Lys Asp Thr Ser Gln Thr Pro Leu His Cys
 850 855 860
 Glu Asn Leu Asp Thr Leu Gly Phe Pro Phe Cys Leu His Arg Asp Trp
 865 870 875 880
 Ile Asn Ser Glu Thr Cys Val His Gly Lys His Asp Ser Ser Trp Val
 885 890 895
 Glu Glu Phe Val Lys Cys Leu His Arg Ala Arg Ile Thr Gly Cys Xaa
 900 905 910
 Gly Thr Ser Leu Gly Leu Ser Phe Tyr Gln Gln Arg Lys Glu Pro Val
 915 920 925
 Ser Asp Ile Leu Lys Leu Lys Thr His Leu Pro Thr Phe Ser Gln Glu
 930 935 940
 Asp
 945

<211> 217
 <212>Amino acid
 <213> Homo sapiens

<400> 1103
 Thr Val Pro Pro Pro Pro Gly Gly Pro Ser Pro Ala Pro Leu His Pro
 1 5 10 15
 Lys Arg Ser Pro Thr Ser Thr Gly Glu Ala Glu Leu Lys Glu Glu Arg
 20 25 30
 Leu Pro Gly Arg Lys Ala Ser Cys Ser Thr Ala Gly Ser Gly Ser Arg
 35 40 45
 Gly Leu Pro Pro Leu Ser Pro Met Val Ser Ser Ala His Asn Pro Asn
 50 55 60
 Lys Ala Glu Ile Pro Glu Arg Arg Lys Asp Ser Thr Ser Thr Pro Asn
 65 70 75 80
 Asn Leu Pro Pro Ser Met Met Thr Arg Arg Asn Thr Tyr Val Cys Thr
 85 90 95
 Glu Arg Pro Gly Ala Glu Arg Pro Ser Leu Leu Pro Asn Gly Lys Glu
 100 105 110
 Asn Ser Ser Gly Thr Pro Arg Val Pro Pro Ala Ser Pro Ser Ser His
 115 120 125
 Ser Leu Ala Pro Pro Ser Gly Glu Arg Ser Arg Leu Ala Arg Gly Ser
 130 135 140
 Thr Ile Arg Ser Thr Phe His Gly Gly Gln Val Arg Asp Arg Arg Ala
 145 150 155 160
 Gly Gly Trp Gly Trp Phe Phe Asn Lys His Ala Leu Gln Arg Ala Pro
 165 170 175
 Arg Asn Ala Gly Ala Pro Ser Leu Met Pro Gly His Arg Thr Val Leu
 180 185 190
 Ile Asn Tyr Gly Gly Gly Gln Asp Leu Lys Asn Trp Glu Thr Cys Leu
 195 200 205
 Ala Ala Pro Pro Asn Lys His Arg Arg
 210 215 217

<210> 1104
 <211> 436
 <212>Amino acid
 <213> Homo sapiens

<400> 1104
 His Thr Leu His His Ser Ser Pro Thr Ser Glu Ala Glu Glu Phe Val
 1 5 10 15
 Ser Arg Leu Ser Thr Gln Asn Tyr Phe Arg Ser Leu Pro Arg Gly Thr
 20 25 30
 Ser Asn Met Thr Tyr Gly Thr Phe Asn Phe Leu Gly Gly Arg Leu Met
 35 40 45
 Ile Pro Asn Thr Gly Ile Ser Leu Leu Ile Pro Pro Asp Ala Ile Pro
 50 55 60
 Arg Gly Lys Ile Tyr Glu Ile Tyr Leu Thr Leu His Lys Pro Glu Asp
 65 70 75 80
 Val Arg Leu Pro Leu Ala Gly Cys Gln Thr Leu Leu Ser Pro Ile Val
 85 90 95
 Ser Cys Gly Pro Pro Gly Val Leu Leu Thr Arg Pro Val Ile Leu Gly
 100 105 110
 Met Asp His Cys Gly Glu Pro Ser Pro Asp Ser Trp Ser Leu Arg Leu

```

      115      120      125
Lys Lys Gln Ser Cys Glu Gly Ser Trp Glu Asp Val Leu His Leu Gly
  130      135      140
Glu Glu Ala Pro Ser His Leu Tyr Tyr Cys Gln Leu Glu Ala Ser Ala
  145      150      155      160
Cys Tyr Val Phe Thr Glu Gln Leu Ser Arg Tyr Ala Leu Val Gly Glu
      165      170      175
Ala Leu Ser Val Ala Ala Ala Lys Arg Leu Lys Leu Leu Leu Phe Ala
      180      185      190
Pro Val Ala Cys Thr Ser Leu Glu Tyr Asn Ile Leu Val Tyr Cys Leu
      195      200      205
His Asp Thr His Asp Ala Leu Asn Val Val Val Gln Leu Glu Lys Gln
      210      215      220
Leu Gln Gly Gln Leu Ile Gln Glu Pro Leu Val Leu His Phe Lys Asp
  225      230      235      240
Ser Tyr His Asn Leu Arg Leu Ser Ile His Asp Val Pro Ser Ser Leu
      245      250      255
Trp Lys Ser Lys Leu Leu Val Ser Tyr Gln Glu Ile Pro Phe Tyr His
      260      265      270
Ile Trp Asn Gly Thr Gln Arg Tyr Leu His Cys Thr Phe Thr Leu Glu
      275      280      285
Arg Val Ser Pro Ser Thr Ser Asp Leu Ala Cys Lys Leu Trp Val Trp
  290      295      300
Gln Val Glu Gly Asp Gly Gln Ser Phe Ser Ile Asn Phe Asn Ile Thr
  305      310      315      320
Lys Asp Thr Arg Phe Ala Glu Leu Leu Ala Leu Glu Ser Glu Ala Gly
      325      330      335
Val Pro Ala Leu Val Gly Pro Ser Ala Phe Lys Ile Pro Phe Leu Ile
      340      345      350
Arg Gln Lys Ile Ile Ser Ser Leu Asp Pro Pro Cys Arg Arg Gly Ala
      355      360      365
Asp Trp Arg Thr Leu Ala Gln Lys Leu His Leu Asp Ser His Leu Ser
  370      375      380
Phe Phe Ala Ser Lys Pro Ser Pro Thr Ala Met Ile Leu Asn Leu Trp
  385      390      395      400
Glu Ala Arg His Phe Pro Asn Gly Asn Leu Ser Gln Leu Ala Ala Ala
      405      410      415
Val Ala Gly Thr Gly Pro Ala Gly Arg Trp Leu Leu Ser Gln Cys Ser
      420      425      430
Glu Ala Glu Cys
      435 436

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<210> 1105
 <211> 113
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 1105
Gly Ser Ala Ala Gly Gln Val Gln Gln Gln Gln Arg Arg His Gln
  1      5      10      15
Gln Gly Lys Val Thr Val Lys Tyr Asp Arg Lys Glu Leu Arg Lys Arg
      20      25      30
Leu Val Leu Glu Glu Trp Ile Val Glu Gln Leu Gly Gln Leu Tyr Gly
      35      40      45
Cys Glu Glu Glu Glu Met Pro Glu Val Glu Ile Asp Ile Asp Asp Leu
      50      55      60
Phe Asp Ala Tyr Ser Asp Glu Gln Arg Ala Ser Lys Leu Gln Glu Ala
      65      70      75      80
Leu Val Asp Cys Tyr Lys Pro Thr Glu Glu Phe Ile Lys Glu Leu Leu

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85 90 95
 Ser Arg Ile Arg Gly Met Arg Lys Leu Ser Pro Pro Gln Lys Lys Ser
 100 105 110
 Val
 113

<210> 1106
 <211> 464
 <212> Amino acid
 <213> Homo sapiens

<400> 1106
 Ile Met Leu Asp Gly Arg Val Arg Trp Leu Thr Pro Val Ile Ser Ala
 1 5 10 15
 Leu Trp Glu Ala Glu Met Glu Asp Val Ile Ala Arg Met Gln Asp Glu
 20 25 30
 Lys Asn Gly Ile Pro Ile Arg Thr Val Lys Ser Phe Leu Ser Lys Ile
 35 40 45
 Pro Ser Val Phe Ser Gly Ser Asp Ile Val Gln Trp Leu Ile Lys Asn
 50 55 60
 Leu Thr Ile Glu Asp Pro Val Glu Ala Leu His Leu Gly Thr Leu Met
 65 70 75 80
 Ala Ala His Gly Tyr Phe Phe Pro Ile Ser Asp His Val Leu Thr Leu
 85 90 95
 Lys Asp Asp Gly Thr Phe Tyr Arg Phe Gln Thr Pro Tyr Phe Trp Pro
 100 105 110
 Ser Asn Cys Trp Glu Pro Glu Asn Thr Asp Tyr Ala Val Tyr Leu Cys
 115 120 125
 Lys Arg Thr Met Gln Asn Lys Ala Arg Leu Glu Leu Ala Asp Tyr Glu
 130 135 140
 Ala Glu Ser Leu Ala Arg Leu Gln Arg Ala Phe Ala Arg Lys Trp Glu
 145 150 155 160
 Phe Ile Phe Met Gln Ala Glu Ala Gln Ala Lys Val Asp Lys Lys Arg
 165 170 175
 Asp Lys Ile Glu Arg Lys Ile Leu Asp Ser Gln Glu Arg Ala Phe Trp
 180 185 190
 Asp Val His Arg Pro Val Pro Gly Cys Val Asn Thr Thr Glu Val Asp
 195 200 205
 Ile Lys Lys Ser Ser Arg Met Arg Asn Pro His Lys Thr Arg Lys Ser
 210 215 220
 Val Tyr Gly Leu Gln Asn Asp Ile Arg Ser His Ser Pro Thr His Thr
 225 230 235 240
 Pro Thr Pro Glu Thr Lys Pro Pro Thr Glu Asp Glu Leu Gln Gln Gln
 245 250 255
 Ile Lys Tyr Trp Gln Ile Gln Leu Asp Arg His Arg Leu Lys Met Ser
 260 265 270
 Lys Val Ala Asp Ser Leu Leu Ser Tyr Thr Glu Gln Tyr Leu Glu Tyr
 275 280 285
 Asp Pro Phe Leu Leu Pro Pro Asp Pro Ser Asn Pro Trp Leu Ser Asp
 290 295 300
 Asp Thr Thr Phe Trp Glu Leu Glu Ala Ser Lys Glu Pro Ser Gln Gln
 305 310 315 320
 Arg Val Lys Arg Trp Gly Phe Gly Met Asp Glu Ala Leu Lys Asp Pro
 325 330 335
 Val Gly Arg Glu Gln Phe Leu Lys Phe Leu Glu Ser Glu Phe Ser Ser
 340 345 350
 Glu Asn Leu Arg Phe Trp Leu Ala Val Glu Asp Leu Lys Lys Arg Pro
 355 360 365
 Ile Lys Glu Val Pro Ser Arg Val Gln Glu Ile Trp Gln Glu Phe Leu

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      370              375              380
Ala Pro Gly Ala Pro Ser Ala Ile Asn Leu Asp Ser Lys Ser Tyr Asp
385              390              395              400
Lys Thr Thr Gln Asn Val Lys Glu Pro Gly Arg Tyr Thr Phe Glu Asp
      405              410              415
Ala Gln Glu His Ile Tyr Lys Leu Met Lys Ser Asp Ser Tyr Pro Arg
      420              425              430
Phe Ile Arg Ser Ser Ala Tyr Gln Glu Leu Leu Gln Ala Lys Lys Lys
      435              440              445
Gly Lys Ser Leu Thr Ser Lys Arg Leu Thr Ser Leu Ala Gln Ser Tyr
      450              455              460              464

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<210> 1107
 <211> 153
 <212>Amino acid
 <213> Homo sapiens

```

<400> 1107
Gly Thr Arg Asp Tyr Pro Arg Ile Val Asn His Leu Asp His Thr Tyr
 1              5              10              15
Val Thr Ala Pro Gln Ala Phe Met Met Phe Gln Tyr Phe Val Lys Val
      20              25              30
Val Pro Thr Val Tyr Met Lys Val Asp Gly Glu Val Leu Thr Thr Asn
      35              40              45
Gln Ile Tyr Val Thr Arg His Glu Lys Ala Ala Tyr Val Leu Met Gly
      50              55              60
Asp Gln Gly Leu Pro Gly Val Phe Ile Leu Tyr Glu Leu Ser Pro Met
      65              70              75              80
Met Val Asn Leu Thr Glu Ile His Thr Phe Phe Ser Leu Phe Leu Thr
      85              90              95
Ile Val Gly Ala Thr Ile Gly Gly Met Phe Phe Glu His Phe Val Ile
      100              105              110
Asn Tyr Leu Thr His Lys Trp Gly Leu Gly Phe Tyr Phe Lys Asn Glu
      115              120              125
Asn Ser Leu Gln Gly Gly His Arg Thr Leu Tyr Gly Val Asn Phe Phe
      130              135              140
Met Tyr Trp Ser Leu Arg Gly Gly Ser
145              150              153

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<210> 1108
 <211> 506
 <212>Amino acid
 <213> Homo sapiens

```

<400> 1108
Ser Val Trp Trp Asn Ser Gln Arg Gln Phe Val Val Arg Ala Trp Gly
 1              5              10              15
Cys Ala Gly Pro Cys Gly Arg Ala Val Phe Leu Ala Phe Gly Leu Gly
      20              25              30
Leu Gly Leu Ile Glu Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser
      35              40              45
Ala Cys Gln Glu Ile Gln Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly

```

50	55	60
Pro Asp Pro Leu Asp Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu		
65	70	75
Tyr Leu Ile Gly Gln Ser Ile Gly Lys Gly Cys Ser Ala Ala Val Tyr		80
	85	90
Glu Ala Thr Met Pro Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser		95
	100	105
Thr Gly Leu Leu Pro Gly Arg Gly Pro Gly Thr Ser Ala Pro Gly Glu		110
	115	120
Gly Gln Glu Arg Ala Pro Gly Ala Pro Ala Phe Pro Leu Ala Ile Lys		125
	130	135
Met Met Trp Asn Ile Ser Ala Gly Ser Ser Ser Glu Ala Ile Leu Asn		140
145	150	155
Thr Met Ser Gln Glu Leu Val Pro Ala Ser Arg Val Ala Leu Ala Gly		160
	165	170
Glu Tyr Gly Ala Val Thr Tyr Arg Lys Ser Lys Arg Gly Pro Lys Gln		175
	180	185
Leu Ala Pro His Pro Asn Ile Ile Arg Val Leu Arg Ala Phe Thr Ser		190
	195	200
Ser Val Pro Leu Leu Pro Gly Ala Leu Val Asp Tyr Pro Asp Val Leu		205
	210	215
Pro Ser Arg Leu His Pro Glu Gly Leu Gly His Gly Arg Thr Leu Phe		220
225	230	235
Leu Val Met Lys Asn Tyr Pro Cys Thr Leu Arg Gln Tyr Leu Cys Val		240
	245	250
Asn Thr Pro Ser Pro Arg Leu Ala Ala Met Met Leu Leu Gln Leu Leu		255
	260	265
Glu Gly Val Asp His Leu Val Gln Gln Gly Ile Ala His Arg Asp Leu		270
	275	280
Lys Ser Asp Asn Ile Leu Val Glu Leu Asp Pro Asp Gly Cys Pro Trp		285
	290	295
Leu Val Ile Ala Asp Phe Gly Cys Cys Leu Ala Asp Glu Ser Ile Gly		300
305	310	315
Leu Gln Leu Pro Phe Ser Ser Trp Tyr Val Asp Arg Gly Gly Asn Gly		320
	325	330
Cys Leu Met Ala Pro Glu Val Ser Thr Ala Arg Pro Gly Pro Arg Ala		335
	340	345
Val Ile Asp Tyr Ser Lys Ala Asp Ala Trp Ala Val Gly Ala Ile Ala		350
	355	360
Tyr Glu Ile Phe Gly Leu Val Asn Pro Phe Tyr Gly Gln Gly Lys Ala		365
	370	375
His Leu Glu Ser Arg Ser Tyr Gln Glu Ala Gln Leu Pro Ala Leu Pro		380
385	390	395
Glu Ser Val Pro Pro Asp Val Arg Gln Leu Val Arg Ala Leu Leu Gln		400
	405	410
Arg Glu Ala Ser Lys Arg Pro Ser Ala Arg Val Ala Ala Asn Val Leu		415
	420	425
His Leu Ser Leu Trp Gly Glu His Ile Leu Ala Leu Lys Asn Leu Lys		430
	435	440
Leu Asp Lys Met Val Gly Trp Leu Leu Gln Gln Ser Ala Ala Thr Leu		445
	450	455
Leu Ala Asn Arg Leu Thr Glu Lys Cys Cys Val Glu Thr Lys Met Lys		460
465	470	475
Met Leu Phe Leu Ala Asn Leu Glu Cys Glu Thr Leu Cys Gln Ala Ala		480
	485	490
Leu Leu Leu Cys Ser Trp Arg Ala Ala Leu		495
	500	505
		506

<210> 1109

<211> 382

<212> Amino acid

<213> Homo sapiens

```

<400> 1109
Arg Pro Leu Leu Arg Leu Ala Glu Leu Pro Asp His Cys Tyr Arg Met
 1          5          10          15
Asn Ser Ser Pro Ala Gly Thr Pro Ser Pro Gln Pro Ser Arg Ala Asn
 20          25          30
Gly Asn Ile Asn Leu Gly Pro Ser Ala Asn Pro Asn Ala Gln Pro Thr
 35          40          45
Asp Phe Asp Phe Leu Lys Val Ile Gly Lys Gly Asn Tyr Gly Lys Val
 50          55          60
Leu Leu Ala Lys Arg Lys Ser Asp Gly Ala Phe Tyr Ala Val Lys Val
 65          70          75          80
Leu Gln Lys Lys Ser Ile Leu Lys Lys Lys Glu Gln Ser His Ile Met
 85          90          95
Ala Glu Arg Ser Val Leu Leu Lys Asn Val Arg His Pro Phe Leu Val
 100          105          110
Gly Leu Arg Tyr Ser Phe Gln Thr Pro Glu Lys Leu Tyr Phe Val Leu
 115          120          125
Asp Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu Arg
 130          135          140
Arg Phe Leu Glu Pro Arg Ala Arg Phe Tyr Ala Ala Glu Val Ala Ser
 145          150          155          160
Ala Ile Gly Tyr Leu His Ser Leu Asn Ile Ile Tyr Arg Asp Leu Lys
 165          170          175
Pro Glu Asn Ile Leu Leu Asp Cys Gln Gly His Val Val Leu Thr Asp
 180          185          190
Phe Gly Leu Cys Lys Glu Gly Val Glu Pro Glu Asp Thr Thr Ser Thr
 195          200          205
Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Arg Lys Glu
 210          215          220
Pro Tyr Asp Arg Ala Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr
 225          230          235          240
Glu Met Leu His Gly Leu Pro Pro Phe Tyr Ser Gln Asp Val Ser Gln
 245          250          255
Met Tyr Glu Asn Ile Leu His Gln Pro Leu Gln Ile Pro Gly Gly Arg
 260          265          270
Thr Val Ala Ala Cys Asp Leu Leu Gln Ser Leu Leu His Lys Asp Gln
 275          280          285
Arg Gln Arg Leu Gly Ser Lys Ala Asp Phe Leu Glu Ile Lys Asn His
 290          295          300
Val Phe Phe Ser Pro Ile Asn Trp Asp Asp Leu Tyr His Lys Arg Leu
 305          310          315          320
Thr Pro Pro Phe Asn Pro Asn Val Thr Gly Pro Ala Asp Leu Lys His
 325          330          335
Phe Asp Pro Glu Phe Thr Gln Glu Ala Val Ser Lys Ser Ile Gly Cys
 340          345          350
Thr Pro Asp Thr Val Ala Ser Ser Ser Gly Ala Ser Ser Ala Phe Leu
 355          360          365
Gly Phe Ser Tyr Ala Pro Glu Asp Asp Asp Ile Leu Asp Cys
 370          375          380          382

```

<210> 1110

<211> 535

<212> Amino acid

<213> Homo sapiens

<400> 1110
 Arg Pro Gln Thr Leu Lys Gly His Gln Glu Lys Ile Arg Gln Arg Gln
 1 5 10 15
 Ser Ile Leu Pro Pro Gln Gly Pro Ala Pro Ile Pro Phe Gln His
 20 25 30
 Arg Gly Gly Asp Ser Pro Glu Ala Lys Asn Arg Val Gly Pro Gln Val
 35 40 45
 Pro Leu Ser Glu Pro Gly Phe Arg Arg Arg Glu Ser Gln Glu Glu Pro
 50 55 60
 Arg Ala Val Leu Ala Gln Lys Ile Glu Lys Glu Thr Gln Ile Leu Asn
 65 70 75 80
 Cys Ala Leu Asp Asp Ile Glu Trp Phe Val Ala Arg Leu Gln Lys Ala
 85 90 95
 Ala Glu Ala Phe Lys Gln Leu Asn Gln Arg Lys Lys Gly Lys Lys Lys
 100 105 110
 Gly Lys Lys Ala Pro Ala Glu Gly Val Leu Thr Leu Arg Ala Arg Pro
 115 120 125
 Pro Ser Glu Gly Glu Phe Ile Asp Cys Phe Gln Lys Ile Lys Leu Ala
 130 135 140
 Ile Asn Leu Leu Ala Lys Leu Gln Lys His Ile Gln Asn Pro Ser Ala
 145 150 155 160
 Ala Glu Leu Val His Phe Leu Phe Gly Pro Leu Asp Leu Ile Val Asn
 165 170 175
 Thr Cys Ser Gly Pro Asp Ile Ala Arg Ser Val Ser Cys Pro Leu Leu
 180 185 190
 Ser Arg Asp Ala Val Asp Phe Leu Arg Gly His Leu Val Pro Lys Glu
 195 200 205
 Met Ser Leu Trp Glu Ser Leu Gly Glu Ser Trp Met Arg Pro Arg Ser
 210 215 220
 Glu Trp Pro Arg Glu Pro Gln Val Pro Leu Tyr Val Pro Lys Phe His
 225 230 235 240
 Ser Gly Trp Glu Pro Pro Val Asp Val Leu Gln Glu Ala Pro Trp Glu
 245 250 255
 Val Glu Gly Leu Ala Ser Ala Pro Ile Glu Glu Val Ser Pro Val Ser
 260 265 270
 Arg Gln Ser Ile Arg Asn Ser Gln Lys His Ser Pro Thr Ser Glu Pro
 275 280 285
 Thr Pro Pro Gly Asp Ala Leu Pro Pro Val Ser Ser Pro His Thr His
 290 295 300
 Arg Gly Tyr Gln Pro Thr Pro Ala Met Ala Lys Tyr Val Lys Ile Leu
 305 310 315 320
 Tyr Asp Phe Thr Ala Arg Asn Ala Asn Glu Leu Ser Val Leu Lys Asp
 325 330 335
 Glu Val Leu Glu Val Leu Glu Asp Gly Arg Gln Trp Trp Lys Leu Arg
 340 345 350
 Ser Arg Ser Gly Gln Ala Gly Tyr Val Pro Cys Asn Ile Leu Gly Glu
 355 360 365
 Ala Arg Pro Glu Asp Ala Gly Ala Pro Phe Glu Gln Ala Gly Gln Lys
 370 375 380
 Tyr Trp Gly Pro Ala Ser Pro Thr His Lys Leu Pro Pro Ser Phe Pro
 385 390 395 400
 Gly Asn Lys Asp Glu Leu Met Gln His Met Asp Glu Val Asn Asp Glu
 405 410 415
 Leu Ile Arg Lys Ile Ser Asn Ile Arg Ala Gln Pro Gln Arg His Phe
 420 425 430
 Arg Val Glu Arg Ser Gln Pro Val Ser Gln Pro Leu Thr Tyr Glu Ser
 435 440 445
 Gly Pro Asp Glu Val Arg Ala Trp Leu Glu Ala Lys Ala Phe Ser Pro
 450 455 460
 Arg Ile Val Glu Asn Leu Gly Ile Leu Thr Gly Pro Gln Leu Phe Ser
 465 470 475 480
 Leu Asn Lys Glu Glu Leu Lys Lys Val Cys Gly Glu Glu Gly Val Arg
 485 490 495
 Val Tyr Ser Gln Leu Thr Met Gln Lys Ala Phe Leu Glu Lys Gln Gln

```
<210> 1111
<211> 346
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(346)
<223> X = any amino acid or stop code
```

638

Gln Lys Val Gly Phe Cys Ile Arg His Leu
 340 345 346

<210> 1112
 <211> 647
 <212> Amino acid
 <213> Homo sapiens

<400> 1112
 Met Ala Ala Gly Leu Ala Thr Trp Leu Pro Phe Ala Arg Ala Ala Ala
 1 5 10 15
 Val Gly Trp Leu Pro Leu Ala Gln Gln Pro Leu Pro Pro Ala Pro Gly
 20 25 30
 Val Lys Ala Ser Arg Gly Asp Glu Val Leu Val Val Asn Val Ser Gly
 35 40 45
 Arg Arg Phe Glu Thr Trp Lys Asn Thr Leu Asp Arg Tyr Pro Asp Thr
 50 55 60
 Leu Leu Gly Ser Ser Glu Lys Glu Phe Phe Tyr Asp Ala Asp Ser Gly
 65 70 75 80
 Glu Tyr Phe Phe Asp Arg Asp Pro Asp Met Phe Arg His Val Leu Asn
 85 90 95
 Phe Tyr Arg Thr Gly Arg Leu His Cys Pro Arg Gln Glu Cys Ile Gln
 100 105 110
 Ala Phe Asp Glu Glu Leu Ala Phe Tyr Gly Leu Val Pro Glu Leu Val
 115 120 125
 Gly Asp Cys Cys Leu Glu Glu Tyr Arg Asp Arg Lys Lys Glu Asn Ala
 130 135 140
 Glu Arg Leu Ala Glu Asp Glu Glu Ala Glu Gln Ala Gly Asp Gly Pro
 145 150 155 160
 Ala Leu Pro Ala Gly Ser Ser Leu Arg Gln Arg Leu Trp Arg Ala Phe
 165 170 175
 Glu Asn Pro His Thr Ser Thr Ala Ala Leu Val Phe Tyr Tyr Val Thr
 180 185 190
 Gly Phe Phe Ile Ala Val Ser Val Ile Ala Asn Val Val Glu Thr Ile
 195 200 205
 Pro Cys Arg Gly Ser Ala Arg Arg Ser Ser Arg Glu Gln Pro Cys Gly
 210 215 220
 Glu Arg Phe Pro Gln Ala Phe Phe Cys Met Asp Thr Ala Cys Val Leu
 225 230 235 240
 Ile Phe Thr Gly Glu Tyr Leu Leu Arg Leu Phe Ala Ala Pro Ser Arg
 245 250 255
 Cys Arg Phe Leu Arg Ser Val Met Ser Leu Ile Asp Val Val Ala Ile
 260 265 270
 Leu Pro Tyr Tyr Ile Gly Leu Leu Val Pro Lys Asn Asp Asp Val Ser
 275 280 285
 Gly Ala Phe Val Thr Leu Arg Val Phe Arg Val Phe Arg Ile Phe Lys
 290 295 300
 Phe Ser Arg His Ser Gln Gly Leu Arg Ile Leu Gly Tyr Thr Leu Lys
 305 310 315 320
 Ser Cys Ala Ser Glu Leu Gly Phe Leu Leu Phe Ser Leu Thr Met Ala
 325 330 335
 Ile Ile Ile Phe Ala Thr Val Met Phe Tyr Ala Glu Lys Gly Thr Asn
 340 345 350
 Lys Thr Asn Phe Thr Ser Ile Pro Ala Ala Phe Trp Tyr Thr Ile Val
 355 360 365
 Thr Met Thr Thr Leu Gly Tyr Gly Asp Met Val Pro Ser Thr Ile Ala
 370 375 380
 Gly Lys Ile Phe Gly Ser Ile Cys Ser Leu Ser Gly Val Leu Val Ile
 385 390 395 400

```
<210> 1113
<211> 220
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(220)
<223> X = any amino acid or stop code
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640

115	120	125
Ser His Gln Ala Val Ala Arg Thr Ala Gly Ser Val Ile Leu Arg Leu		
130	135	140
Ser Asp Ser Phe Phe Leu Pro Leu Lys Val Ser Asp Tyr Ser Glu Thr		
145	150	155
Leu Arg Ser Phe Leu Gln Ala Ala Gln Gln Asp Leu Gly Ala Leu Leu		
165	170	175
Glu Gln His Ser Ile Ser Leu Gly Pro Leu Val Thr Ala Val Glu Lys		
180	185	190
Phe Glu Ala Glu Ala Ala Ala Leu Gly Gln Arg Ile Ser Thr Leu Gln		
195	200	205
Lys Gly Ser Pro Asp Pro Leu Gln Val Arg Met Leu		
210	215	220

<210> 1114

<211> 382

<212> Amino acid

<213> Homo sapiens

<400> 1114

Gly Ile Arg Gly Gly Gly Ser Leu Ala Ser Gly Gly Pro Gly Pro Gly		
1	5	10
His Ala Ser Leu Ser Gln Arg Leu Arg Leu Tyr Leu Ala Asp Ser Trp		
20	25	30
Asn Gln Cys Asp Leu Val Ala Leu Thr Cys Phe Leu Leu Gly Val Gly		
35	40	45
Cys Arg Leu Thr Pro Gly Leu Tyr His Leu Gly Arg Thr Val Leu Cys		
50	55	60
Ile Asp Phe Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val		
65	70	75
Asn Lys Gln Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys		
85	90	95
Asp Val Phe Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr		
100	105	110
Gly Val Ala Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro		
115	120	125
Ser Ile Leu Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly		
130	135	140
Gln Ile Pro Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn		
145	150	155
Cys Ser Ser Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala		
165	170	175
Gly Thr Cys Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu		
180	185	190
Val Ile Phe Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile		
195	200	205
Ala Met Phe Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu		
210	215	220
Tyr Trp Lys Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg		
225	230	235
Pro Ala Leu Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu		
245	250	255
Leu Arg Gln Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro		
260	265	270
Ala Leu Glu His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys		
275	280	285
Leu Leu Thr Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg		
290	295	300
Ala Arg Asp Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser		

305 310 315 320
 Gln Lys Val Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr
 325 330 335
 Glu Gln Arg Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg
 340 345 350
 Val Leu Gly Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro
 355 360 365
 Pro Gly Gly Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
 370 375 380 382

<210> 1115
 <211> 109
 <212> Amino acid
 <213> Homo sapiens

<400> 1115
 Leu Ile Lys Leu Cys Lys Ser Lys Ala Lys Ser Cys Glu Asn Asp Leu
 1 5 10 15
 Glu Met Gly Met Leu Asn Ser Lys Phe Lys Lys Thr Arg Tyr Gln Ala
 20 25 30
 Gly Met Arg Asn Ser Glu Asn Leu Thr Ala Asn Asn Thr Leu Ser Lys
 35 40 45
 Pro Thr Arg Tyr Gln Gly Glu Leu Lys Glu Ile Lys Gln Asp Ile Ser
 50 55 60
 Ser Leu Arg Tyr Glu Leu Leu Glu Glu Lys Ser Gln Ala Thr Gly Glu
 65 70 75 80
 Leu Ala Asp Leu Ile Gln Gln Leu Ser Glu Lys Phe Gly Lys Asn Leu
 85 90 95
 Asn Lys Asp His Leu Arg Val Asn Lys Gly Lys Asp Ile
 100 105 109

<210> 1116
 <211> 679
 <212> Amino acid
 <213> Homo sapiens

<400> 1116
 Leu Pro Leu Leu His Ala Gly Phe Asn Arg Arg Phe Met Glu Asn Ser
 1 5 10 15
 Ser Ile Ile Ala Cys Tyr Asn Glu Leu Ile Gln Ile Glu His Gly Glu
 20 25 30
 Val Arg Ser Gln Phe Lys Leu Arg Ala Cys Asn Ser Val Phe Thr Ala
 35 40 45
 Leu Asp His Cys His Glu Ala Ile Glu Ile Thr Ser Asp Asp His Val
 50 55 60
 Ile Gln Tyr Val Asn Pro Ala Phe Glu Arg Met Met Gly Tyr His Lys
 65 70 75 80
 Gly Glu Leu Leu Gly Lys Glu Leu Ala Asp Leu Pro Lys Ser Asp Lys
 85 90 95
 Asn Arg Ala Asp Leu Leu Asp Thr Ile Asn Thr Cys Ile Lys Lys Gly
 100 105 110
 Lys Glu Trp Gln Gly Val Tyr Tyr Ala Arg Arg Lys Ser Gly Asp Ser
 115 120 125
 Ile Gln Gln His Val Lys Ile Thr Pro Val Ile Gly Gln Gly Gly Lys

643

Pro	Ser	Asp	Arg	Leu	Lys	Pro	Ser	His	Arg	Gly	Gly	Leu	Leu	Thr	Asp
			660					665						670	
Lys	Gly	His	Cys	Glu	Ser	Gln									
		675				679									

```
<210> 1117
<211> 1193
<212> Amino acid
<213> Homo sapiens
```

<400> 1117																	
Ala	Phe	Leu	Ser	Lys	Val	Glu	Glu	Asp	Asp	Tyr	Pro	Ser	Glu	Glu	Leu		
1				5					10					15			
Leu	Glu	Asp	Glu	Asn	Ala	Ile	Asn	Ala	Lys	Arg	Ser	Lys	Glu	Lys	Asn		
			20					25					30				
Pro	Gly	Asn	Gln	Gly	Arg	Gln	Phe	Asp	Val	Asn	Leu	Gln	Val	Pro	Asp		
		35					40					45					
Arg	Ala	Val	Leu	Gly	Thr	Ile	His	Pro	Asp	Pro	Glu	Ile	Glu	Glu	Ser		
	50				55				60								
Lys	Gln	Glu	Thr	Ser	Met	Ile	Leu	Asp	Ser	Glu	Lys	Thr	Ser	Glu	Thr		
65				70					75					80			
Ala	Ala	Lys	Gly	Val	Asn	Thr	Gly	Gly	Arg	Glu	Pro	Asn	Thr	Met	Val		
			85					90					95				
Glu	Lys	Glu	Arg	Pro	Leu	Ala	Asp	Lys	Lys	Ala	Gln	Arg	Pro	Phe	Glu		
		100					105				110						
Arg	Ser	Asp	Phe	Ser	Asp	Ser	Ile	Lys	Ile	Gln	Thr	Pro	Glu	Leu	Gly		
	115				120					125							
Glu	Val	Phe	Gln	Asn	Lys	Asp	Ser	Asp	Tyr	Leu	Lys	Asn	Asp	Asn	Pro		
	130			135					140								
Glu	Glu	His	Leu	Lys	Thr	Ser	Gly	Leu	Ala	Gly	Glu	Pro	Glu	Gly	Glu		
145				150					155					160			
Leu	Ser	Lys	Glu	Asp	His	Glu	Asn	Thr	Glu	Lys	Tyr	Met	Gly	Thr	Glu		
			165					170					175				
Ser	Gln	Gly	Ser	Ala	Ala	Ala	Glu	Pro	Glu	Asp	Asp	Ser	Phe	His	Trp		
		180					185					190					
Thr	Pro	His	Thr	Ser	Val	Glu	Pro	Gly	His	Ser	Asp	Lys	Arg	Glu	Asp		
	195				200						205						
Leu	Leu	Ile	Ile	Ser	Ser	Phe	Phe	Lys	Glu	Gln	Gln	Ser	Leu	Gln	Arg		
	210				215				220								
Phe	Gln	Lys	Tyr	Phe	Asn	Val	His	Glu	Leu	Glu	Ala	Leu	Leu	Gln	Glu		
225				230					235					240			
Met	Ser	Ser	Lys	Leu	Lys	Ser	Ala	Gln	Gln	Glu	Ser	Leu	Pro	Tyr	Asn		
			245					250					255				
Met	Glu	Lys	Val	Leu	Asp	Lys	Val	Phe	Arg	Ala	Ser	Glu	Ser	Gln	Ile		
		260					265					270					
Leu	Ser	Ile	Ala	Glu	Lys	Met	Leu	Asp	Thr	Arg	Val	Ala	Glu	Asn	Arg		
	275						280					285					
Asp	Leu	Gly	Met	Asn	Glu	Asn	Asn	Ile	Phe	Glu	Glu	Ala	Ala	Val	Leu		
	290			295					300								
Asp	Asp	Ile	Gln	Asp	Leu	Ile	Tyr	Phe	Val	Arg	Tyr	Lys	His	Ser			

370	375	380
Ser Gln Lys Pro Asn Thr	Glu Lys Asp Leu Asp Pro Gly Pro Val Thr	
385	390	395
Thr Glu Asp Thr Pro Met Asp Ala Ile Asp Ala Asn Lys Gln Pro Glu		400
	405	410
Thr Ala Ala Glu Pro Ala Ser Val Thr Pro Leu Glu Asn Ala Ile		415
	420	425
Leu Leu Ile Tyr Ser Phe Met Phe Tyr Leu Thr Lys Ser Leu Val Ala		430
	435	440
Thr Leu Pro Asp Asp Val Gln Pro Gly Pro Asp Phe Tyr Gly Leu Pro		445
	450	455
Trp Lys Pro Val Phe Ile Thr Ala Phe Leu Gly Ile Ala Ser Phe Ala		460
465	470	475
Ile Phe Leu Trp Arg Thr Val Leu Val Val Lys Asp Arg Val Tyr Gln		480
	485	490
Val Thr Glu Gln Gln Ile Ser Glu Lys Leu Lys Thr Ile Met Lys Glu		495
	500	505
Asn Thr Glu Leu Val Gln Lys Leu Ser Asn Tyr Glu Gln Lys Ile Lys		510
	515	520
Glu Ser Lys Lys His Val Gln Glu Thr Arg Lys Gln Asn Met Ile Leu		525
	530	535
Ser Asp Glu Ala Ile Lys Tyr Lys Asp Lys Ile Lys Thr Leu Glu Lys		540
545	550	555
Asn Gln Glu Ile Leu Asp Asp Thr Ala Lys Asn Leu Arg Val Met Leu		560
	565	570
Glu Ser Glu Arg Glu Gln Asn Val Lys Asn Gln Asp Leu Ile Ser Glu		575
	580	585
Asn Lys Lys Ser Ile Glu Lys Leu Lys Asp Val Ile Ser Met Asn Ala		590
	595	600
Ser Glu Phe Ser Glu Val Gln Ile Ala Leu Asn Glu Ala Lys Leu Ser		605
	610	615
Glu Glu Lys Val Lys Ser Glu Cys His Arg Val Gln Glu Glu Asn Ala		620
625	630	635
Arg Leu Lys Lys Lys Lys Glu Gln Leu Gln Gln Glu Ile Glu Asp Trp		640
	645	650
Ser Lys Leu His Ala Glu Leu Ser Glu Gln Ile Lys Ser Phe Glu Lys		655
	660	665
Ser Gln Lys Asp Leu Glu Val Ala Leu Thr His Lys Asp Asp Asn Ile		670
	675	680
Asn Ala Leu Thr Asn Cys Ile Thr Gln Leu Asn Leu Leu Glu Cys Glu		685
	690	695
Ser Glu Ser Glu Gly Gln Asn Lys Gly Gly Asn Asp Ser Asp Glu Leu		700
705	710	715
Ala Asn Gly Glu Val Gly Gly Asp Arg Asn Glu Lys Met Lys Asn Gln		720
	725	730
Ile Lys Gln Met Met Asp Val Ser Arg Thr Gln Thr Ala Ile Ser Val		735
	740	745
Val Glu Glu Asp Leu Lys Leu Leu Gln Leu Lys Leu Arg Ala Ser Val		750
	755	760
Ser Thr Lys Cys Asn Leu Glu Asp Gln Val Lys Lys Leu Glu Asp Asp		765
	770	775
Arg Asn Ser Leu Gln Ala Ala Lys Ala Gly Leu Glu Asp Glu Cys Lys		780
785	790	795
Thr Leu Arg Gln Lys Val Glu Ile Leu Asn Glu Leu Tyr Gln Gln Lys		800
	805	810
Glu Met Ala Leu Gln Lys Lys Leu Ser Gln Glu Glu Tyr Glu Arg Gln		815
	820	825
Glu Arg Glu His Arg Leu Ser Ala Ala Asp Glu Lys Ala Val Ser Ala		830
	835	840
Ala Glu Glu Val Lys Thr Tyr Lys Arg Arg Ile Glu Glu Met Glu Asp		845
	850	855
Glu Leu Gln Lys Thr Glu Arg Ser Phe Lys Asn Gln Ile Ala Thr His		860
865	870	875
Glu Lys Lys Ala His Glu Asn Trp Leu Lys Ala Arg Ala Ala Glu Arg		880

885 890 895
 Ala Ile Ala Glu Glu Lys Arg Glu Ala Ala Asn Leu Arg His Lys Leu
 900 905 910
 Leu Asp Leu Thr Gln Lys Met Ala Met Leu Gln Glu Glu Pro Val Ile
 915 920 925
 Val Lys Pro Met Pro Gly Lys Pro Asn Thr Gln Asn Pro Pro Arg Arg
 930 935 940
 Gly Pro Leu Ser Gln Asn Gly Ser Phe Gly Pro Ser Pro Val Ser Gly
 945 950 955 960
 Gly Glu Cys Ser Pro Pro Leu Thr Val Glu Pro Pro Val Arg Pro Leu
 965 970 975
 Ser Ala Thr Leu Asn Arg Arg Asp Met Pro Arg Ser Glu Phe Gly Ser
 980 985 990
 Leu Asp Gly Pro Leu Pro His Pro Arg Trp Ser Ala Glu Ala Ser Gly
 995 1000 1005
 Lys Pro Ser Pro Ser Asp Pro Gly Ser Gly Thr Ala Thr Met Met Asn
 1010 1015 1020
 Ser Ser Ser Arg Gly Ser Ser Pro Thr Arg Val Leu Asp Glu Gly Lys
 1025 1030 1035 1040
 Val Asn Met Ala Pro Lys Gly Pro Pro Pro Phe Pro Gly Val Pro Leu
 1045 1050 1055
 Met Ser Thr Pro Met Gly Gly Pro Val Pro Pro Pro Ile Arg Tyr Gly
 1060 1065 1070
 Pro Pro Pro Gln Leu Cys Gly Pro Phe Gly Pro Arg Pro Leu Pro Pro
 1075 1080 1085
 Pro Phe Gly Pro Gly Met Arg Pro Pro Leu Gly Leu Arg Glu Phe Ala
 1090 1095 1100
 Pro Gly Val Pro Pro Gly Arg Arg Asp Leu Pro Leu His Pro Arg Gly
 1105 1110 1115 1120
 Phe Leu Pro Gly His Ala Pro Phe Arg Pro Leu Gly Ser Leu Gly Pro
 1125 1130 1135
 Arg Glu Tyr Phe Ile Pro Gly Thr Arg Leu Pro Pro Pro Thr His Gly
 1140 1145 1150
 Pro Gln Glu Tyr Pro Pro Pro Pro Ala Val Arg Asp Leu Leu Pro Ser
 1155 1160 1165
 Gly Ser Arg Asp Glu Pro Pro Pro Ala Ser Gln Ser Thr Ser Gln Asp
 1170 1175 1180
 Cys Ser Gln Ala Leu Lys Gln Ser Pro
 1185 1190 1193

<210> 1118

<211> 981

<212> Amino acid

<213> Homo sapiens

<400> 1118

Met Ala Ala Asp Ser Glu Pro Glu Ser Glu Val Phe Glu Ile Thr Asp
 1 5 10 15
 Phe Thr Thr Ala Ser Glu Trp Glu Arg Phe Ile Ser Lys Val Glu Glu
 20 25 30
 Val Leu Asn Asp Trp Lys Leu Ile Gly Asn Ser Leu Gly Lys Pro Leu
 35 40 45
 Glu Lys Gly Ile Phe Thr Ser Gly Thr Trp Glu Glu Lys Ser Asp Glu
 50 55 60
 Ile Ser Phe Ala Asp Phe Lys Phe Ser Val Thr His His Tyr Leu Val
 65 70 75 80
 Gln Glu Ser Thr Asp Lys Glu Gly Lys Asp Glu Leu Leu Glu Asp Val
 85 90 95
 Val Pro Gln Ser Met Gln Asp Leu Leu Gly Met Asn Asn Asp Phe Pro

100	105	110
Pro Arg Ala His Cys Leu Val	Arg Trp Tyr Gly Leu Arg	Glu Phe Val
115	120	125
Val Ile Ala Pro Ala Ala His	Ser Asp Ala Val Leu Ser	Glu Ser Lys
130	135	140
Cys Asn Leu Leu Leu Ser Ser	Val Ser Ile Ala Leu Gly	Asn Thr Gly
145	150	155
Cys Gln Val Pro Leu Phe Val	Gln Ile His His Lys Trp	Arg Arg Met
165	170	175
Tyr Val Gly Glu Cys Gln Gly	Pro Gly Val Arg Thr Asp	Phe Glu Met
180	185	190
Val His Leu Arg Lys Val Pro	Asn Gln Tyr Thr His Leu	Ser Gly Leu
195	200	205
Leu Asp Ile Phe Lys Ser Lys	Ile Gly Cys Pro Leu Thr	Pro Leu Pro
210	215	220
Pro Val Ser Ile Ala Ile Arg	Phe Thr Tyr Val Leu Gln	Asp Trp Gln
225	230	235
Gln Tyr Phe Trp Pro Gln Gln	Pro Pro Asp Ile Asp Ala	Leu Val Gly
245	250	255
Gly Glu Val Gly Gly Leu Glu	Phe Gly Lys Leu Pro Phe	Gly Ala Cys
260	265	270
Glu Asp Pro Ile Ser Glu Leu	His Leu Ala Thr Thr Trp	Pro His Leu
275	280	285
Thr Glu Gly Ile Ile Val Asp	Asn Asp Val Tyr Ser Asp	Leu Asp Pro
290	295	300
Ile Gln Ala Pro His Trp Ser	Val Arg Val Arg Lys Ala	Glu Asn Pro
305	310	315
Gln Cys Leu Leu Gly Asp Phe	Val Thr Glu Phe Phe Lys	Ile Cys Arg
325	330	335
Arg Lys Glu Ser Thr Asp Glu	Ile Leu Gly Arg Ser Ala	Phe Glu Glu
340	345	350
Glu Gly Lys Glu Thr Ala Asp	Ile Thr His Ala Leu Ser	Lys Leu Thr
355	360	365
Glu Pro Ala Ser Val Pro Ile	His Lys Leu Ser Val Ser	Asn Met Val
370	375	380
His Thr Ala Lys Lys Lys Ile	Arg Lys His Arg Gly Val	Glu Glu Ser
385	390	395
Pro Leu Asn Asn Asp Val Leu	Asn Thr Ile Leu Leu Phe	Leu Phe Pro
405	410	415
Asp Ala Val Ser Glu Lys Pro	Leu Asp Gly Thr Thr Ser	Thr Asp Asn
420	425	430
Asn Asn Pro Pro Ser Glu Ser	Glu Asp Tyr Asn Leu Tyr	Asn Gln Phe
435	440	445
Lys Ser Ala Pro Ser Asp Ser	Leu Thr Tyr Lys Leu Ala	Leu Cys Leu
450	455	460
Cys Met Ile Asn Phe Tyr His	Gly Gly Leu Lys Gly Val	Ala His Leu
465	470	475
Trp Gln Glu Phe Val Leu Glu	Met Arg Phe Arg Trp Glu	Asn Asn Phe
485	490	495
Leu Ile Pro Gly Leu Ala Ser	Gly Pro Pro Asp Leu Arg	Cys Cys Leu
500	505	510
Leu His Gln Lys Leu Gln Met	Leu Asn Cys Cys Ile Glu	Arg Lys Lys
515	520	525
Ala Arg Asp Glu Gly Lys Lys	Thr Ser Ala Ser Asp Val	Thr Asn Ile
530	535	540
Tyr Pro Gly Asp Ala Gly Lys	Ala Gly Asp Gln Leu Val	Pro Asp Asn
545	550	555
Leu Lys Glu Thr Asp Lys Glu	Lys Gly Glu Val Gly Lys	Ser Trp Asp
565	570	575
Ser Trp Ser Asp Ser Glu Glu	Glu Glu Phe Glu Cys Leu	Ser Asp Thr
580	585	590
Glu Glu Leu Lys Gly Asn Gly	Gln Glu Ser Gly Lys Lys	Gly Gly Pro
595	600	605
Lys Glu Met Ala Asn Leu Arg	Pro Glu Gly Arg Leu Tyr	Gln His Gly

```

        610                615                620
Lys Leu Thr Leu Leu His Asn Gly Glu Pro Leu Tyr Ile Pro Val Thr
625                630                635                640
Gln Glu Pro Ala Pro Met Thr Glu Asp Leu Leu Glu Glu Gln Ser Glu
        645                650                655
Val Leu Ala Lys Leu Gly Thr Ser Ala Glu Gly Ala His Leu Arg Ala
        660                665                670
Arg Met Gln Ser Ala Cys Leu Leu Ser Asp Met Glu Ser Phe Lys Ala
        675                680                685
Ala Asn Pro Gly Cys Ser Leu Glu Asp Phe Val Arg Trp Tyr Ser Pro
        690                695                700
Arg Asp Tyr Ile Glu Glu Glu Val Ile Asp Glu Lys Gly Asn Val Val
705                710                715                720
Leu Lys Gly Glu Leu Ser Ala Arg Met Lys Ile Pro Ser Asn Met Trp
        725                730                735
Val Glu Ala Trp Glu Thr Ala Lys Pro Ile Pro Ala Arg Arg Gln Arg
        740                745                750
Arg Leu Phe Asp Asp Thr Arg Glu Ala Glu Lys Val Leu His Tyr Leu
        755                760                765
Ala Ile Gln Lys Pro Ala Asp Leu Ala Arg His Leu Leu Pro Cys Val
770                775                780
Ile His Ala Ala Val Leu Lys Val Lys Glu Glu Glu Ser Leu Glu Asn
785                790                795                800
Ile Ser Ser Val Lys Lys Ile Ile Lys Gln Ile Ile Ser His Ser Ser
        805                810                815
Lys Val Leu His Phe Pro Asn Pro Glu Asp Lys Lys Leu Glu Glu Ile
        820                825                830
Ile His Gln Ile Thr Asn Val Glu Ala Leu Ile Ala Arg Ala Arg Ser
        835                840                845
Leu Lys Ala Lys Phe Gly Thr Glu Lys Cys Glu Gln Glu Glu Lys
        850                855                860
Glu Asp Leu Glu Arg Phe Val Ser Cys Leu Leu Glu Gln Pro Glu Val
865                870                875                880
Leu Val Thr Gly Ala Gly Arg Gly His Ala Gly Arg Ile Ile His Lys
        885                890                895
Leu Phe Val Asn Ala Gln Arg Ala Ala Ala Met Thr Pro Pro Glu Glu
        900                905                910
Glu Leu Lys Arg Met Gly Ser Pro Glu Glu Arg Arg Gln Asn Ser Val
        915                920                925
Ser Asp Phe Pro Pro Pro Ala Gly Arg Glu Phe Ile Leu Arg Thr Thr
        930                935                940
Val Pro Arg Pro Ala Pro Tyr Ser Lys Ala Leu Pro Gln Arg Met Tyr
945                950                955                960
Ser Val Leu Thr Lys Glu Asp Phe Arg Leu Ala Gly Ala Phe Ser Ser
        965                970                975
Asp Thr Ser Phe Phe
        980 981

```

<210> 1119

<211> 554

<212> Amino acid

<213> Homo sapiens

<400> 1119

```

Ser Pro Thr Arg Thr Gly Asp Arg Ser Val Ser Leu Ile Val Phe Leu
1                5                10                15
Thr Glu Gly Lys Pro Thr Val Gly Glu Thr His Thr Leu Lys Ile Leu
        20                25                30
Asn Asn Thr Arg Glu Ala Ala Arg Gly Gln Val Cys Ile Phe Thr Ile

```

649

545

550

554

<210> 1120
 <211> 107
 <212> Amino acid
 <213> Homo sapiens

<400> 1120
 Val Pro Leu Glu Ser Leu Ser Cys Ser His Ala Asp Asn Trp Lys Gln
 1 5 10 15
 Glu Leu Thr Lys Phe Ile Ser Pro Asp Gln Leu Pro Val Glu Phe Gly
 20 25 30
 Gly Thr Met Thr Asp Pro Asp Gly Asn Pro Lys Cys Leu Thr Lys Ile
 35 40 45
 Asn Tyr Gly Gly Glu Val Pro Lys Ser Tyr Tyr Leu Cys Lys Gln Val
 50 55 60
 Arg Leu Gln Tyr Glu His Thr Arg Ser Val Gly Arg Gly Ser Ser Leu
 65 70 75 80
 Gln Val Glu Asn Glu Ile Leu Phe Pro Gly Cys Val Leu Arg Cys Pro
 85 90 95
 Glu Val Leu Gln His Leu Gln Pro Gly Ser Phe
 100 105 107

<210> 1121
 <211> 1241
 <212> Amino acid
 <213> Homo sapiens

<400> 1121
 Pro Ala Ala Pro Glu His Thr Asp Pro Ser Glu Pro Arg Gly Ser Val
 1 5 10 15
 Ser Cys Cys Ser Leu Leu Arg Gly Leu Ser Ser Gly Trp Ser Ser Pro
 20 25 30
 Leu Leu Pro Ala Pro Val Cys Asn Pro Asn Lys Ala Ile Phe Thr Val
 35 40 45
 Asp Ala Lys Thr Thr Glu Ile Leu Val Ala Asn Asp Lys Ala Cys Gly
 50 55 60
 Leu Leu Gly Tyr Ser Ser Gln Asp Leu Ile Gly Gln Lys Leu Thr Gln
 65 70 75 80
 Phe Phe Leu Arg Ser Asp Ser Asp Val Val Glu Ala Leu Ser Glu Glu
 85 90 95
 His Met Glu Ala Asp Gly His Ala Ala Val Val Phe Gly Thr Val Val
 100 105 110
 Asp Ile Ile Ser Arg Ser Gly Glu Lys Ile Pro Val Ser Val Trp Met
 115 120 125
 Lys Arg Met Arg Gln Glu Arg Arg Leu Cys Cys Val Val Leu Glu
 130 135 140
 Pro Val Glu Arg Val Ser Thr Trp Val Ala Phe Gln Ser Asp Gly Thr
 145 150 155 160
 Val Thr Ser Cys Asp Ser Leu Phe Ala His Leu His Gly Tyr Val Ser
 165 170 175
 Gly Glu Asp Val Ala Gly Gln His Ile Thr Asp Leu Ile Pro Ser Val
 180 185 190
 Gln Leu Pro Pro Ser Gly Gln His Ile Pro Lys Asn Leu Lys Ile Gln

195	200	205
Arg Ser Val Gly Arg Ala Arg Asp Gly Thr Thr Phe Pro Leu Ser Leu		
210	215	220
Lys Leu Lys Ser Gln Pro Ser Ser Glu Glu Ala Thr Thr Gly Glu Ala		
225	230	235
Ala Pro Val Ser Gly Tyr Arg Ala Ser Val Trp Val Phe Cys Thr Ile		
245	250	255
Ser Gly Leu Ile Thr Leu Leu Pro Asp Gly Thr Ile His Gly Ile Asn		
260	265	270
His Ser Phe Ala Leu Thr Leu Phe Gly Tyr Gly Lys Thr Glu Leu Leu		
275	280	285
Gly Lys Asn Ile Thr Phe Leu Ile Pro Gly Phe Tyr Ser Tyr Met Asp		
290	295	300
Leu Ala Tyr Asn Ser Ser Leu Gln Leu Pro Asp Leu Ala Ser Cys Leu		
305	310	315
Asp Val Gly Asn Glu Ser Gly Cys Gly Glu Arg Thr Leu Asp Pro Trp		
325	330	335
Gln Gly Gln Asp Pro Ala Glu Gly Gly Gln Asp Pro Arg Ile Asn Val		
340	345	350
Val Leu Ala Gly Gly His Val Val Pro Arg Asp Glu Ile Arg Lys Leu		
355	360	365
Met Glu Ser Gln Asp Ile Phe Thr Gly Thr Gln Thr Glu Leu Ile Ala		
370	375	380
Gly Gly Gln Leu Leu Ser Cys Leu Ser Pro Gln Pro Ala Pro Gly Val		
385	390	395
Asp Asn Val Pro Glu Gly Ser Leu Pro Val His Gly Glu Gln Ala Leu		
405	410	415
Pro Lys Asp Gln Gln Ile Thr Ala Leu Gly Arg Glu Glu Pro Val Ala		
420	425	430
Ile Glu Ser Pro Gly Gln Asp Leu Leu Gly Glu Ser Arg Ser Glu Pro		
435	440	445
Val Asp Val Lys Pro Phe Ala Ser Cys Glu Asp Ser Glu Ala Pro Val		
450	455	460
Pro Ala Glu Asp Gly Gly Ser Asp Ala Gly Met Cys Gly Leu Cys Gln		
465	470	475
Lys Ala Gln Leu Glu Arg Met Gly Val Ser Gly Pro Ser Gly Ser Asp		
485	490	495
Leu Trp Ala Gly Ala Ala Val Ala Lys Pro Gln Ala Lys Gly Gln Leu		
500	505	510
Ala Gly Gly Ser Leu Leu Met His Cys Pro Cys Tyr Gly Ser Glu Trp		
515	520	525
Gly Leu Trp Trp Arg Ser Gln Asp Leu Ala Pro Ser Pro Ser Gly Met		
530	535	540
Ala Gly Leu Ser Phe Gly Thr Pro Thr Leu Asp Glu Pro Trp Leu Gly		
545	550	555
Val Glu Asn Asp Arg Glu Glu Leu Gln Thr Cys Leu Ile Lys Glu Gln		
565	570	575
Leu Ser Gln Leu Ser Leu Ala Gly Ala Leu Asp Val Pro His Ala Glu		
580	585	590
Leu Val Pro Thr Glu Cys Gln Ala Val Thr Ala Pro Val Ser Ser Cys		
595	600	605
Asp Leu Gly Gly Arg Asp Leu Cys Gly Gly Cys Thr Gly Ser Ser Ser		
610	615	620
Ala Cys Tyr Ala Leu Ala Thr Asp Leu Pro Gly Gly Leu Glu Ala Val		
625	630	635
Glu Ala Gln Glu Val Asp Val Asn Ser Phe Ser Trp Asn Leu Lys Glu		
645	650	655
Leu Phe Phe Ser Asp Gln Thr Asp Gln Thr Ser Ser Asn Cys Ser Cys		
660	665	670
Ala Thr Ser Glu Leu Arg Glu Thr Pro Ser Ser Leu Ala Val Gly Ser		
675	680	685
Asp Pro Asp Val Gly Ser Leu Gln Glu Gln Gly Ser Cys Val Leu Asp		
690	695	700
Asp Arg Glu Leu Leu Leu Leu Thr Gly Thr Cys Val Asp Leu Gly Gln		

705		710		715		720
Gly Arg Arg Phe Arg Glu Ser Cys Val Gly His Asp Pro Thr Glu Pro						
	725			730		735
Leu Glu Val Cys Leu Val Ser Ser Glu His Tyr Ala Ala Ser Asp Arg						
	740			745		750
Glu Ser Pro Gly His Val Pro Ser Thr Leu Asp Ala Gly Pro Glu Asp						
	755			760		765
Thr Cys Pro Ser Ala Glu Glu Pro Arg Leu Asn Val Gln Val Thr Ser						
	770			775		780
Thr Pro Val Ile Val Met Arg Gly Ala Ala Gly Leu Gln Arg Glu Ile						
	785			790		795
Gln Glu Gly Ala Tyr Ser Gly Ser Cys Tyr His Arg Asp Gly Leu Arg						
	805			810		815
Leu Ser Ile Gln Phe Glu Val Arg Arg Val Glu Leu Gln Gly Pro Thr						
	820			825		830
Pro Leu Phe Cys Cys Trp Leu Val Lys Asp Leu Leu His Ser Gln Arg						
	835			840		845
Asp Ser Ala Ala Arg Thr Arg Leu Phe Leu Ala Ser Leu Pro Gly Ser						
	850			855		860
Thr His Ser Thr Ala Ala Glu Leu Thr Gly Pro Ser Leu Val Glu Val						
	865			870		875
Leu Arg Ala Arg Pro Trp Phe Glu Glu Pro Pro Lys Ala Val Glu Leu						
	885			890		895
Glu Gly Leu Ala Ala Cys Glu Gly Glu Tyr Ser Gln Lys Tyr Ser Thr						
	900			905		910
Met Ser Pro Leu Gly Ser Gly Ala Phe Gly Phe Val Trp Thr Ala Val						
	915			920		925
Asp Lys Glu Lys Asn Lys Glu Val Val Val Lys Phe Ile Lys Lys Glu						
	930			935		940
Lys Val Leu Glu Asp Cys Trp Ile Glu Asp Pro Lys Leu Gly Lys Val						
	945			950		955
Thr Leu Glu Ile Ala Ile Leu Ser Arg Val Glu His Ala Asn Ile Ile						
	965			970		975
Lys Val Leu Asp Ile Phe Glu Asn Gln Gly Phe Phe Gln Leu Val Met						
	980			985		990
Glu Lys His Gly Ser Gly Leu Asp Leu Phe Ala Phe Ile Asp Arg His						
	995			1000		1005
Pro Arg Leu Asp Glu Pro Leu Ala Ser Tyr Ile Phe Arg Gln Val Arg						
	1010			1015		1020
Ala Gly Gln Ser Arg Leu Val Ser Ala Val Gly Tyr Leu Arg Leu Lys						
	1025			1030		1035
Asp Ile Ile His Arg Asp Ile Lys Asp Glu Asn Ile Val Ile Ala Glu						
	1045			1050		1055
Asp Phe Thr Ile Lys Leu Ile Asp Phe Gly Ser Ala Ala Tyr Leu Glu						
	1060			1065		1070
Arg Gly Lys Leu Phe Tyr Thr Phe Cys Gly Thr Ile Glu Tyr Cys Ala						
	1075			1080		1085
Pro Glu Val Leu Met Gly Asn Pro Tyr Arg Gly Pro Glu Leu Glu Met						
	1090			1095		1100
Trp Ser Leu Gly Val Thr Leu Tyr Thr Leu Val Phe Glu Glu Asn Pro						
	1105			1110		1115
Phe Cys Glu Leu Glu Glu Thr Val Glu Ala Ala Ile His Pro Pro Tyr						
	1125			1130		1135
Leu Val Ser Lys Glu Leu Met Ser Leu Val Ser Gly Leu Leu Gln Pro						
	1140			1145		1150
Val Pro Glu Arg Arg Thr Thr Leu Glu Lys Leu Val Thr Asp Pro Trp						
	1155			1160		1165
Val Thr Gln Pro Val Asn Leu Ala Asp Tyr Thr Trp Glu Glu Val Phe						
	1170			1175		1180
Arg Val Asn Lys Pro Glu Ser Gly Val Leu Ser Ala Ala Ser Leu Glu						
	1185			1190		1195
Met Gly Asn Arg Ser Leu Ser Asp Val Ala Gln Ala Gln Glu Leu Cys						
	1205			1210		1215
Gly Gly Pro Val Pro Gly Glu Ala Pro Asn Gly Gln Gly Cys Leu His						

1220 1225 1230
 Pro Gly Asp Pro Arg Leu Leu Thr Ser
 1235 1240 1241

<210> 1122
 <211> 395
 <212> Amino acid
 <213> Homo sapiens

<400> 1122
 Pro Gly Thr Ser Ala Ala Thr Cys Arg Phe Leu Ser Pro Pro Val Ile
 1 5 10 15
 Ser Leu Ser Phe Thr Gly Leu Cys Ile Ser Asp Leu Val Val Ala Val
 20 25 30
 Asn Gly Val Trp Ile Leu Val Glu Thr Phe Met Leu Lys Gly Gly Asn
 35 40 45
 Phe Phe Ser Lys His Val Pro Trp Ser Tyr Leu Val Phe Leu Thr Ile
 50 55 60
 Tyr Gly Val Glu Leu Phe Leu Lys Val Ala Gly Leu Gly Pro Val Glu
 65 70 75 80
 Tyr Leu Ser Ser Gly Trp Asn Leu Phe Asp Phe Ser Val Thr Val Phe
 85 90 95
 Ala Phe Leu Gly Leu Leu Ala Leu Ala Leu Asn Met Glu Pro Phe Tyr
 100 105 110
 Phe Ile Val Val Leu Arg Pro Leu Gln Leu Leu Arg Leu Phe Lys Leu
 115 120 125
 Lys Glu Arg Tyr Arg Asn Val Leu Asp Thr Met Phe Glu Leu Leu Pro
 130 135 140
 Arg Met Ala Ser Leu Gly Leu Thr Leu Leu Ile Phe Tyr Tyr Ser Phe
 145 150 155 160
 Ala Ile Val Gly Met Glu Phe Phe Cys Gly Ile Val Phe Pro Asn Cys
 165 170 175
 Cys Asn Thr Ser Thr Val Ala Asp Ala Tyr Arg Trp Arg Asn His Thr
 180 185 190
 Val Gly Asn Arg Thr Val Val Glu Gly Tyr Tyr Tyr Leu Asn Asn
 195 200 205
 Phe Asp Asn Ile Leu Asn Ser Phe Val Thr Leu Phe Glu Leu Thr Val
 210 215 220
 Val Asn Asn Trp Tyr Ile Ile Met Glu Gly Val Thr Ser Gln Thr Ser
 225 230 235 240
 His Trp Ser Arg Leu Tyr Phe Met Thr Phe Tyr Ile Val Thr Met Val
 245 250 255
 Val Met Thr Ile Ile Val Ala Phe Ile Leu Glu Ala Phe Val Phe Arg
 260 265 270
 Met Asn Tyr Ser Arg Lys Asn Gln Asp Ser Glu Val Asp Gly Gly Ile
 275 280 285
 Thr Leu Glu Lys Glu Ile Ser Lys Glu Glu Leu Val Ala Val Leu Glu
 290 295 300
 Leu Tyr Arg Glu Ala Arg Gly Ala Ser Ser Asp Val Thr Arg Leu Leu
 305 310 315 320
 Glu Thr Leu Ser Gln Met Glu Arg Tyr Gln Gln His Ser Met Val Phe
 325 330 335
 Leu Gly Arg Arg Ser Arg Thr Lys Ser Asp Leu Ser Leu Lys Met Tyr
 340 345 350
 Gln Glu Glu Ile Gln Glu Trp Tyr Glu Glu His Ala Arg Glu Gln Glu
 355 360 365
 Gln Gln Arg Gln Leu Ser Ser Ser Ala Ala Pro Ala Ala Gln Gln Pro
 370 375 380
 Pro Gly Ser Arg Gln Arg Ser Gln Thr Val Thr

385

390

395

<210> 1123

<211> 328

<212>Amino acid

<213> Homo sapiens

<400> 1123

```

Leu Ala Gly Val Gly Thr Gln Ala Pro Pro Arg Arg Pro Gly Gly Glu
 1           5           10           15
Met Ala Ala Gly Gln Asn Gly His Glu Glu Trp Val Gly Ser Ala Tyr
      20           25           30
Leu Phe Val Glu Ser Ser Leu Asp Lys Val Val Leu Ser Asp Ala Tyr
      35           40           45
Ala His Pro Gln Gln Lys Val Ala Val Tyr Arg Ala Leu Gln Ala Ala
      50           55           60
Leu Ala Glu Ser Gly Gly Ser Pro Asp Val Leu Gln Met Leu Lys Ile
      65           70           75           80
His Arg Ser Asp Pro Gln Leu Ile Val Gln Leu Arg Phe Cys Gly Arg
      85           90           95
Gln Pro Cys Gly Arg Phe Leu Arg Ala Tyr Arg Glu Gly Ala Leu Arg
      100          105          110
Ala Ala Leu Gln Arg Ser Leu Ala Ala Leu Ala Gln His Ser Val
      115          120          125
Pro Leu Gln Leu Asp Leu Arg Ala Gly Ala Glu Arg Leu Glu Ala Leu
      130          135          140
Leu Ala Asp Glu Glu Arg Cys Leu Ser Cys Ile Leu Ala Gln Gln Pro
      145          150          155          160
Asp Arg Leu Arg Asp Glu Glu Leu Ala Glu Leu Glu Asp Ala Leu Arg
      165          170          175
Asn Leu Lys Cys Gly Ser Gly Ala Arg Gly Gly Asp Gly Glu Val Ala
      180          185          190
Ser Ala Pro Leu Gln Pro Pro Val Pro Ser Leu Ser Glu Val Lys Pro
      195          200          205
Pro Pro Pro Pro Pro Pro Ala Gln Thr Phe Leu Phe Gln Gly Gln Pro
      210          215          220
Val Val Asn Arg Pro Leu Ser Leu Lys Asp Gln Gln Thr Phe Ala Arg
      225          230          235          240
Ser Val Gly Leu Lys Trp Arg Lys Val Gly Arg Ser Leu Gln Arg Gly
      245          250          255
Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Glu Tyr
      260          265          270
Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg Arg Phe
      275          280          285
Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu Val Glu Ala
      290          295          300
Leu Glu Glu Asn Glu Leu Thr Ser Leu Ala Glu Asp Leu Leu Gly Leu
      305          310          315          320
Thr Asp Pro Asn Gly Gly Leu Ala
      325          328

```

<210> 1124

<211> 667

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(667)

<223> X = any amino acid or stop code

<400> 1124

```

Ser Ser Lys Pro Lys Leu Lys Lys Arg Phe Ser Leu Arg Ser Val Gly
 1      5      10      15
Arg Ser Val Arg Gly Ser Val Arg Gly Ile Leu Gln Trp Arg Gly Thr
      20      25      30
Val Asp Pro Pro Ser Ser Ala Gly Pro Leu Glu Thr Ser Ser Gly Pro
      35      40      45
Pro Val Leu Gly Gly Asn Ser Asn Ser Asn Ser Ser Gly Gly Ala Gly
      50      55      60
Thr Val Gly Arg Gly Leu Val Ser Asp Gly Thr Ser Pro Gly Glu Arg
      65      70      75      80
Trp Thr His Arg Phe Glu Arg Leu Arg Leu Ser Arg Gly Gly Gly Ala
      85      90      95
Leu Lys Asp Gly Ala Gly Met Val Gln Arg Glu Glu Leu Leu Ser Phe
      100      105      110
Met Gly Ala Glu Glu Ala Ala Pro Asp Pro Ala Gly Val Gly Arg Gly
      115      120      125
Gly Gly Val Ala Gly Pro Pro Ser Gly Gly Gly Gly Gln Pro Gln Trp
      130      135      140
Gln Lys Cys Arg Leu Leu Leu Arg Ser Glu Gly Glu Gly Gly Gly Gly
      145      150      155      160
Ser Arg Leu Glu Phe Val Pro Pro Lys Ala Ser Arg Pro Arg Leu
      165      170      175
Ser Ile Pro Cys Ser Ser Ile Thr Asp Val Arg Thr Thr Thr Ala Leu
      180      185      190
Glu Met Pro Asp Arg Glu Asn Thr Phe Val Val Lys Val Glu Gly Pro
      195      200      205
Ser Glu Tyr Ile Met Glu Thr Val Asp Ala Gln His Val Lys Ala Trp
      210      215      220
Val Ser Asp Ile Gln Glu Cys Leu Ser Pro Gly Pro Cys Pro Ala Thr
      225      230      235      240
Ser Pro Arg Pro Met Thr Leu Pro Leu Ala Pro Gly Thr Ser Phe Leu
      245      250      255
Thr Arg Glu Asn Thr Asp Ser Leu Glu Leu Ser Cys Leu Asn His Ser
      260      265      270
Glu Ser Leu Pro Ser Gln Asp Leu Leu Leu Gly Pro Ser Glu Ser Asn
      275      280      285
Asp Arg Leu Ser Gln Gly Ala Tyr Gly Gly Leu Ser Asp Arg Pro Ser
      290      295      300
Ala Ser Ile Ser Pro Ser Ser Ala Ser Ile Ala Ala Ser His Phe Asp
      305      310      315      320
Ser Met Glu Leu Leu Pro Pro Glu Leu Pro Pro Arg Ile Pro Ile Glu
      325      330      335
Glu Gly Pro Pro Ala Gly Thr Val His Pro Leu Ser Ala Pro Tyr Pro
      340      345      350
Pro Leu Asp Thr Pro Glu Thr Ala Thr Gly Ser Phe Leu Phe Gln Gly
      355      360      365
Glu Pro Glu Gly Gly Glu Gly Asp Gln Pro Leu Ser Gly Tyr Pro Trp
      370      375      380
Phe His Gly Met Leu Ser Arg Leu Lys Ala Ala Gln Leu Val Leu Thr
      385      390      395      400
Gly Gly Thr Gly Ser His Gly Val Phe Leu Val Arg Gln Ser Glu Thr
      405      410      415
Arg Arg Gly Glu Tyr Val Leu Thr Phe Asn Phe Gln Gly Lys Ala Lys
      420      425      430
His Leu Arg Leu Ser Leu Asn Glu Glu Gly Gln Cys Arg Val Gln His
      435      440      445

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```

Leu Trp Phe Gln Ser Ile Phe Asp Met Leu Glu His Phe Arg Val His
 450          455          460
Pro Ile Pro Leu Glu Ser Gly Gly Ser Ser Asp Val Val Leu Val Ser
465          470          475          480
Tyr Val Pro Ser Ser Gln Arg Gln Gln Gly Glu Gln Ser Arg Ser Ala
          485          490          495
Gly Glu Glu Val Pro Val His Pro Arg Ser Glu Ala Gly Ser Arg Leu
          500          505          510
Gly Ala Met Arg Gly Cys Ala Arg Glu Met Asp Ala Thr Pro Asn Ala
          515          520          525
Ser Cys Thr Leu Met Pro Phe Gly Ala Ser Asp Cys Glu Pro Thr Thr
          530          535          540
Ser His Asp Pro Pro Gln Pro Pro Glu Pro Pro Ser Trp Thr Asp Pro
545          550          555          560
Pro Gln Pro Gly Glu Glu Glu Ala Ser Arg Ala Pro Gly Ser Gly Gly
          565          570          575
Gln Gln Ala Ala Ala Ala Lys Glu Arg Gln Glu Lys Glu Lys Ala
          580          585          590
Gly Gly Gly Gly Val Pro Glu Glu Leu Val Pro Val Val Xaa Leu Val
          595          600          605
Pro Val Gly Glu Leu Gly Glu Gly His Arg Pro Gln Ala Gln Glu Ala
          610          615          620
Gln Gly Arg Leu Gly Pro Gly Gly Asp Ala Gly Val Pro Pro Met Val
625          630          635          640
Gln Leu Gln Gln Ser Pro Leu Gly Gly Asp Gly Glu Glu Gly Gly His
          645          650          655
Pro Arg Ala Ile Asn Asn Gln Tyr Ser Phe Val
          660          665          667

```

<210> 1125

<211> 387

<212>Amino acid

<213> Homo sapiens

<400> 1125

```

Phe Arg Ala Pro Val Gly Thr Ala Ala Arg Ser Pro Gln Val Val Ile
 1          5          10          15
Arg Arg Leu Pro Pro Gly Leu Thr Lys Glu Gln Leu Glu Glu Gln Leu
          20          25          30
Arg Pro Leu Pro Ala His Asp Tyr Phe Glu Phe Phe Ala Ala Asp Leu
          35          40          45
Ser Leu Tyr Pro His Leu Tyr Ser Arg Ala Tyr Ile Asn Phe Arg Asn
          50          55          60
Pro Asp Asp Ile Leu Leu Phe Arg Asp Arg Phe Asp Gly Tyr Ile Phe
          65          70          75          80
Leu Asp Ser Lys Asp Pro Glu Tyr Lys Lys Phe Leu Glu Thr Tyr Cys
          85          90          95
Val Glu Glu Glu Lys Thr Ser Ala Asn Pro Glu Thr Leu Leu Gly Glu
          100          105          110
Met Glu Ala Lys Thr Arg Glu Leu Ile Ala Arg Arg Thr Thr Pro Leu
          115          120          125
Leu Glu Tyr Ile Lys Asn Arg Lys Leu Glu Lys Gln Arg Ile Arg Glu
          130          135          140
Glu Lys Arg Glu Glu Arg Arg Arg Glu Leu Glu Lys Lys Arg Leu
145          150          155          160
Arg Glu Glu Glu Lys Arg Arg Arg Arg Glu Glu Arg Cys Lys Lys
          165          170          175
Lys Glu Thr Asp Lys Gln Lys Lys Ile Ala Glu Lys Glu Val Arg Ile
          180          185          190

```

Lys Leu Leu Lys Lys Pro Glu Lys Gly Glu Glu Pro Thr Thr Glu Lys
 195 200 205
 Pro Lys Glu Arg Gly Glu Glu Ile Asp Thr Gly Gly Gly Lys Gln Glu
 210 215 220
 Ser Cys Ala Pro Gly Ala Val Val Lys Ala Arg Pro Met Glu Gly Ser
 225 230 235 240
 Leu Glu Glu Pro Gln Glu Thr Ser His Ser Gly Ser Asp Lys Glu His
 245 250 255
 Arg Asp Val Glu Arg Ser Gln Glu Gln Glu Ser Glu Ala Gln Arg Tyr
 260 265 270
 His Val Asp Asp Gly Arg Arg His Arg Ala His His Glu Pro Glu Arg
 275 280 285
 Leu Ser Arg Arg Ser Glu Asp Glu Gln Arg Trp Gly Lys Gly Pro Gly
 290 295 300
 Gln Asp Arg Gly Lys Lys Gly Ser Gln Asp Ser Gly Ala Pro Gly Glu
 305 310 315 320
 Ala Met Glu Arg Leu Gly Arg Ala Gln Arg Cys Asp Asp Ser Pro Ala
 325 330 335
 Pro Arg Lys Glu Arg Leu Ala Asn Lys Asp Arg Pro Ala Leu Gln Leu
 340 345 350
 Tyr Asp Pro Gly Ala Arg Phe Arg Ala Arg Glu Cys Gly Gly Asn Arg
 355 360 365
 Arg Ile Cys Lys Ala Glu Gly Ser Gly Thr Gly Pro Glu Lys Arg Glu
 370 375 380
 Glu Ala Glu
 385 387

<210> 1126

<211> 208

<212> Amino acid

<213> Homo sapiens

<400> 1126

Gly Val Trp Gly Val Cys Val Ser Gly Leu Leu Gln Val Gly Ser Gln
 1 5 10 15
 Arg Ala Gln Ala Trp Arg Ala Trp Ser Pro Met Glu Thr Pro Leu Thr
 20 25 30
 Gly Thr Phe Leu Trp Pro His Ile Pro Gln Gly Leu Phe Phe Asp Asp
 35 40 45
 Ser Tyr Gly Phe Tyr Pro Gly Gln Val Leu Ile Gly Pro Ala Lys Ile
 50 55 60
 Phe Ser Ser Val Gln Trp Leu Ser Gly Val Lys Pro Val Leu Ser Thr
 65 70 75 80
 Lys Ser Lys Phe Arg Val Val Val Glu Glu Val Gln Val Val Glu Leu
 85 90 95
 Lys Val Thr Trp Ile Thr Lys Ser Phe Cys Pro Gly Gly Thr Asp Ser
 100 105 110
 Val Ser Pro Pro Pro Ser Val Ile Thr Gln Glu Asn Leu Gly Arg Val
 115 120 125
 Lys Arg Leu Gly Cys Phe Asp His Ala Gln Arg His Ala Trp Gly Ala
 130 135 140
 Leu Ser Val Cys Leu Pro Ser Gln Gly Arg Ala Ser Gln Asp Cys Leu
 145 150 155 160
 Gly Met Ser Arg Lys Lys Leu Arg Pro Gly Gly Gly Leu Tyr Gly Gln
 165 170 175
 Glu Gly Glu Ala Pro Val Glu Glu Ala Gly Cys Ala Asp His Val Met
 180 185 190
 Leu Pro Arg His Pro Val Phe Pro Gly Pro Phe His Gly Arg Pro Arg
 195 200 205 208

<210> 1127
 <211> 670
 <212> Amino acid
 <213> Homo sapiens

<400> 1127
 Phe Arg Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys Leu Ser
 1 5 10 15
 Gly Glu Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro Asp Cys
 20 25 30
 Lys Asp Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys Arg Pro
 35 40 45
 Asp Glu Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser Arg Gln
 50 55 60
 Cys Asp Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val Gly Cys
 65 70 75 80
 Val Asn Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys His Ser
 85 90 95
 Gly Glu Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg Asp Cys
 100 105 110
 Arg Asp Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn Glu Cys
 115 120 125
 Leu Asp Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu Lys Ile
 130 135 140
 Gly Tyr Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala Gln Arg
 145 150 155 160
 Arg Cys Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys Ser Gln
 165 170 175
 Leu Cys Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu Glu Gly
 180 185 190
 Phe Gln Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly Ser Ile
 195 200 205
 Ala Tyr Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met Thr Leu
 210 215 220
 Asp Arg Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn Val Val
 225 230 235 240
 Ala Leu Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser Asp Leu
 245 250 255
 Ser Gln Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val
 260 265 270
 Ser Ser Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly
 275 280 285
 Leu Ala Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp Ser Val
 290 295 300
 Leu Gly Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg Lys Thr
 305 310 315 320
 Leu Phe Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val Asp Pro
 325 330 335
 Val His Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile
 340 345 350
 Lys Lys Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu
 355 360 365
 Asn Ile Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser Gly Arg
 370 375 380
 Leu Tyr Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile Asp Val
 385 390 395 400

Asn Gly Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg Leu Ala
 405 410 415
 His Pro Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp
 420 425 430
 Ile Ile Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp
 435 440 445
 Val Asn Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met Val Leu
 450 455 460
 Phe His Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu Arg Thr
 465 470 475 480
 Thr Leu Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala Pro Gln
 485 490 495
 Ile Asn Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met
 500 505 510
 Leu Leu Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Gly Glu Ala Ala
 515 520 525
 Val Ala Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser Ser Thr
 530 535 540
 Ala Val Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp Thr Ser
 545 550 555 560
 Arg Leu Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr
 565 570 575
 Met Ser His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys
 580 585 590
 Lys Pro Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu
 595 600 605
 Leu Val Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg
 610 615 620
 Leu Lys Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys
 625 630 635 640
 Thr Thr Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly Tyr Ser
 645 650 655
 Tyr Pro Ser Arg Gln Met Val Ser Leu Glu Asp Asp Val Ala
 660 665 670

<210> 1128

<211> 383

<212> Amino acid

<213> Homo sapiens

<400> 1128

Arg Ile Pro Gly Leu Gly Pro Pro Gly Ser Pro Pro Pro Pro Pro His
 1 5 10 15
 Val Arg Gly Met Pro Gly Cys Pro Cys Pro Gly Cys Gly Met Ala Gly
 20 25 30
 Pro Arg Leu Leu Phe Leu Thr Ala Leu Ala Leu Glu Leu Leu Gly Arg
 35 40 45
 Ala Gly Gly Ser Gln Pro Ala Leu Arg Ser Arg Gly Thr Ala Thr Ala
 50 55 60
 Cys Arg Leu Asp Asn Lys Glu Ser Glu Ser Trp Gly Ala Leu Leu Ser
 65 70 75 80
 Gly Glu Arg Leu Asp Thr Trp Ile Cys Ser Leu Leu Gly Ser Leu Met
 85 90 95
 Val Gly Leu Ser Gly Val Phe Pro Leu Leu Val Ile Pro Leu Glu Met
 100 105 110
 Gly Thr Met Leu Arg Ser Glu Ala Gly Ala Trp Arg Leu Lys Gln Leu
 115 120 125
 Leu Ser Phe Ala Leu Gly Gly Leu Leu Gly Asn Val Phe Leu His Leu
 130 135 140

Leu Pro Glu Ala Trp Ala Tyr Thr Cys Ser Ala Ser Pro Gly Gly Glu
 145 150 155 160
 Gly Gln Ser Leu Gln Gln Gln Gln Gln Leu Gly Leu Trp Val Ile Ala
 165 170 175
 Gly Ile Leu Thr Phe Leu Ala Leu Glu Lys Met Phe Leu Asp Ser Lys
 180 185 190
 Glu Glu Gly Thr Ser Gln Ala Pro Asn Lys Asp Pro Thr Ala Ala Ala
 195 200 205
 Ala Ala Leu Asn Gly Gly His Cys Leu Ala Gln Pro Ala Ala Glu Pro
 210 215 220
 Gly Leu Gly Ala Val Val Arg Ser Ile Lys Val Ser Gly Tyr Leu Asn
 225 230 235 240
 Leu Leu Ala Asn Thr Ile Asp Asn Phe Thr His Gly Leu Ala Val Ala
 245 250 255
 Ala Ser Phe Leu Val Ser Lys Lys Ile Gly Leu Leu Thr Thr Met Ala
 260 265 270
 Ile Leu Leu His Glu Ile Pro His Glu Val Gly Asp Phe Ala Ile Leu
 275 280 285
 Leu Arg Ala Gly Phe Asp Arg Trp Ser Ala Ala Lys Leu Gln Leu Ser
 290 295 300
 Thr Ala Leu Gly Gly Leu Leu Gly Ala Gly Phe Ala Ile Cys Thr Gln
 305 310 315 320
 Ser Pro Lys Gly Val Glu Glu Thr Ala Ala Trp Val Leu Pro Phe Thr
 325 330 335
 Ser Gly Gly Phe Leu Tyr Ile Ala Leu Val Asn Val Leu Pro Asp Leu
 340 345 350
 Leu Glu Glu Glu Asp Pro Trp Arg Ser Leu Gln Gln Leu Leu Leu Leu
 355 360 365
 Cys Ala Gly Ile Val Val Met Val Leu Phe Ser Leu Phe Val Asp
 370 375 380 383

<210> 1129

<211> 174

<212> Amino acid

<213> Homo sapiens

<400> 1129

Gly Lys Val Ser Ala Gly Gln Ala Gly Ala Asp Arg Thr Leu Arg Arg
 1 5 10 15
 Ala Pro Glu Pro Arg Phe Ser Gln Glu Pro Thr Gly Asn Ser Ala Tyr
 20 25 30
 Pro Gln Leu Arg Pro Phe Leu Asp Pro Gln Gly Arg Asp Leu Lys Pro
 35 40 45
 Ser Ala Leu Val Pro Pro Thr Arg Ser His Thr Gly Arg Arg Pro Trp
 50 55 60
 Leu His Thr Gln Pro Leu Pro Gly Pro Gln Gly Arg Ala Trp Gly Pro
 65 70 75 80
 Thr Cys Thr Pro Ala Cys Val Asp Arg Val Leu Glu Ser Glu Glu Gly
 85 90 95
 Arg Arg Glu Tyr Leu Ala Phe Pro Thr Ser Lys Ser Ser Gly Gln Lys
 100 105 110
 Gly Arg Lys Glu Leu Leu Lys Gly Asn Gly Arg Arg Ile Asp Tyr Met
 115 120 125
 Leu His Ala Glu Glu Gly Leu Cys Pro Asp Trp Lys Ala Glu Val Glu
 130 135 140
 Glu Phe Ser Phe Ile Thr Gln Leu Ser Gly Leu Thr Asp His Leu Pro
 145 150 155 160
 Val Ala Met Arg Leu Met Val Ser Ser Gly Glu Glu Glu Ala
 165 170 174

<210> 1130
 <211> 231
 <212>Amino acid
 <213> Homo sapiens

<400> 1130
 Pro Cys Gly Gly Ile Arg Leu Ser Ala Ser Glu Ala Ala Thr Leu Phe
 1 5 10 15
 Gly Tyr Leu Val Val Pro Ala Gly Gly Gly Thr Phe Leu Gly Gly
 20 25 30
 Phe Phe Val Asn Lys Leu Arg Leu Arg Gly Ser Ala Val Ile Lys Phe
 35 40 45
 Cys Leu Phe Cys Thr Val Val Ser Leu Leu Gly Ile Leu Val Phe Ser
 50 55 60
 Leu His Cys Pro Ser Val Pro Met Ala Gly Val Thr Ala Ser Tyr Gly
 65 70 75 80
 Gly Ser Leu Leu Pro Glu Gly His Leu Asn Leu Thr Ala Pro Cys Asn
 85 90 95
 Ala Ala Cys Ser Cys Gln Pro Glu His Tyr Ser Pro Val Cys Gly Ser
 100 105 110
 Asp Gly Leu Met Tyr Phe Ser Leu Cys His Ala Gly Cys Pro Ala Ala
 115 120 125
 Thr Glu Thr Asn Val Asp Gly Gln Lys Val Ser Gly Ala Ala Ala Tyr
 130 135 140
 Arg Pro Cys Pro Pro Leu Asp Pro Gly Lys Gly Pro Pro Cys Leu Pro
 145 150 155 160
 Leu Val Ile Gly Ala Ile Val Gly Leu Pro Arg Cys Thr Glu Thr Val
 165 170 175
 Ala Val Ser Leu Arg Ile Phe Pro Leu Val Leu Ala Met His Cys Arg
 180 185 190
 Glu Met His Phe Asn Leu Ser Glu Lys Ala Pro Pro Ser Gly Phe His
 195 200 205
 Ile Arg Cys Asn Phe Leu Tyr Ile Pro Gln Gln His Ser Cys Thr Asn
 210 215 220
 Gly Asn Ser Thr Met Cys Pro
 225 230 231

<210> 1131
 <211> 234
 <212>Amino acid
 <213> Homo sapiens

<400> 1131
 Leu Leu Arg Lys Val Gly Ala Pro Gly Gly Ala Arg Gly Val Ile Arg
 1 5 10 15
 Leu Leu Asp Trp Phe Glu Arg Pro Asp Gly Phe Leu Leu Val Leu Glu
 20 25 30
 Arg Pro Glu Pro Ala Gln Asp Leu Phe Asp Phe Ile Thr Glu Arg Gly
 35 40 45
 Ala Leu Asp Glu Pro Leu Ala Arg Arg Phe Phe Ala Gln Val Leu Ala
 50 55 60
 Ala Val Arg His Cys His Ser Cys Gly Val Val His Arg Asp Ile Lys
 65 70 75 80

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Asp Glu Asn Leu Leu Val Asp Leu Arg Ser Gly Glu Leu Lys Leu Ile
      85                      90                      95
Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe
      100                      105                      110
Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp Ile Arg Tyr His Arg
      115                      120                      125
Tyr His Gly Arg Ser Ala Thr Val Trp Ser Leu Gly Val Leu Leu Tyr
      130                      135                      140
Asp Met Val Cys Gly Asp Ile Pro Phe Glu Gln Asp Glu Glu Ile Leu
      145                      150                      155                      160
Arg Gly Arg Leu Leu Phe Arg Arg Arg Val Ser Pro Glu Cys Gln Gln
      165                      170                      175
Leu Ile Arg Trp Cys Leu Ser Leu Arg Pro Ser Glu Arg Pro Ser Leu
      180                      185                      190
Asp Gln Ile Ala Ala His Pro Trp Met Leu Gly Ala Asp Gly Gly Ala
      195                      200                      205
Pro Glu Ser Cys Asp Leu Arg Leu Cys Thr Leu Asp Pro Asp Asp Val
      210                      215                      220
Ala Ser Thr Thr Ser Ser Ser Glu Ser Leu
      225                      230                      234

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<210> 1132
<211> 270
<212>Amino acid
<213> Homo sapiens

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<400> 1132
Gly Lys Asn Ser Gln Lys Ala Ser Pro Val Asp Asp Glu Gln Leu Ser
  1      5      10      15
Val Cys Leu Ser Gly Phe Leu Asp Glu Val Met Lys Lys Tyr Gly Ser
      20      25      30
Leu Val Pro Leu Ser Glu Lys Glu Val Leu Gly Arg Leu Lys Asp Val
      35      40      45
Phe Asn Glu Asp Phe Ser Asn Arg Lys Pro Phe Ile Asn Arg Glu Ile
      50      55      60
Thr Asn Tyr Arg Ala Arg His Gln Lys Cys Asn Phe Arg Ile Phe Tyr
      65      70      75      80
Asn Lys His Met Leu Asp Met Asp Asp Leu Ala Thr Leu Asp Gly Gln
      85      90      95
Asn Trp Leu Asn Asp Gln Val Ile Asn Met Tyr Gly Glu Leu Ile Met
      100      105      110
Asp Ala Val Pro Asp Lys Val His Phe Phe Asn Ser Phe Phe His Arg
      115      120      125
Gln Leu Val Thr Lys Gly Tyr Asn Gly Val Lys Arg Trp Thr Lys Lys
      130      135      140
Val Asp Leu Phe Lys Lys Ser Leu Leu Leu Ile Pro Ile His Leu Glu
      145      150      155      160
Val His Trp Ser Leu Ile Thr Val Thr Leu Ser Asn Arg Ile Ile Ser
      165      170      175
Phe Tyr Asp Ser Gln Gly Ile His Phe Lys Phe Cys Val Glu Asn Ile
      180      185      190
Arg Lys Tyr Leu Leu Thr Glu Ala Arg Glu Lys Asn Arg Leu Asn Leu
      195      200      205
Gln Gly Trp Gln Thr Ala Val Thr Lys Cys Ile Pro Gln Gln Lys Asn
      210      215      220
Asp Ser Asp Cys Gly Val Phe Val Leu Gln Tyr Cys Lys Cys Leu Ala
      225      230      235      240
Leu Lys Gln Pro Phe Gln Phe Ser Gln Glu Asp Met Pro Arg Val Arg
      245      250      255

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Lys Arg Ile Tyr Lys Glu Leu Cys Glu Cys Arg Leu Met Asp
 260 265 270

<210> 1133
 <211> 204
 <212>Amino acid
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(204)
 <223> X = any amino acid or stop code

<400> 1133
 Pro Pro Gly Gly Xaa Gln Gly Ser Ala Ala Lys His Arg Phe Pro Lys
 1 5 10 15
 Gly Tyr Arg His Pro Ala Leu Glu Ala Arg Leu Gly Arg Arg Arg Thr
 20 25 30
 Val Gln Glu Ala Arg Ala Leu Leu Arg Cys Arg Arg Ala Gly Ile Ser
 35 40 45
 Ala Pro Val Val Phe Phe Val Asp Tyr Ala Ser Asn Cys Leu Tyr Met
 50 55 60
 Glu Glu Ile Glu Gly Ser Val Thr Val Arg Asp Tyr Ile Gln Ser Thr
 65 70 75 80
 Met Glu Thr Glu Lys Thr Pro Gln Gly Leu Ser Asn Leu Ala Lys Thr
 85 90 95
 Ile Gly Gln Val Leu Ala Arg Met His Asp Glu Asp Leu Ile His Gly
 100 105 110
 Asp Leu Thr Thr Ser Asn Met Leu Leu Lys Pro Pro Leu Glu Gln Leu
 115 120 125
 Asn Ile Val Leu Ile Asp Phe Gly Leu Ser Phe Ile Ser Ala Leu Pro
 130 135 140
 Glu Asp Lys Gly Val Asp Leu Tyr Val Leu Glu Lys Ala Phe Leu Ser
 145 150 155 160
 Thr His Pro Asn Thr Glu Thr Val Phe Glu Ala Phe Leu Lys Ser Tyr
 165 170 175
 Ser Thr Ser Ser Lys Lys Ala Arg Pro Val Leu Lys Lys Leu Asp Glu
 180 185 190
 Val Arg Leu Arg Gly Lys Lys Arg Ser Met Val Gly
 195 200 204

<210> 1134
 <211> 531
 <212>Amino acid
 <213> Homo sapiens

<400> 1134
 Arg Ala Cys Val Phe Arg Pro Glu Asp Met Met Gln Gly Glu Ala His
 1 5 10 15
 Pro Ser Ala Ser Leu Ile Asp Arg Thr Ile Lys Met Arg Lys Glu Thr
 20 25 30
 Glu Ala Arg Lys Val Val Leu Ala Trp Gly Leu Leu Asn Val Ser Met
 35 40 45
 Ala Gly Met Ile Tyr Thr Glu Met Thr Gly Lys Leu Ile Ser Ser Tyr

	50						55						60					
Tyr 65	Asn	Val	Thr	Tyr	Trp	Pro	Leu	Trp	Tyr	Ile	Glu	Leu	Ala	Leu	Ala			
Ser	Leu	Phe	Ser	Leu	Asn	Ala	Leu	Phe	Asp	Phe	Trp	Arg	Tyr	Phe	Lys			
				85					90					95				
Tyr	Thr	Val	Ala	Pro	Thr	Ser	Leu	Val	Val	Ser	Pro	Gly	Gln	Gln	Thr			
			100					105					110					
Leu	Leu	Gly	Leu	Lys	Thr	Ala	Val	Val	Gln	Thr	Thr	Pro	Pro	His	Asp			
		115					120					125						
Leu	Ala	Ala	Thr	Gln	Ile	Pro	Pro	Ala	Pro	Pro	Ser	Pro	Ser	Ile	Gln			
	130					135					140							
Gly	Gln	Ser	Val	Leu	Ser	Tyr	Ser	Pro	Ser	Arg	Ser	Pro	Ser	Thr	Ser			
145					150					155					160			
Pro	Lys	Phe	Thr	Thr	Ser	Cys	Met	Thr	Gly	Tyr	Ser	Pro	Gln	Leu	Gln			
			165						170					175				
Gly	Leu	Ser	Ser	Gly	Gly	Ser	Gly	Ser	Tyr	Ser	Pro	Gly	Val	Thr	Tyr			
			180					185					190					
Ser	Pro	Val	Ser	Gly	Tyr	Asn	Lys	Leu	Ala	Ser	Phe	Ser	Pro	Ser	Pro			
		195				200						205						
Pro	Ser	Pro	Tyr	Pro	Thr	Thr	Val	Gly	Pro	Val	Glu	Ser	Ser	Gly	Leu			
	210					215					220							
Arg	Ser	Arg	Tyr	Arg	Ser	Ser	Pro	Thr	Val	Tyr	Asn	Ser	Pro	Thr	Asp			
225					230					235					240			
Lys	Glu	Asp	Tyr	Met	Thr	Asp	Leu	Arg	Thr	Leu	Asp	Thr	Phe	Leu	Arg			
			245						250					255				
Ser	Glu	Glu	Glu	Lys	Gln	His	Arg	Val	Lys	Leu	Gly	Ser	Pro	Asp	Ser			
			260					265					270					
Thr	Ser	Pro	Ser	Ser	Ser	Pro	Thr	Phe	Trp	Asn	Tyr	Ser	Arg	Ser	Met			
		275				280						285						
Gly	Asp	Tyr	Ala	Gln	Thr	Leu	Lys	Lys	Phe	Gln	Tyr	Gln	Leu	Ala	Cys			
	290					295				300								
Arg	Ser	Gln	Ala	Pro	Cys	Ala	Asn	Lys	Asp	Glu	Ala	Asp	Leu	Ser	Ser			
305					310					315					320			
Lys	Gln	Ala	Ala	Glu	Glu	Val	Trp	Ala	Arg	Val	Ala	Met	Asn	Arg	Gln			
			325						330					335				
Leu	Leu	Asp	His	Met	Asp	Ser	Trp	Thr	Ala	Lys	Phe	Arg	Asn	Trp	Ile			
			340					345					350					
Asn	Glu	Thr	Ile	Leu	Val	Pro	Leu	Val	Gln	Glu	Ile	Glu	Ser	Val	Ser			
		355				360						365						
Thr	Gln	Met	Arg	Arg	Met	Gly	Cys	Pro	Glu	Leu	Gln	Ile	Gly	Glu	Ala			
	370					375					380							
Ser	Ile	Thr	Ser	Leu	Lys	Gln	Ala	Ala	Leu	Val	Lys	Ala	Pro	Leu	Ile			
385					390					395					400			
Pro	Thr	Leu	Asn	Thr	Ile	Val	Gln	Tyr	Leu	Asp	Leu	Thr	Pro	Asn	Gln			
			405						410					415				
Glu	Tyr	Leu	P															

<210> 1135

<211> 508
 <212> Amino acid
 <213> Homo sapiens

<400> 1135
 Ser Ser Ala Val Glu Phe Ile Asn Arg Asn Asn Ser Val Val Gln Val
 1 5 10 15
 Leu Leu Ala Ala Gly Ala Asp Pro Asn Leu Gly Asp Asp Phe Ser Ser
 20 25 30
 Val Tyr Lys Thr Ala Lys Glu Gln Gly Ile His Ser Leu Glu Val Leu
 35 40 45
 Ile Thr Arg Glu Asp Asp Phe Asn Asn Arg Leu Asn Asn Arg Ala Ser
 50 55 60
 Phe Lys Gly Cys Thr Ala Leu His Tyr Ala Val Leu Ala Asp Asp Tyr
 65 70 75 80
 Arg Thr Val Lys Glu Leu Leu Asp Gly Gly Ala Asn Pro Leu Gln Arg
 85 90 95
 Asn Glu Met Gly His Thr Pro Leu Asp Tyr Ala Arg Glu Gly Glu Val
 100 105 110
 Met Lys Leu Leu Arg Thr Ser Glu Ala Lys Tyr Gln Glu Lys Gln Arg
 115 120 125
 Lys Arg Glu Ala Glu Glu Arg Arg Arg Phe Pro Leu Glu Gln Arg Leu
 130 135 140
 Lys Glu His Ile Ile Gly Gln Glu Ser Ala Ile Ala Thr Val Gly Ala
 145 150 155 160
 Ala Ile Arg Arg Lys Glu Asn Gly Trp Tyr Asp Glu Glu His Pro Leu
 165 170 175
 Val Phe Leu Phe Leu Gly Ser Ser Gly Ile Gly Lys Thr Glu Leu Ala
 180 185 190
 Lys Gln Thr Ala Lys Tyr Met His Lys Asp Ala Lys Lys Gly Phe Ile
 195 200 205
 Arg Leu Asp Met Ser Glu Phe Gln Glu Arg His Glu Val Ala Lys Phe
 210 215 220
 Ile Gly Ser Pro Pro Gly Tyr Val Gly His Glu Glu Gly Gly Gln Leu
 225 230 235 240
 Thr Lys Lys Leu Lys Gln Cys Pro Asn Ala Val Val Leu Phe Asp Glu
 245 250 255
 Val Asp Lys Ala His Pro Asp Val Leu Thr Ile Met Leu Gln Leu Phe
 260 265 270
 Asp Glu Gly Arg Leu Thr Asp Gly Lys Gly Lys Thr Ile Asp Cys Lys
 275 280 285
 Asp Ala Ile Phe Ile Met Thr Ser Asn Val Ala Ser Asp Glu Ile Ala
 290 295 300
 Gln His Ala Leu Gln Leu Arg Gln Glu Ala Leu Glu Met Ser Arg Asn
 305 310 315 320
 Arg Ile Ala Glu Asn Leu Gly Asp Val Gln Ile Ser Asp Lys Ile Thr
 325 330 335
 Ile Ser Lys Asn Phe Lys Glu Asn Val Ile Arg Pro Ile Leu Lys Ala
 340 345 350
 His Phe Arg Arg Asp Glu Phe Leu Gly Arg Ile Asn Glu Ile Val Tyr
 355 360 365
 Phe Leu Pro Phe Cys His Ser Glu Leu Ile Gln Leu Val Asn Lys Glu
 370 375 380
 Leu Asn Phe Trp Ala Lys Arg Ala Lys Gln Arg His Asn Ile Thr Leu
 385 390 395 400
 Leu Trp Asp Arg Glu Val Ala Asp Val Leu Val Asp Gly Tyr Asn Val
 405 410 415
 His Tyr Gly Ala Arg Ser Ile Lys His Glu Val Glu Arg Arg Val Gly
 420 425 430
 Asn Gln Leu Ala Ala Ala Tyr Glu Gln Asp Leu Leu Pro Gly Gly Cys

435	440	445
Thr Leu Arg Ile Thr Val Glu Asp Ser Asp Lys Gln Leu Leu Lys Ser		
450	455	460
Pro Glu Leu Pro Ser Pro Gln Ala Glu Lys Arg Leu Pro Lys Leu Arg		
465	470	475
Leu Glu Ile Ile Asp Lys Asp Ser Lys Thr Arg Arg Leu Asp Ile Arg		480
	485	490
Ala Pro Leu His Pro Glu Lys Val Cys Asn Thr Ile		495
500	505	508

<210> 1136
 <211> 81
 <212> Amino acid
 <213> Homo sapiens

<400> 1136
Ser Ser Cys Asp Arg Glu Arg His Gly Ser Leu Gly Met Met Ser Gly
1 5 10 15
Ser Phe Ile Leu Cys Leu Ala Leu Val Thr Arg Trp Ser Pro Gln Ala
20 25 30
Ser Ser Val Pro Leu Ala Val Tyr Glu Ser Lys Thr Arg Lys Ser Tyr
35 40 45
Arg Ser Gln Arg Asp Arg Asp Gly Lys Asp Arg Ser Gln Gly Met Gly
50 55 60
Leu Ser Leu Leu Val Glu Thr Arg Lys Leu Leu Leu Ser Ala Asn Gln
65 70 75 80
Gly
81

<210> 1137
 <211> 260
 <212> Amino acid
 <213> Homo sapiens

<400> 1137
His Thr Pro Met Ala Phe Phe Leu Ser Phe Leu Ser Thr Ser Glu Thr
1 5 10 15
Val Tyr Thr Phe Val Ile Leu Pro Lys Met Leu Ile Asn Leu Leu Ser
20 25 30
Val Ala Arg Thr Ile Ser Phe Asn Cys Cys Ala Leu Gln Met Phe Phe
35 40 45
Phe Leu Gly Phe Ala Ile Thr Asn Cys Leu Leu Leu Gly Val Met Gly
50 55 60
Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu His Tyr Pro Thr Leu
65 70 75 80
Met Ser Trp Gln Val Cys Gly Lys Leu Ala Ala Ala Cys Ala Ile Gly
85 90 95
Gly Phe Leu Ala Ser Leu Thr Val Val Asn Leu Val Phe Ser Leu Pro
100 105 110
Phe Cys Ser Thr Asn Lys Val Asn His Tyr Phe Cys Asp Ile Ser Ala
115 120 125
Val Ile Leu Leu Ala Cys Thr Asn Thr Asp Val Asn Gly Phe Val Ile
130 135 140
Phe Ile Cys Gly Val Leu Val Leu Val Val Pro Phe Leu Phe Ile Cys

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145          150          155          160
Val Ser Tyr Phe Cys Ile Leu Arg Thr Ile Leu Lys Ile Pro Ser Ala
          165          170          175
Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser Val
          180          185          190
Val Ile Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr
          195          200          205
Ala Asn Tyr Val Ser Asn Lys Asp Arg Leu Val Thr Val Thr Tyr Thr
          210          215          220
Ile Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Leu Arg Asn Lys
225          230          235          240
Asp Val Gln Leu Ala Ile Arg Lys Val Leu Gly Lys Lys Gly Ser Leu
          245          250          255
Lys Leu Tyr Asn
          260

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<210> 1138
<211> 393
<212>Amino acid
<213> Homo sapiens

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<400> 1138
Arg Pro Pro Ala Ala Thr Arg Tyr Pro Arg Glu Lys Leu Lys Ser Met
 1          5          10          15
Thr Ser Arg Asp Asn Tyr Lys Ala Gly Ser Arg Glu Ala Ala Ala Ala
          20          25          30
Ala Ala Ala Ala Val Ala Ala Ala Ala Ala Ala Ala Ala Ala Glu
          35          40          45
Pro Tyr Pro Val Ser Gly Ala Lys Arg Lys Tyr Leu Glu Asp Ser Asp
          50          55          60
Pro Glu Arg Ser Asp Tyr Glu Glu Gln Gln Leu Gln Glu Glu Glu Glu
          65          70          75          80
Ala Arg Lys Val Lys Ser Gly Ile Arg Gln Met Arg Leu Phe Ser Gln
          85          90          95
Asp Glu Cys Ala Lys Ile Glu Ala Arg Ile Asp Glu Val Val Ser Arg
          100          105          110
Ala Glu Lys Gly Leu Tyr Asn Glu His Thr Val Asp Arg Ala Pro Leu
          115          120          125
Arg Asn Lys Tyr Phe Phe Gly Glu Gly Tyr Thr Tyr Gly Ala Gln Leu
          130          135          140
Gln Lys Arg Gly Pro Gly Gln Glu Arg Leu Tyr Pro Pro Gly Asp Val
145          150          155          160
Asp Glu Ile Pro Glu Trp Val His Gln Leu Val Ile Gln Lys Leu Val
          165          170          175
Glu His Arg Val Ile Pro Glu Gly Phe Val Asn Ser Ala Val Ile Asn
          180          185          190
Asp Tyr Gln Pro Gly Gly Cys Ile Val Ser His Val Asp Pro Ile His
          195          200          205
Ile Phe Glu Arg Pro Ile Val Ser Val Ser Phe Phe Ser Asp Ser Ala
          210          215          220
Leu Cys Phe Gly Cys Lys Phe Gln Phe Lys Pro Ile Arg Val Ser Glu
225          230          235          240
Pro Val Leu Ser Leu Pro Val Arg Arg Gly Ser Val Thr Val Leu Ser
          245          250          255
Gly Tyr Ala Ala Asp Glu Ile Thr His Cys Ile Arg Pro Gln Asp Ile
          260          265          270
Lys Glu Arg Arg Ala Val Ile Ile Leu Arg Lys Thr Arg Leu Asp Ala
          275          280          285
Pro Arg Leu Glu Thr Lys Ser Leu Ser Ser Ser Val Leu Pro Pro Ser

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290 295 300
 Tyr Ala Ser Asp Arg Leu Ser Gly Asn Asn Arg Asp Pro Ala Leu Lys
 305 310 315 320
 Pro Lys Arg Ser His Arg Lys Ala Asp Pro Asp Ala Ala His Arg Pro
 325 330 335
 Arg Ile Leu Glu Met Asp Lys Glu Glu Asn Arg Arg Ser Val Leu Leu
 340 345 350
 Pro Thr His Arg Arg Arg Gly Ser Phe Ser Ser Glu Asn Tyr Trp Arg
 355 360 365
 Lys Ser Tyr Glu Ser Ser Glu Asp Cys Ser Glu Ala Ala Gly Ser Pro
 370 375 380
 Ala Arg Lys Val Lys Met Arg Arg His
 385 390 393

<210> 1139
 <211> 545
 <212> Amino acid
 <213> Homo sapiens

<400> 1139
 Val Thr Trp His Phe Tyr Phe Cys Ser Asp His Lys Asn Gly His Tyr
 1 5 10 15
 Ile Ile Pro Gln Met Ala Asp Arg Ser Arg Gln Lys Cys Met Ser Gln
 20 25 30
 Ser Leu Asp Leu Ser Glu Leu Ala Lys Ala Ala Lys Lys Lys Leu Gln
 35 40 45
 Ala Leu Ser Asn Arg Leu Phe Glu Glu Leu Ala Met Asp Val Tyr Asp
 50 55 60
 Glu Val Asp Arg Arg Glu Asn Asp Ala Val Trp Leu Ala Thr Gln Asn
 65 70 75 80
 His Ser Thr Leu Val Thr Glu Arg Ser Ala Val Pro Phe Leu Pro Val
 85 90 95
 Asn Pro Glu Tyr Ser Ala Thr Arg Asn Gln Gly Arg Gln Lys Leu Ala
 100 105 110
 Arg Phe Asn Ala Arg Glu Phe Ala Thr Leu Ile Ile Asp Ile Leu Ser
 115 120 125
 Glu Ala Lys Arg Arg Gln Gln Gly Lys Ser Leu Ser Ser Pro Thr Asp
 130 135 140
 Asn Leu Glu Leu Ser Leu Arg Ser Gln Ser Asp Leu Asp Asp Gln His
 145 150 155 160
 Asp Tyr Asp Ser Val Ala Ser Asp Glu Asp Thr Asp Gln Glu Pro Leu
 165 170 175
 Arg Ser Thr Gly Ala Thr Arg Ser Asn Arg Ala Arg Ser Met Asp Ser
 180 185 190
 Ser Asp Leu Ser Asp Gly Ala Val Thr Leu Gln Glu Tyr Leu Glu Leu
 195 200 205
 Lys Lys Ala Leu Ala Thr Ser Glu Ala Lys Val Gln Gln Leu Met Lys
 210 215 220
 Val Asn Ser Ser Leu Ser Asp Glu Leu Arg Arg Leu Gln Arg Glu His
 225 230 235 240
 Phe Ala Pro Ile Ile His Lys Leu Gln Ala Glu Asn Leu Gln Leu Arg
 245 250 255
 Gln Pro Pro Gly Pro Val Pro Thr Pro Pro Leu Pro Ser Glu Arg Ala
 260 265 270
 Glu His Thr Pro Met Ala Pro Gly Ser Thr His Arg Arg Asp Arg
 275 280 285
 Gln Ala Phe Ser Met Tyr Glu Pro Gly Ser Ala Leu Lys Pro Phe Gly
 290 295 300
 Gly Pro Pro Gly Asp Glu Leu Thr Thr Arg Leu Gln Pro Phe His Ser

305 310 315 320
 Thr Glu Leu Glu Asp Asp Ala Ile Tyr Ser Val His Val Pro Ala Gly
 325 330 335
 Leu Tyr Arg Ile Arg Lys Gly Val Ser Ala Ser Ala Val Pro Phe Thr
 340 345 350
 Pro Ser Ser Pro Leu Leu Ser Cys Ser Gln Glu Gly Ser Arg His Thr
 355 360 365
 Ser Lys Leu Ser Arg His Gly Ser Gly Ala Asp Ser Asp Tyr Glu Asn
 370 375 380
 Thr Gln Ser Gly Asp Pro Leu Leu Gly Leu Glu Gly Lys Arg Phe Leu
 385 390 395 400
 Glu Leu Gly Lys Glu Glu Asp Phe His Pro Glu Leu Glu Ser Leu Asp
 405 410 415
 Gly Asp Leu Asp Pro Gly Leu Pro Ser Thr Glu Asp Val Ile Leu Lys
 420 425 430
 Thr Glu Gln Val Thr Lys Asn Ile Gln Glu Leu Leu Arg Ala Ala Gln
 435 440 445
 Glu Phe Lys His Asp Ser Phe Val Pro Cys Ser Glu Lys Ile His Leu
 450 455 460
 Ala Val Thr Glu Met Ala Ser Leu Phe Pro Lys Arg Pro Ala Leu Glu
 465 470 475 480
 Pro Val Arg Ser Ser Leu Arg Leu Leu Asn Ala Ser Ala Tyr Arg Leu
 485 490 495
 Gln Ser Glu Cys Arg Lys Thr Val Pro Pro Glu Pro Gly Ala Pro Val
 500 505 510
 Asp Phe Gln Leu Leu Thr Gln Gln Val Ile Gln Cys Ala Tyr Asp Ile
 515 520 525
 Ala Lys Ala Ala Lys Gln Leu Val Thr Ile Thr Thr Arg Glu Lys Lys
 530 535 540
 Gln
 545

<210> 1140

<211> 621

<212> Amino acid

<213> Homo sapiens

<400> 1140

Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu Val Asp
 1 5 10 15
 Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val Cys Thr
 20 25 30
 Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly Ser Ile
 35 40 45
 Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala Leu Ser
 50 55 60
 Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile Ser Ser
 65 70 75 80
 Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro Pro Asp
 85 90 95
 Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu Leu Ser
 100 105 110
 Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu Asn Asp
 115 120 125
 Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr Ile Glu
 130 135 140
 Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg Leu His
 145 150 155 160
 Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr Trp Ala

				165					170					175			
Tyr	Ile	Phe	Asp	His	Arg	Glu	Ser	Arg	Trp	Met	Lys	Tyr	Asn	Asp	Ile		
			180						185					190			
Ala	Val	Thr	Lys	Ser	Ser	Trp	Glu	Glu	Leu	Val	Arg	Asp	Ser	Phe	Gly		
		195					200					205					
Gly	Tyr	Arg	Asn	Ala	Ser	Ala	Tyr	Cys	Leu	Met	Tyr	Ile	Asn	Asp	Lys		
	210				215						220						
Ala	Gln	Phe	Leu	Ile	Gln	Glu	Glu	Phe	Asn	Lys	Glu	Thr	Gly	Gln	Pro		
225					230					235					240		
Leu	Val	Gly	Ile	Glu	Thr	Leu	Pro	Pro	Asp	Leu	Arg	Asp	Phe	Val	Glu		
			245						250					255			
Glu	Asp	Asn	Gln	Arg	Phe	Glu	Lys	Glu	Leu	Glu	Glu	Trp	Asp	Ala	Gln		
		260						265					270				
Leu	Ala	Gln	Lys	Ala	Leu	Gln	Glu	Lys	Leu	Leu	Ala	Ser	Gln	Lys	Leu		
	275						280					285					
Arg	Glu	Ser	Glu	Thr	Ser	Val	Thr	Thr	Ala	Gln	Ala	Ala	Gly	Asp	Pro		
	290				295						300						
Lys	Tyr	Leu	Glu	Gln	Pro	Ser	Arg	Ser	Asp	Phe	Ser	Lys	His	Leu	Lys		
305					310					315					320		
Glu	Glu	Thr	Ile	Gln	Ile	Ile	Thr	Lys	Ala	Ser	His	Glu	His	Glu	Asp		
			325						330					335			
Lys	Ser	Pro	Glu	Thr	Val	Leu	Gln	Ser	Ala	Ile	Lys	Leu	Glu	Tyr	Ala		
		340					345						350				
Arg	Leu	Val	Lys	Leu	Ala	Gln	Glu	Asp	Thr	Pro	Pro	Glu	Thr	Asp	Tyr		
	355					360						365					
Arg	Leu	His	His	Val	Val	Val	Tyr	Phe	Ile	Gln	Asn	Gln	Ala	Pro	Lys		
	370				375						380						
Lys	Ile	Ile	Glu	Lys	Thr	Leu	Leu	Glu	Gln	Phe	Gly	Asp	Arg	Asn	Leu		
385				390						395					400		
Ser	Phe	Asp	Glu	Arg	Cys	His	Asn	Ile	Met	Lys	Val	Ala	Gln	Ala	Lys		
			405						410				415				
Leu	Glu	Met	Ile	Lys	Pro	Glu	Glu	Val	Asn	Leu	Glu	Glu	Tyr	Glu	Glu		
		420					425						430				
Trp	His	Gln	Asp	Tyr	Arg	Lys	Phe	Arg	Glu	Thr	Thr	Met	Tyr	Leu	Ile		
	435						440					445					
Ile	Gly	Leu	Glu	Asn	Phe	Gln	Arg	Glu	Ser	Tyr	Ile	Asp	Ser	Leu	Leu		
	450				455						460						
Phe	Leu	Ile	Cys	Ala	Tyr	Gln	Asn	Asn	Lys	Glu	Leu	Leu	Ser	Lys	Gly		
465				470						475					480		
Leu	Tyr	Arg	Gly	His	Asp	Glu	Glu	Leu	Ile	Ser	His	Tyr	Arg	Arg	Glu		
			485						490					495			
Cys	Leu	Leu	Lys	Leu	Asn	Glu	Gln	Ala	Ala	Glu	Leu	Phe	Glu	Ser	Gly		
		500					505						510				
Glu	Asp	Arg	Glu	Val	Asn	Asn	Gly	Leu	Ile	Ile	Met	Asn	Glu	Phe	Ile		
	515						520					525					
Val	Pro	Phe	Leu	Pro	Leu	Leu	Leu	Val	Asp	Glu	Met	Glu	Glu	Lys	Asp		
	530				535							540					
Ile	Leu	Ala	Val	Glu	Asp	Met	Arg	Asn	Arg	Trp	Cys	Ser	Tyr	Leu	Gly		
545				550						555					560		
Gln	Glu	Met	Glu	Pro	His	Leu	Gln	Glu	Lys	Leu	Thr	Asp	Phe	Leu	Pro		
			565						570					575			
Lys	Leu	Leu	Asp	Cys	Ser	Met	Glu	Ile	Lys	Ser	Phe	His	Glu	Pro	Pro		
		580					585						590				
Lys	Leu	Pro	Ser	Tyr	Ser	Thr	His	Glu	Leu	Cys	Glu	Arg	Phe	Ala	Arg		
	595					600						605					
Ile	Met	Leu	Ser	Leu	Ser	Arg	Thr	Pro	Ala	Asp	Gly	Arg					
	610					615					620	621					

<210> 1141

<211> 154

<212> Amino acid

<213> Homo sapiens

<400> 1141
 Ala Gln Val Tyr Val Arg Met Asp Ser Phe Asp Glu Asp Leu Ala Arg
 1 5 10 15
 Pro Ser Gly Leu Leu Ala Gln Glu Arg Lys Leu Cys Arg Asp Leu Val
 20 25 30
 His Ser Asn Lys Lys Glu Gln Glu Phe Arg Ser Ile Phe Gln His Ile
 35 40 45
 Gln Ser Ala Gln Ser Gln Arg Ser Pro Ser Glu Leu Phe Ala Gln His
 50 55 60
 Met Val Pro Ile Val His His Val Lys Glu His His Phe Gly Ser Ser
 65 70 75 80
 Gly Met Thr Leu His Glu Arg Phe Thr Lys Tyr Leu Lys Arg Gly Thr
 85 90 95
 Glu Gln Glu Ala Ala Lys Asn Lys Lys Ser Pro Glu Ile His Arg Arg
 100 105 110
 Ile Asp Ile Ser Pro Ser Thr Phe Arg Lys His Gly Leu Ala His Asp
 115 120 125
 Glu Met Lys Ser Pro Arg Glu Pro Gly Tyr Lys Asp Gly His Asn Ser
 130 135 140
 Lys Asn Glu Leu Gln Arg Val Asn Phe Tyr
 145 150 154

<210> 1142
 <211> 121
 <212>Amino acid
 <213> Homo sapiens

<400> 1142
 Thr Tyr Thr Phe Cys Phe Ser Leu Met Ile Ile Leu Leu Thr Ile Ile
 1 5 10 15
 Gln Gly Leu Ile Leu Glu Ala Phe Gly Glu Leu Arg Asp Gln Leu Asp
 20 25 30
 Gln Val Lys Glu Asp Met Glu Thr Lys Cys Phe Ile Cys Gly Ile Gly
 35 40 45
 Asn Asp Tyr Phe Asp Thr Val Pro His Gly Phe Glu Thr His Thr Leu
 50 55 60
 Gln Glu His Asn Leu Ala Asn Tyr Leu Phe Phe Leu Met Tyr Leu Ile
 65 70 75 80
 Asn Lys Asp Glu Thr Glu His Thr Gly Gln Glu Ser Tyr Val Trp Lys
 85 90 95
 Met Tyr Gln Glu Arg Cys Trp Glu Phe Phe Pro Ala Gly Asp Cys Phe
 100 105 110
 Arg Lys Gln Tyr Glu Asp Gln Leu Asn
 115 120 121

<210> 1143
 <211> 851
 <212>Amino acid
 <213> Homo sapiens

<400> 1143

Phe	Arg	Arg	Lys	Gly	Gly	Gly	Gly	Pro	Lys	Asp	Phe	Gly	Ala	Gly	Leu	1	5	10	15
Lys	Tyr	Asn	Ser	Arg	His	Glu	Lys	Val	Asn	Gly	Leu	Glu	Glu	Gly	Val	20	25	30	
Glu	Phe	Leu	Pro	Val	Asn	Asn	Val	Lys	Lys	Val	Glu	Lys	His	Gly	Pro	35	40	45	
Gly	Arg	Trp	Val	Val	Leu	Ala	Val	Leu	Ile	Gly	Leu	Leu	Leu	Val		50	55	60	
Leu	Leu	Gly	Ile	Gly	Phe	Leu	Val	Trp	His	Leu	Gln	Tyr	Arg	Asp	Val	65	70	75	80
Arg	Val	Gln	Lys	Val	Phe	Asn	Gly	Tyr	Met	Arg	Ile	Thr	Asn	Glu	Asn	85	90	95	
Phe	Val	Asp	Ala	Tyr	Glu	Asn	Ser	Asn	Ser	Thr	Glu	Phe	Val	Ser	Leu	100	105	110	
Ala	Ser	Lys	Val	Lys	Asp	Ala	Leu	Lys	Leu	Leu	Tyr	Ser	Gly	Val	Pro	115	120	125	
Phe	Leu	Gly	Pro	Tyr	His	Lys	Glu	Ser	Ala	Val	Thr	Ala	Phe	Ser	Glu	130	135	140	
Gly	Ser	Val	Ile	Ala	Tyr	Trp	Ser	Glu	Phe	Ser	Ile	Pro	Gln	His		145	150	155	160
Leu	Val	Glu	Glu	Ala	Glu	Arg	Val	Met	Ala	Glu	Glu	Arg	Val	Val	Met	165	170	175	
Leu	Pro	Pro	Arg	Ala	Arg	Ser	Leu	Lys	Ser	Phe	Val	Val	Thr	Ser	Val	180	185	190	
Val	Ala	Phe	Pro	Thr	Asp	Ser	Lys	Thr	Val	Gln	Arg	Thr	Gln	Asp	Asn	195	200	205	
Ser	Cys	Ser	Phe	Gly	Leu	His	Ala	Arg	Gly	Val	Glu	Leu	Met	Arg	Phe	210	215	220	
Thr	Thr	Pro	Gly	Phe	Pro	Asp	Ser	Pro	Tyr	Pro	Ala	His	Ala	Arg	Cys	225	230	235	240
Gln	Trp	Ala	Leu	Arg	Gly	Asp	Ala	Asp	Ser	Val	Leu	Ser	Leu	Thr	Phe	245	250	255	
Arg	Ser	Phe	Asp	Leu	Ala	Ser	Cys	Asp	Glu	Arg	Gly	Arg	His	Leu	Val	260	265	270	
Thr	Val	Tyr	Asn	Thr	Leu	Ser	Pro	Met	Glu	Pro	His	Ala	Leu	Val	Gln	275	280	285	
Leu	Cys	Gly	Thr	Tyr	Pro	Pro	Ser	Tyr	Asn	Leu	Thr	Phe	His	Ser	Ser	290	295	300	
Gln	Asn	Val	Leu	Leu	Ile	Thr	Leu	Ile	Thr	Asn	Thr	Glu	Arg	Arg	His	305	310	315	320
Pro	Gly	Phe	Glu	Ala	Thr	Phe	Phe	Gln	Leu	Pro	Arg	Met	Ser	Ser	Cys	325	330	335	
Gly	Gly	Arg	Leu	Arg	Lys	Ala	Gln	Gly	Thr	Phe	Asn	Ser	Pro	Tyr	Tyr	340	345	350	
Pro	Gly	His	Tyr	Pro	Pro	Asn	Ile	Asp	Cys	Thr	Trp	Asn	Ile	Glu	Val	355	360	365	
Pro	Asn	Asn	Gln	His	Val	Lys	Val	Arg	Phe	Lys	Phe	Phe	Tyr	Leu	Leu	370	375	380	
Glu	Pro	Gly	Val	Pro	Ala	Gly	Thr	Cys	Pro	Lys	Asp	Tyr	Val	Glu	Ile	385	390	395	400
Asn	Gly	Glu	Lys	Tyr	Cys	Gly	Glu	Arg	Ser	Gln	Phe	Val	Val	Thr	Ser	405	410	415	
Asn	Ser	Asn	Lys	Ile	Thr	Val	Arg	Phe	His	Ser	Asp	Gln	Ser	Tyr	Thr	420	425	430	
Asp	Thr	Gly	Phe	Leu	Ala	Glu	Tyr	Leu	Ser	Tyr	Asp	Ser	Ser	Asp	Pro	435	440	445	
Cys	Pro	Gly	Gln	Phe	Thr	Cys	Arg	Thr	Gly	Arg	Cys	Ile	Arg	Lys	Glu	450	455	460	
Leu	Arg	Cys	Asp	Gly	Trp	Ala	Asp	Cys	Thr	Asp	His	Ser	Asp	Glu	Leu	465	470	475	480
Asn	Cys	Ser	Cys	Asp	Ala	Gly	His	Gln	Phe	Thr	Cys	Lys	Asn	Lys	Phe	485	490	495	
Cys	Lys	Pro	Leu	Phe	Trp	Val	Cys	Asp	Ser	Leu	Asn	Asp	Cys	Gly	Asp				

```

      500      505      510
Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln Thr Phe Arg Cys
      515      520      525
Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys Asn Gly Lys Asp
      530      535      540
Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro Lys Val Asn Val
      545      550      555      560
Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu
      565      570      575
Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly
      580      585      590
Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln
      595      600      605
Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp
      610      615      620
Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser
      625      630      635      640
Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp
      645      650      655
Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu
      660      665      670
Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg
      675      680      685
Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe
      690      695      700
Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser
      705      710      715      720
Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro
      725      730      735
Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly
      740      745      750
Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn
      755      760      765
Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met
      770      775      780
Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp
      785      790      795      800
Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln
      805      810      815
Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro
      820      825      830
Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn
      835      840      845
Thr Gly Val
      850 851

```

<210> 1144

<211> 346

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(346)

<223> X = any amino acid or stop code

<400> 1144

```

Arg His Glu Glu Asp Leu Gly Asn Leu Trp Glu Asn Thr Arg Phe Thr
  1           5           10           15

```

```

Asp Cys Ser Phe Phe Val Arg Gly Gln Glu Phe Lys Ala His Lys Ser
      20      25      30
Val Leu Ala Ala Arg Ser Pro Val Phe Asn Ala Met Phe Glu His Glu
      35      40      45
Met Glu Glu Ser Lys Lys Asn Arg Val Glu Ile Asn Asp Leu Asp Pro
      50      55      60
Glu Val Phe Lys Glu Met Met Arg Phe Ile Tyr Thr Gly Arg Ala Pro
      65      70      75      80
Asn Leu Asp Lys Met Ala Asp Asn Leu Leu Ala Ala Ala Asp Lys Tyr
      85      90      95
Ala Leu Glu Arg Leu Lys Val Met Cys Glu Lys Ala Leu Cys Ser Asn
      100      105      110
Leu Ser Val Glu Asn Val Ala Asp Thr Leu Val Leu Ala Asp Leu His
      115      120      125
Ser Ala Glu Gln Leu Lys Ala Gln Ala Ile Asp Phe Ile Asn Arg Cys
      130      135      140
Ser Val Leu Arg Gln Leu Gly Cys Lys Asp Gly Lys Asn Trp Asn Ser
      145      150      155      160
Asn Gln Ala Thr Asp Ile Met Glu Thr Ser Gly Gly Lys Ser Met Ile
      165      170      175
Gln Ser His Pro His Leu Val Ala Glu Ala Phe Arg Ala Leu Ala Ser
      180      185      190
Ala Gln Gly Pro Gln Phe Gly Ile Pro Arg Lys Arg Leu Lys Gln Ser
      195      200      205
Xaa Asn Leu Gly Asn Leu Trp Glu Asn Thr Arg Phe Thr Asp Cys Ser
      210      215      220
Phe Phe Val Arg Gly Gln Glu Phe Lys Ala His Lys Ser Val Leu Ala
      225      230      235      240
Ala Arg Ser Pro Val Phe Asn Ala Met Phe Glu His Glu Met Glu Glu
      245      250      255
Ser Lys Lys Asn Arg Val Glu Ile Asn Asp Leu Asp Pro Glu Val Phe
      260      265      270
Lys Glu Met Met Arg Phe Ile Tyr Thr Gly Arg Ala Pro Asn Leu Asp
      275      280      285
Lys Met Ala Asp Asn Leu Leu Ala Ala Ala Asp Lys Tyr Ala Leu Glu
      290      295      300
Arg Leu Lys Val Met Cys Glu Lys Ala Leu Cys Ser Asn Leu Ser Val
      305      310      315      320
Glu Asn Val Ala Asp Thr Leu Val Leu Ala Asp Leu His Ser Gly Arg
      325      330      335
Thr Val Glu Ser Thr Ser His Arg Leu Tyr
      340      345 346

```

<210> 1145

<211> 339

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(339)

<223> X = any amino acid or stop code

<400> 1145

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Gln Arg Gly Gly Ile Pro Gly Lys Phe Gln Glu Asp Ser Gly Ser Val
  1      5      10      15
Asp Trp Ala Leu Gly Pro Phe Trp Gly Ile Phe Gln Ala Asp Phe Gly
      20      25      30
Cys Met Arg Phe Tyr Leu Ser Ala Gln Thr Ser Asp Pro Val Leu Arg

```

```

      35      40      45
Met Xaa Trp Gly Pro Ser Pro Ile Ser His Pro Thr Ser Leu Cys Pro
  50      55      60
Gly Gly Gly Gly Ala Gly Gln Thr Thr Gly Ser Leu Cys Leu Gly Gln
  65      70      75      80
Gln Cys Cys Pro Leu Ser Cys Pro Asn Ile Pro Ser Arg His Lys Arg
      85      90      95
Trp Arg Leu Xaa Ala Ala Leu Val Ala Gly Ser Arg Gly Ser Cys Thr
      100      105      110
Leu Arg Ser Xaa Arg Xaa Arg Thr Pro Leu Pro Val Thr Arg Asn Leu
      115      120      125
Pro Arg Cys His Leu His Leu His Pro Thr Gly Asp Leu Arg Val His
      130      135      140
Val His Gln His Cys Leu Leu His Gly His Val Pro Pro Gly Ala Ala
      145      150      155      160
Leu Leu Gln Cys Gly Gly Cys Asp Leu Arg Gly Glu Ala Ala Gly Leu
      165      170      175
Leu Phe Leu Gly His Ala Cys Leu Arg Gly Ser Val Asn Leu Arg Arg
      180      185      190
Asp Gln Trp Leu Pro Val Pro Tyr Ser Arg Leu Cys Phe Ser Gly Ala
      195      200      205
Arg Glu Gly His Leu Pro Ser Leu Leu Ala Met Ile His Val Arg His
      210      215      220
Cys Thr Pro Ile Pro Ala Leu Leu Val Cys Pro Ile Lys Val Asn Leu
      225      230      235      240
Leu Ile Pro Val Ala Tyr Leu Val Phe Trp Ala Phe Leu Leu Val Phe
      245      250      255
Ser Phe Ile Ser Glu His Met Val Cys Gly Val Gly Val Ile Ile Ile
      260      265      270
Leu Thr Gly Val Pro Ile Phe Phe Leu Gly Val Phe Trp Arg Ser Lys
      275      280      285
Pro Lys Cys Val His Arg Leu Thr Glu Ser Met Thr His Trp Gly Gln
      290      295      300
Glu Leu Cys Phe Val Val Tyr Pro Gln Asp Ala Pro Glu Glu Glu Glu
      305      310      315      320
Asn Gly Pro Cys Pro Pro Ser Leu Leu Pro Ala Thr Asp Lys Pro Ser
      325      330      335
Lys Pro Gln
      339

```

<210> 1146

<211> 425

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(425)

<223> X = any amino acid or stop code

<400> 1146

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Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala Leu Leu Glu Asp His Arg
  1      5      10      15
His Leu Pro Val Gly Cys Val Ser Phe Gln Asn Ile Ser Ser Asn Val
      20      25      30
Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile Leu Ser Pro Asp Glu Glu
      35      40      45
Gly Phe Cys Ser Gly Lys His Phe Thr Glu Leu Gly Leu Val Gly Leu
      50      55      60

```

Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met Gly Gly Leu Tyr Glu Ala
 65 70 75 80
 Val Asn Glu Val Tyr Lys Asn Leu Ile Pro Ile Leu Glu Ala His Arg
 85 90 95
 Asp Tyr Lys Lys Leu Ala Ala Val His Gly Lys Leu Gln Glu Ala Phe
 100 105 110
 Thr Lys Ile Met His Gln Ser Ser Gly Trp Glu Arg Val Phe Gly Thr
 115 120 125
 Tyr Phe Arg Val Gly Phe Tyr Gly Ala His Phe Gly Asp Leu Asp Glu
 130 135 140
 Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile Thr Lys Leu Ala Glu Ile
 145 150 155 160
 Ser His Arg Leu Glu Glu Phe Tyr Thr Glu Arg Phe Gly Asp Asp Val
 165 170 175
 Val Glu Ile Ile Lys Asp Ser Asn Pro Val Asp Lys Ser Lys Leu Asp
 180 185 190
 Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp
 195 200 205
 Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr Phe Asp Arg Asn Tyr Gly
 210 215 220
 Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe Thr Pro Asp Gly Arg Ala
 225 230 235 240
 His Gly Glu Leu Pro Glu Gln His Lys Arg Lys Thr Leu Leu Ser Thr
 245 250 255
 Asp His Ala Phe Pro Tyr Ile Lys Thr Arg Ile Arg Val Cys His Arg
 260 265 270
 Glu Glu Thr Val Leu Thr Pro Val Glu Val Ala Ile Glu Asp Met Gln
 275 280 285
 Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr Glu Gln Asp Pro Pro Asp
 290 295 300
 Ala Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Pro Thr Val
 305 310 315 320
 Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro
 325 330 335
 Glu Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe
 340 345 350
 Lys Asp Phe Xaa Lys Lys Cys Glu Asp Ala Leu Arg Lys Asn Lys Ala
 355 360 365
 Leu Ile Gly Pro Asp Gln Lys Glu Tyr His Arg Glu Leu Glu Arg Asn
 370 375 380
 Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro Leu Leu Thr Gln Arg Leu
 385 390 395 400
 Pro Gln Leu Met Ala Pro Thr Pro Pro Gly Leu Arg Asn Ser Leu Asn
 405 410 415
 Arg Ala Ser Phe Arg Lys Ala Asp Leu
 420 425

<210> 1147

<211> 198

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(198)

<223> X = any amino acid or stop code

<400> 1147

Gly Glu Gly Gln Gln Trp Gln Ser Thr Pro Leu Ser Pro Leu Gln Pro

1	5	10	15
Thr Val Ala Asp Phe Leu Asn Leu Ala Trp Trp Thr Ser Ala Ala Ala			
20	25	30	
Trp Xaa Val Leu Ser Gly Arg Trp Val Glu Lys Val Leu Pro Gly Arg			
35	40	45	
Glu Gly Ser Glu Glu Lys Xaa Gly Met Ala Ser Ser Ser Ala Asp His			
50	55	60	
Leu His Ser Ala Pro Arg Ala Leu Gln Ser Leu Phe Gln Gln Leu Leu			
65	70	75	80
Tyr Gly Leu Ile Tyr His Ser Trp Phe Gln Ala Gly Arg Xaa Gly Phe			
85	90	95	
Gly Gly Ala Ser Ser Ser Pro Gly Pro Gln Ser Glu Leu Arg Arg Leu			
100	105	110	
His Gly Glu Gly Gly Val Tyr Asp Xaa Gly Arg Pro Glu Thr Leu Pro			
115	120	125	
Gly Ser Val Gly Gly Ala Glu Ala Leu Trp Ala Leu Ala Asp Pro Ala			
130	135	140	
Glu Ala Glu Gly Ser Pro Glu Thr Arg Glu Ser Ser Cys Val Met Lys			
145	150	155	160
Gln Thr Gln Tyr Tyr Phe Gly Ser Val Asn Ala Ser Tyr Asn Ala Ile			
165	170	175	
Ile Asp Cys Gly Asn Cys Ser Arg Cys Trp Gln Trp Gly Gly Thr Arg			
180	185	190	
Gly Gln Gly Arg Asn Leu			
195	198		

<210> 1148

<211> 317

<212> Amino acid

<213> Homo sapiens

<400> 1148

Val Ala Gly Ile Pro Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu Ala			
1	5	10	15
Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Ser Lys Pro Thr Phe Arg			
20	25	30	
Ala Val Glu Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr			
35	40	45	
Glu Asn Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu			
50	55	60	
Ser Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Glu Ser Leu			
65	70	75	80
Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser Trp			
85	90	95	
Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys Gly Gly			
100	105	110	
Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His Cys Phe Arg			
115	120	125	
Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala Gly Ser Asp Lys			
130	135	140	
Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys Ile Ile Ile Ile Glu			
145	150	155	160
Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp Ile Ala Leu Met Lys Leu			
165	170	175	
Gln Phe Pro Leu Thr Phe Ser Gly Thr Val Arg Pro Ile Cys Leu Pro			
180	185	190	
Phe Phe Asp Glu Glu Leu Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly			
195	200	205	
Trp Gly Phe Thr Lys Gln Asn Gly Gly Lys Met Ser Asp Ile Leu Leu			

210	215	220
Gln Ala Ser Val Gln Val Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp		
225	230	235
Ala Tyr Gln Gly Glu Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro		240
	245	250
Glu Gly Gly Val Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met		255
	260	265
Tyr Gln Ser Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr		270
	275	280
Gly Cys Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala		285
	290	295
Tyr Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu		300
305	310	315
		317

<210> 1149

<211> 320

<212> Amino acid

<213> Homo sapiens

<400> 1149

Thr Ile Ser Thr Val Arg Trp Asn Ser Arg Ile Gly Met Val Leu Gly		
1	5	10
Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Tyr Ala Phe Glu Glu		15
	20	25
Ala Tyr Ala Arg Ala Asp Lys Glu Ala Pro Arg Pro Cys His Lys Gly		30
	35	40
Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln Ala Phe Met		45
	50	55
Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser Ser Ala Tyr		60
	65	70
Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu His Gln Leu		75
	85	90
Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val Tyr Pro Trp		95
	100	105
Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu His Lys Asp		110
	115	120
Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser Tyr Asn Ile		125
	130	135
Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr Val Leu Gly		140
	145	150
Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu Thr Lys Ile		155
	165	170
Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val Cys Ser Ser		175
	180	185
Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe His His Cys		190
	195	200
Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu Asn Lys Ser		205
	210	215
Ser Tyr Leu Gly Lys Asp Leu Pro Glu Asn Tyr Asn Glu Ala Lys Cys		220
	225	230
Val Thr Phe Ser Leu Leu Phe Asn Phe Val Ser Trp Ile Ala Phe Phe		235
	245	250
Thr Thr Ala Ser Val Tyr Asp Gly Lys Tyr Leu Pro Ala Ala Asn Met		255
	260	265
Met Ala Gly Leu Ser Ser Leu Ser Gly Phe Gly Gly Tyr Phe Leu		270
	275	280
Pro Lys Cys Tyr Val Ile Leu Cys Arg Pro Asp Leu Asn Ser Thr Glu		285
	290	295
His Phe Gln Ala Ser Ile Gln Asp Tyr Thr Arg Arg Cys Gly Ser Thr		300

305

310

315

320

<210> 1150
 <211> 458
 <212> Amino acid
 <213> Homo sapiens

<400> 1150
 Val Ala Arg Gly Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser
 1 5 10 15
 Pro Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser
 20 25 30
 Thr Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu
 35 40 45
 His Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala
 50 55 60
 Thr Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile
 65 70 75 80
 Ala Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln
 85 90 95
 Asp Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro
 100 105 110
 Ala Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr
 115 120 125
 Gln Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe
 130 135 140
 Thr Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys
 145 150 155 160
 Val Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu
 165 170 175
 Ser Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn
 180 185 190
 Trp Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser
 195 200 205
 Asn Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe
 210 215 220
 Pro Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val
 225 230 235 240
 Asp Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val
 245 250 255
 Gly Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn
 260 265 270
 Thr Ala Gly Ala Gly Ala Thr Gly Gly Ile Ile Gly Gly Ile Ile Ala
 275 280 285
 Ala Ile Ile Ala Thr Ala Asp Ala Thr Gly Ile Leu Ile Cys Arg Gln
 290 295 300
 Gln Arg Lys Glu Gln Thr Leu Gln Gly Ala Glu Glu Asp Glu Asp Leu
 305 310 315 320
 Glu Gly Pro Pro Ser Tyr Lys Pro Pro Thr Pro Lys Ala Lys Leu Glu
 325 330 335
 Ala Gln Glu Met Pro Ser Gln Leu Phe Thr Leu Gly Ala Ser Glu His
 340 345 350
 Ser Pro Leu Lys Thr Pro Tyr Phe Asp Ala Gly Ala Ser Cys Thr Glu
 355 360 365
 Gln Glu Met Pro Arg Tyr His Glu Leu Pro Thr Leu Glu Glu Arg Ser
 370 375 380
 Gly Pro Leu His Pro Gly Ala Thr Ser Leu Gly Ser Pro Ile Pro Val

385 390 395 400
 Pro Pro Gly Pro Pro Ala Val Glu Asp Val Ser Leu Asp Leu Glu Asp
 405 410 415
 Glu Glu Gly Glu Glu Glu Glu Tyr Leu Asp Lys Ile Asn Pro Ile
 420 425 430
 Tyr Asp Ala Leu Ser Tyr Ser Ser Pro Ser Asp Ser Tyr Gln Gly Lys
 435 440 445
 Gly Phe Val Met Ser Arg Ala Met Tyr Val
 450 455 458

<210> 1151

<211> 608

<212> Amino acid

<213> Homo sapiens

<400> 1151

Gly Thr Arg Leu Arg Glu Asp Lys Asn His Asn Met Tyr Val Ala Gly
 1 5 10 15
 Cys Thr Glu Val Glu Val Lys Ser Thr Glu Glu Ala Phe Glu Val Phe
 20 25 30
 Trp Arg Gly Gln Lys Lys Arg Arg Ile Ala Asn Thr His Leu Asn Arg
 35 40 45
 Glu Ser Ser Arg Ser His Ser Val Phe Asn Ile Lys Leu Val Gln Ala
 50 55 60
 Pro Leu Asp Ala Asp Gly Asp Asn Val Leu Gln Glu Lys Glu Gln Ile
 65 70 75 80
 Thr Ile Ser Gln Leu Ser Leu Val Asp Leu Ala Gly Ser Glu Arg Thr
 85 90 95
 Asn Arg Thr Arg Ala Glu Gly Asn Arg Leu Arg Glu Ala Gly Asn Ile
 100 105 110
 Asn Gln Ser Leu Met Thr Leu Arg Thr Cys Met Asp Val Leu Arg Glu
 115 120 125
 Asn Gln Met Tyr Gly Thr Asn Lys Met Val Pro Tyr Arg Asp Ser Lys
 130 135 140
 Leu Thr His Leu Phe Lys Asn Tyr Phe Asp Gly Glu Gly Lys Val Arg
 145 150 155 160
 Met Ile Val Cys Val Asn Pro Lys Ala Glu Asp Tyr Glu Glu Asn Leu
 165 170 175
 Gln Val Met Arg Phe Ala Glu Val Thr Gln Glu Val Glu Val Ala Arg
 180 185 190
 Pro Val Asp Lys Ala Ile Cys Gly Leu Thr Pro Gly Arg Arg Tyr Arg
 195 200 205
 Asn Gln Pro Arg Gly Pro Ile Gly Asn Glu Pro Leu Val Thr Asp Val
 210 215 220
 Val Leu Gln Ser Phe Pro Pro Leu Pro Ser Cys Glu Ile Leu Asp Ile
 225 230 235 240
 Asn Asp Glu Gln Thr Leu Pro Arg Leu Ile Glu Ala Leu Glu Lys Arg
 245 250 255
 His Asn Leu Arg Gln Met Met Ile Asp Glu Phe Asn Lys Gln Ser Asn
 260 265 270
 Ala Phe Lys Ala Leu Leu Gln Glu Phe Asp Asn Ala Val Leu Ser Lys
 275 280 285
 Glu Asn His Met Gln Gly Lys Leu Asn Glu Lys Glu Lys Met Ile Ser
 290 295 300
 Gly Gln Lys Leu Glu Ile Glu Arg Leu Glu Lys Lys Asn Lys Thr Leu
 305 310 315 320
 Glu Tyr Lys Ile Glu Ile Leu Glu Lys Thr Thr Thr Ile Tyr Glu Glu
 325 330 335
 Asp Lys Arg Asn Leu Gln Gln Glu Leu Glu Thr Gln Asn Gln Lys Leu

			340				345				350				
Gln	Arg	Gln	Phe	Ser	Asp	Lys	Arg	Arg	Leu	Glu	Ala	Arg	Leu	Gln	Gly
			355				360				365				
Met	Val	Thr	Glu	Thr	Thr	Met	Lys	Trp	Glu	Lys	Glu	Cys	Glu	Arg	Arg
			370				375				380				
Val	Ala	Ala	Lys	Gln	Leu	Glu	Met	Gln	Asn	Lys	Leu	Trp	Val	Lys	Asp
385			390				395				400				
Glu	Lys	Leu	Lys	Gln	Leu	Lys	Ala	Ile	Val	Thr	Glu	Pro	Lys	Thr	Glu
			405				410				415				
Lys	Pro	Glu	Arg	Pro	Ser	Arg	Glu	Arg	Asp	Arg	Glu	Lys	Val	Thr	Gln
			420				425				430				
Arg	Ser	Val	Ser	Pro	Ser	Pro	Val	Pro	Leu	Leu	Phe	Gln	Pro	Asp	Gln
			435				440				445				
Asn	Ala	Pro	Pro	Ile	Arg	Leu	Arg	His	Arg	Arg	Ser	Arg	Ser	Ala	Gly
450			455				460								
Asp	Arg	Trp	Val	Asp	His	Lys	Pro	Ala	Ser	Asn	Met	Gln	Thr	Glu	Thr
465			470				475				480				
Val	Met	Gln	Pro	His	Val	Pro	His	Ala	Ile	Thr	Val	Ser	Val	Ala	Asn
			485				490				495				
Glu	Lys	Ala	Leu	Ala	Lys	Cys	Glu	Lys	Tyr	Met	Leu	Thr	His	Gln	Glu
			500				505				510				
Leu	Ala	Ser	Asp	Gly	Glu	Ile	Glu	Thr	Lys	Leu	Ile	Lys	Gly	Asp	Ile
515			520				525								
Tyr	Lys	Thr	Arg	Gly	Gly	Gly	Gln	Ser	Val	Gln	Phe	Thr	Asp	Ile	Glu
530			535				540								
Thr	Leu	Lys	Gln	Glu	Ser	Pro	Asn	Gly	Ser	Arg	Lys	Arg	Arg	Ser	Ser
545			550				555				560				
Thr	Val	Ala	Pro	Ala	Gln	Pro	Asp	Gly	Ala	Glu	Ser	Glu	Trp	Thr	Asp
			565				570				575				
Val	Glu	Thr	Arg	Cys	Ser	Val	Ala	Val	Glu	Met	Arg	Ala	Gly	Ser	Gln
			580				585				590				
Leu	Gly	Pro	Gly	Tyr	Gln	His	His	Ala	Gln	Pro	Lys	Arg	Lys	Lys	Pro
595			600				605				608				

<210> 1152

<211> 111

<212>Amino acid

<213> Homo sapiens

	<400> 1152															
Pro	Phe	Ser	Ser	Ser	Ser	Val	Ser	Ser	Lys	Gly	Ser	Asp	Pro	Phe	Gly	
1				5					10					15		
Thr	Leu	Asp	Pro	Phe	Gly	Ser	Gly	Ser	Phe	Asn	Ser	Ala	Glu	Gly	Phe	
			20					25					30			
Ala	Asp	Phe	Ser	Gln	Met	Ser	Lys	Gly	Lys	Ser	Thr	Pro	Val	Ser	Gln	
		35					40					45				
Leu	Gly	Ser	Ala	Asp	Phe	Pro	Glu	Ala	Pro	Asp	Pro	Phe	Gln	Pro	Leu	
	50					55					60					
Gly	Ala	Asp	Ser	Gly	Asp	Pro	Phe	Gln	Ser	Lys	Lys	Gly	Phe	Gly	Asp	
65				70						75				80		
Pro	Phe	Ser	Gly	Lys	Asp	Pro	Phe	Val	Pro	Ser	Ser	Ala	Ala	Lys	Pro	
				85					90					95		
Ser	Lys	Ala	Ser	Ala	Ser	Gly	Phe	Ala	Asp	Phe	Thr	Ser	Val	Ser		
			100					105					110	111		

<210> 1153

<211> 444

<212> Amino acid

<213> Homo sapiens

<400> 1153

```

Met Ser Leu Met Val Val Ser Met Ala Cys Val Gly Leu Phe Leu Val
 1          5          10          15
Gln Arg Ala Gly Pro His Met Gly Gly Gln Asp Lys Pro Phe Leu Ser
          20          25          30
Ala Trp Pro Ser Ala Val Val Pro Arg Gly Gly His Val Thr Leu Arg
          35          40          45
Cys His Tyr Arg His Arg Phe Asn Asn Phe Met Leu Tyr Lys Glu Asp
          50          55          60
Arg Ile His Ile Pro Ile Phe His Gly Arg Ile Phe Gln Glu Ser Phe
          65          70          75          80
Asn Met Ser Pro Val Thr Thr Ala His Ala Gly Asn Tyr Thr Cys Arg
          85          90          95
Gly Ser His Pro His Ser Pro Thr Gly Trp Ser Ala Pro Ser Asn Pro
          100          105          110
Val Val Ile Met Val Thr Gly Asn His Arg Lys Pro Ser Leu Leu Ala
          115          120          125
His Pro Gly Pro Leu Val Lys Ser Gly Glu Arg Val Ile Leu Gln Cys
          130          135          140
Trp Ser Asp Ile Met Phe Glu His Phe Phe Leu His Lys Glu Gly Ile
          145          150          155          160
Ser Lys Asp Pro Ser Arg Leu Val Gly Gln Ile His Asp Gly Val Ser
          165          170          175
Lys Ala Asn Phe Ser Ile Gly Pro Met Met Gln Asp Leu Ala Gly Thr
          180          185          190
Tyr Arg Cys Tyr Gly Ser Val Thr His Ser Pro Tyr Gln Leu Ser Ala
          195          200          205
Pro Ser Asp Pro Leu Asp Ile Val Ile Thr Gly Leu Tyr Glu Lys Pro
          210          215          220
Ser Leu Ser Ala Gln Pro Gly Pro Thr Val Leu Ala Gly Glu Ser Val
          225          230          235          240
Thr Leu Ser Cys Ser Ser Arg Ser Ser Tyr Asp Met Tyr His Leu Ser
          245          250          255
Arg Glu Gly Glu Ala His Glu Arg Arg Phe Ser Ala Gly Pro Lys Val
          260          265          270
Asn Gly Thr Phe Gln Ala Asp Phe Pro Leu Gly Pro Ala Thr His Gly
          275          280          285
Gly Thr Tyr Arg Cys Phe Gly Ser Phe Arg Asp Ser Pro Tyr Glu Trp
          290          295          300
Ser Asn Ser Ser Asp Pro Leu Leu Val Ser Val Thr Gly Asn Pro Ser
          305          310          315          320
Asn Ser Trp Pro Ser Pro Thr Glu Pro Ser Ser Glu Thr Gly Asn Pro
          325          330          335
Arg His Leu His Val Leu Ile Gly Thr Ser Val Val Ile Ile Leu Phe
          340          345          350
Ile Leu Leu Leu Phe Phe Leu Leu His Arg Trp Cys Ser Asn Lys Lys
          355          360          365
Asn Ala Ala Val Met Asp Gln Glu Ser Ala Gly Asn Arg Thr Ala Asn
          370          375          380
Ser Glu Asp Ser Asp Glu Gln Asp Pro Gln Glu Val Thr Tyr Thr Gln
          385          390          395          400
Leu Asn His Cys Val Phe Thr Gln Arg Lys Ile Thr Arg Pro Ser Gln
          405          410          415
Arg Pro Lys Thr Pro Pro Thr Asp Ile Ile Val Tyr Thr Glu Leu Pro
          420          425          430
Asn Ala Glu Ser Arg Ser Lys Val Val Ser Cys Pro

```

435

440

444

<210> 1154
 <211> 522
 <212> Amino acid
 <213> Homo sapiens

<400> 1154
 Met Ser Leu Arg Val His Thr Leu Pro Thr Leu Leu Gly Ala Val Val
 1 5 10 15
 Arg Pro Gly Cys Arg Glu Leu Leu Cys Leu Leu Met Ile Thr Val Thr
 20 25 30
 Val Gly Pro Gly Ala Ser Gly Val Cys Pro Thr Ala Cys Ile Cys Ala
 35 40 45
 Thr Asp Ile Val Ser Cys Thr Asn Lys Asn Leu Ser Lys Val Pro Gly
 50 55 60
 Asn Leu Phe Arg Leu Ile Lys Arg Leu Asp Leu Ser Tyr Asn Arg Ile
 65 70 75 80
 Gly Leu Leu Asp Ser Glu Trp Ile Pro Val Ser Phe Ala Lys Leu Asn
 85 90 95
 Thr Leu Ile Leu Arg His Asn Asn Ile Thr Ser Ile Ser Thr Gly Ser
 100 105 110
 Phe Ser Thr Thr Pro Asn Leu Lys Cys Leu Asp Leu Ser Ser Asn Lys
 115 120 125
 Leu Lys Thr Val Lys Asn Ala Val Phe Gln Glu Leu Lys Val Leu Glu
 130 135 140
 Val Leu Leu Leu Tyr Asn Asn His Ile Ser Tyr Leu Asp Pro Ser Ala
 145 150 155 160
 Phe Gly Gly Leu Ser Gln Leu Gln Lys Leu Tyr Leu Ser Gly Asn Phe
 165 170 175
 Leu Thr Gln Phe Pro Met Asp Leu Tyr Val Gly Arg Phe Lys Leu Ala
 180 185 190
 Glu Leu Met Phe Leu Asp Val Ser Tyr Asn Arg Ile Pro Ser Met Pro
 195 200 205
 Met His His Ile Asn Leu Val Pro Gly Lys Gln Leu Arg Gly Ile Tyr
 210 215 220
 Leu His Gly Asn Pro Phe Val Cys Asp Cys Ser Leu Val Ser Leu Leu
 225 230 235 240
 Val Phe Trp Tyr Arg Arg His Phe Ser Ser Val Met Asp Phe Lys Asn
 245 250 255
 Asp Tyr Thr Cys Arg Leu Trp Ser Asp Ser Arg His Ser Arg Gln Val
 260 265 270
 Leu Leu Leu Gln Asp Ser Phe Met Asn Cys Ser Asp Ser Ile Ile Asn
 275 280 285
 Gly Ser Phe Arg Ala Leu Gly Phe Ile His Glu Ala Gln Val Gly Glu
 290 295 300
 Arg Leu Met Val His Cys Asp Ser Lys Thr Gly Asn Ala Asn Thr Asp
 305 310 315 320
 Phe Ile Trp Val Gly Pro Asp Asn Arg Leu Leu Glu Pro Asp Lys Glu
 325 330 335
 Met Glu Asn Phe Tyr Val Phe His Asn Gly Ser Leu Val Ile Glu Ser
 340 345 350
 Pro Arg Phe Glu Asp Ala Gly Val Tyr Ser Cys Ile Ala Met Asn Lys
 355 360 365
 Gln Arg Leu Leu Asn Glu Thr Val Asp Val Thr Ile Asn Val Ser Asn
 370 375 380
 Phe Thr Val Ser Arg Ser His Ala His Glu Ala Phe Asn Thr Ala Phe
 385 390 395 400
 Thr Thr Leu Ala Ala Cys Val Ala Ser Ile Val Leu Val Leu Leu Tyr

405 410 415
 Leu Tyr Leu Thr Pro Cys Pro Cys Lys Cys Lys Thr Lys Arg Gln Lys
 420 425 430
 Asn Met Leu His Gln Ser Asn Ala His Ser Ser Ile Leu Ser Pro Gly
 435 440 445
 Pro Ala Ser Asp Ala Ser Ala Asp Glu Arg Lys Ala Gly Ala Gly Lys
 450 455 460
 Arg Val Val Phe Leu Glu Pro Leu Lys Asp Thr Ala Ala Gly Gln Asn
 465 470 475 480
 Gly Lys Val Arg Leu Phe Pro Ser Glu Ala Val Ile Ala Glu Gly Ile
 485 490 495
 Leu Lys Ser Thr Arg Gly Lys Ser Asp Ser Asp Ser Val Asn Ser Val
 500 505 510
 Phe Ser Asp Thr Pro Phe Val Ala Ser Thr
 515 520 522

<210> 1155

<211> 642

<212> Amino acid

<213> Homo sapiens

<400> 1155

Ala Ser Asp Phe Ile Arg Ser Leu Asp His Cys Gly Tyr Leu Ser Leu
 1 5 10 15
 Glu Gly Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser
 20 25 30
 Ser Val Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr
 35 40 45
 Thr Ala Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe
 50 55 60
 Gln Glu Tyr Thr Ala Gly Arg Arg Leu Ser Ser Leu Leu Thr Ser His
 65 70 75 80
 Glu Pro Glu Glu Val Thr Lys Gly Asn Gly Tyr Leu Gln Lys Met Val
 85 90 95
 Ser Ile Ser Asp Ile Thr Ser Thr Tyr Ser Ser Leu Leu Arg Tyr Thr
 100 105 110
 Cys Gly Ser Ser Val Glu Ala Thr Arg Ala Val Met Lys His Leu Ala
 115 120 125
 Ala Val Tyr Gln His Gly Cys Leu Leu Gly Leu Ser Ile Ala Lys Arg
 130 135 140
 Pro Leu Trp Arg Gln Glu Ser Leu Gln Ser Val Lys Asn Thr Thr Glu
 145 150 155 160
 Gln Glu Ile Leu Lys Ala Ile Asn Ile Asn Ser Phe Val Glu Cys Gly
 165 170 175
 Ile His Leu Tyr Gln Glu Ser Thr Ser Lys Ser Ala Leu Ser Gln Glu
 180 185 190
 Phe Glu Ala Phe Phe Gln Gly Lys Ser Leu Tyr Ile Asn Ser Gly Asn
 195 200 205
 Ile Pro Asp Tyr Leu Phe Asp Phe Phe Glu His Leu Pro Asn Cys Ala
 210 215 220
 Ser Ala Leu Asp Phe Ile Lys Leu Gly Phe Tyr Gly Gly Ala Met Ala
 225 230 235 240
 Ser Trp Glu Lys Ala Ala Glu Asp Thr Gly Gly Ile His Met Glu Glu
 245 250 255
 Ala Pro Glu Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn
 260 265 270
 Trp Lys Gln Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser
 275 280 285
 Lys Leu Asn Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser

290 295 300
 Ala Thr Ser Leu Arg Leu Gln Ile Lys Arg Cys Ala Gly Val Ala Gly
 305 310 315 320
 Ser Leu Ser Leu Val Leu Ser Thr Cys Lys Asn Ile Tyr Ser Leu Met
 325 330 335
 Val Glu Ala Ser Pro Leu Thr Ile Glu Asp Glu Arg His Ile Thr Ser
 340 345 350
 Val Thr Asn Leu Lys Thr Leu Ser Ile His Asp Leu Gln Asn Gln Arg
 355 360 365
 Leu Pro Gly Gly Leu Thr Asp Ser Leu Gly Asn Leu Lys Asn Leu Thr
 370 375 380
 Lys Leu Ile Met Asp Asn Ile Lys Met Asn Glu Glu Asp Ala Ile Lys
 385 390 395 400
 Leu Ala Glu Gly Leu Lys Asn Leu Lys Lys Met Cys Leu Phe His Leu
 405 410 415
 Thr His Leu Ser Asp Ile Gly Glu Gly Met Asp Tyr Ile Val Lys Ser
 420 425 430
 Leu Ser Ser Glu Pro Cys Asp Leu Glu Glu Ile Gln Leu Val Ser Cys
 435 440 445
 Cys Leu Ser Ala Asn Ala Val Lys Ile Leu Ala Gln Asn Leu His Asn
 450 455 460
 Leu Val Lys Leu Ser Ile Leu Asp Leu Ser Glu Asn Tyr Leu Glu Lys
 465 470 475 480
 Asp Gly Asn Glu Ala Leu His Glu Leu Ile Asp Arg Met Asn Val Leu
 485 490 495
 Glu Gln Leu Thr Ala Leu Met Leu Pro Trp Gly Cys Asp Val Gln Gly
 500 505 510
 Ser Leu Ser Ser Leu Leu Lys His Leu Glu Glu Val Pro Gln Leu Val
 515 520 525
 Lys Leu Gly Leu Lys Asn Trp Arg Leu Thr Asp Thr Glu Ile Arg Ile
 530 535 540
 Leu Gly Ala Phe Phe Gly Lys Asn Pro Leu Lys Asn Phe Gln Gln Leu
 545 550 555 560
 Asn Leu Ala Gly Asn Arg Val Ser Ser Asp Gly Trp Leu Ala Phe Met
 565 570 575
 Gly Val Phe Glu Asn Leu Lys Gln Leu Val Phe Phe Asp Phe Ser Thr
 580 585 590
 Lys Glu Phe Leu Pro Asp Pro Ala Leu Val Arg Lys Leu Ser Gln Val
 595 600 605
 Leu Ser Lys Leu Thr Phe Leu Gln Glu Ala Arg Leu Val Gly Trp Gln
 610 615 620
 Phe Asp Asp Asp Asp Leu Ser Val Ile Thr Gly Ala Phe Lys Leu Val
 625 630 635 640
 Thr Ala
 642

<210> 1156

<211> 125

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (125)

<223> X = any amino acid or stop code

<400> 1156

Ala Ser Asp Arg Lys Val Ala Met Thr Cys Asp Cys Phe Trp Phe Arg
 1 5 10 15

```

Thr Met Leu Asp Gln His Ala Ser Cys Met Glu Val Gly Thr Glu Arg
      20          25          30
Glu Arg Gln Ala Gly Gly Leu Val Met Phe Asp Pro Ser Gly Phe Pro
      35          40          45
Thr Gly Glu Lys Val Leu Gln Asp Asp Glu Phe Thr Cys Asp Leu Phe
      50          55          60
Arg Phe Leu Gln Leu Leu Cys Glu Gly His Asn Ser Gly Leu Xaa Val
      65          70          75          80
Pro Gly Thr Ser Asp Asp Thr Lys Ala Xaa Ile Met Phe Ser Ser Gln
      85          90          95
Xaa Xaa Gln Glu Pro Val Ser Ser Asn Tyr Ala Ser Phe Xaa Arg Gln
      100          105          110
Gln Ile Ile Leu Glu His Gly Ser Ala Leu Gly Ser Gly
      115          120          125

```

<210> 1157

<211> 91

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(91)

<223> X = any amino acid or stop code

<400> 1157

```

Glu Ile Thr His Ile Val Gly Glu Thr Ala Ala Phe Leu Cys Pro Arg
  1          5          10          15
Leu Arg Leu Arg Arg Gly Gly Lys Asp Gly Ser Pro Lys Pro Gly Phe
      20          25          30
Leu Ala Ser Val Ile Pro Val Asp Arg Arg Pro Gly Glu Xaa Asp Ile
      35          40          45
Thr His Ile Val Gly Glu Thr Ala Ala Phe Leu Cys Pro Arg Leu Arg
      50          55          60
Leu Arg Arg Gly Gly Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala
      65          70          75          80
Ser Val Ile Pro Val Asp Arg Arg Pro Gly Glu
      85          90  91

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<210> 1158

<211> 254

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(254)

<223> X = any amino acid or stop code

<400> 1158

```

Ser Lys Phe Ile Phe Tyr Val Asp Ser Gln Ser Met Ile Phe Phe Phe
  1          5          10          15
Gln Thr Pro Thr Arg His Lys Val Leu Ile Met Glu Phe Cys Pro Cys
      20          25          30

```


Gly Ser Leu Tyr Thr Val Leu Glu Glu Pro Ser Asn Ala Tyr Gly Leu
 35 40 45
 Pro Glu Ser Glu Phe Leu Ile Val Leu Arg Asp Val Val Gly Gly Met
 50 55 60
 Asn His Leu Arg Glu Asn Gly Ile Val His Arg Asp Ile Lys Pro Gly
 65 70 75 80
 Asn Ile Met Arg Val Ile Gly Glu Asp Gly Gln Ser Val Tyr Lys Leu
 85 90 95
 Thr Asp Phe Gly Ala Ala Arg Glu Leu Glu Asp Asp Glu Gln Phe Val
 100 105 110
 Ser Leu Tyr Gly Thr Glu Glu Tyr Leu His Pro Asp Met Tyr Glu Arg
 115 120 125
 Ala Val Leu Arg Lys Asp His Gln Lys Lys Tyr Gly Ala Thr Val Asp
 130 135 140
 Leu Trp Ser Ile Gly Val Thr Phe Tyr Gln Gly Lys Pro Thr Gly Ser
 145 150 155 160
 Leu Ala Ile Xaa His Pro Phe Glu Gly Ala Ser Val Arg Asn Lys Ala
 165 170 175
 Ser Asp Gly Ile Lys Ile Ile Thr Gly Lys Gly Leu Leu Gly Ala Ile
 180 185 190
 Ser Gly Val Gln Lys Ser Lys Lys Asn Gly Pro Ile Asp Trp Glu Trp
 195 200 205
 Glu Asp Met Pro Val Ser Cys Ser Pro Ser Ser Gly Val Leu Arg Val
 210 215 220
 Pro Asn Leu Pro Pro Val Leu Ala Asn Ile Leu Glu Ser Arg Ser Arg
 225 230 235 240
 Lys Lys Cys Trp Gly Phe Xaa Pro Ser Phe Leu Gln Glu Asn
 245 250 254

<210> 1159

<211> 162

<212> Amino acid

<213> Homo sapiens

<400> 1159

Gly Ser Thr Ile Ser Cys Glu Arg Ser Leu Arg Ser Leu Trp Thr Ala
 1 5 10 15
 His Trp Ala Leu Pro Glu Met Asp Ser Arg Ile Pro Tyr Asp Asp Tyr
 20 25 30
 Pro Val Val Phe Leu Pro Ala Tyr Glu Asn Pro Pro Ala Trp Ile Pro
 35 40 45
 Pro His Glu Arg Val His His Pro Asp Tyr Asn Asn Glu Leu Thr Gln
 50 55 60
 Phe Leu Pro Arg Thr Ile Thr Leu Lys Lys Pro Pro Gly Ala Gln Leu
 65 70 75 80
 Gly Phe Asn Ile Arg Gly Gly Lys Ala Ser Gln Leu Gly Ile Phe Ile
 85 90 95
 Ser Lys Val Ile Pro Asp Ser Asp Ala His Arg Ala Gly Leu Gln Glu
 100 105 110
 Gly Asp Gln Val Leu Ala Val Asn Asp Val Asp Phe Gln Asp Ile Glu
 115 120 125
 His Ser Lys Ala Val Glu Ile Leu Lys Thr Ala Arg Glu Ile Ser Met
 130 135 140
 Arg Val Arg Phe Phe Pro Tyr Asn Tyr His Arg Gln Lys Glu Arg Thr
 145 150 155 160
 Val His
 162

<210> 1160
 <211> 295
 <212>Amino acid
 <213> Homo sapiens

<400> 1160
 His Glu Gln Val Ser Ala Leu His Arg Arg Ile Lys Ala Ile Val Glu
 1 5 10 15
 Val Ala Ala Met Cys Gly Val Asn Ile Ile Cys Phe Gln Glu Ala Trp
 20 25 30
 Thr Met Pro Phe Ala Phe Cys Thr Arg Glu Lys Leu Pro Trp Thr Glu
 35 40 45
 Phe Ala Glu Ser Ala Glu Asp Gly Pro Thr Thr Arg Phe Cys Gln Lys
 50 55 60
 Leu Ala Lys Asn His Asp Met Val Val Val Ser Pro Ile Leu Glu Arg
 65 70 75 80
 Asp Ser Glu His Gly Asp Val Leu Trp Asn Thr Ala Val Val Ile Ser
 85 90 95
 Asn Ser Gly Ala Val Leu Gly Lys Thr Arg Lys Asn His Ile Pro Arg
 100 105 110
 Val Gly Asp Phe Asn Glu Ser Thr Tyr Tyr Met Glu Gly Asn Leu Gly
 115 120 125
 His Pro Val Phe Gln Thr Gln Phe Gly Arg Ile Ala Val Asn Ile Cys
 130 135 140
 Tyr Gly Arg His His Pro Leu Asn Trp Leu Met Tyr Ser Ile Asn Gly
 145 150 155 160
 Ala Glu Ile Ile Phe Asn Pro Ser Ala Thr Ile Gly Ala Leu Ser Glu
 165 170 175
 Ser Leu Trp Pro Ile Glu Ala Arg Asn Ala Ala Ile Ala Asn His Cys
 180 185 190
 Phe Thr Cys Ala Ile Asn Arg Val Gly Thr Glu His Phe Pro Asn Glu
 195 200 205
 Phe Thr Ser Gly Asp Gly Lys Lys Ala His Gln Asp Phe Gly Tyr Phe
 210 215 220
 Tyr Gly Ser Ser Tyr Val Ala Ala Pro Asp Ser Ser Arg Thr Pro Gly
 225 230 235 240
 Leu Ser Arg Ser Arg Asp Gly Leu Leu Val Ala Lys Leu Asp Leu Asn
 245 250 255
 Leu Cys Gln Gln Val Asn Asp Val Trp Asn Phe Lys Met Thr Gly Arg
 260 265 270
 Tyr Glu Met Tyr Ala Arg Glu Leu Ala Glu Ala Val Lys Ser Asn Tyr
 275 280 285
 Ser Pro Thr Ile Val Lys Glu
 290 295

<210> 1161
 <211> 1621
 <212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(1621)
 <223> X = any amino acid or stop code

<400> 1161

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Met Ala Lys Ser Gly Gly Cys Gly Ala Gly Ala Gly Val Gly Gly Gly
 1          5          10          15
Asn Gly Ala Leu Thr Trp Val Asn Asn Ala Ala Lys Lys Glu Glu Ser
          20          25          30
Glu Thr Ala Asn Lys Asn Asp Ser Ser Lys Lys Leu Ser Val Glu Arg
          35          40          45
Val Tyr Gln Lys Lys Thr Gln Leu Glu His Ile Leu Leu Arg Pro Asp
          50          55          60
Thr Tyr Ile Gly Ser Val Glu Pro Leu Thr Gln Phe Met Trp Val Tyr
          65          70          75          80
Asp Glu Asp Val Gly Met Asn Cys Arg Glu Val Thr Phe Val Pro Gly
          85          90          95
Leu Tyr Lys Ile Phe Asp Glu Ile Leu Val Asn Ala Ala Asp Asn Lys
          100          105          110
Gln Arg Asp Lys Asn Met Thr Cys Ile Lys Val Ser Ile Asp Pro Glu
          115          120          125
Ser Asn Ile Ile Ser Ile Trp Asn Asn Gly Lys Gly Ile Pro Val Val
          130          135          140
Glu His Lys Val Glu Lys Val Tyr Val Pro Ala Leu Ile Phe Gly Gln
          145          150          155          160
Leu Leu Thr Ser Ser Asn Tyr Asp Asp Asp Glu Lys Lys Val Thr Gly
          165          170          175
Gly Arg Asn Gly Tyr Gly Ala Lys Leu Cys Asn Ile Phe Ser Thr Lys
          180          185          190
Phe Thr Val Glu Thr Ala Cys Lys Glu Tyr Lys His Ser Phe Lys Gln
          195          200          205
Thr Trp Met Asn Asn Met Met Lys Thr Ser Glu Ala Lys Ile Lys His
          210          215          220
Phe Asp Gly Glu Asp Tyr Thr Cys Ile Thr Phe Gln Pro Asp Leu Ser
          225          230          235          240
Lys Phe Lys Met Glu Lys Leu Asp Lys Asp Ile Val Ala Leu Met Thr
          245          250          255
Arg Arg Ala Tyr Asp Leu Ala Gly Ser Cys Arg Gly Val Lys Val Met
          260          265          270
Phe Asn Gly Lys Lys Leu Pro Val Asn Gly Phe Arg Ser Tyr Val Asp
          275          280          285
Leu Tyr Val Lys Asp Lys Leu Asp Glu Thr Gly Val Ala Leu Lys Val
          290          295          300
Ile His Glu Leu Ala Asn Glu Arg Trp Asp Val Cys Leu Thr Leu Ser
          305          310          315          320
Glu Lys Gly Phe Gln Gln Ile Ser Phe Val Asn Ser Ile Ala Thr Thr
          325          330          335
Lys Gly Gly Arg His Val Asp Tyr Val Val Asp Gln Val Val Gly Lys
          340          345          350
Leu Ile Glu Val Val Lys Lys Lys Asn Lys Ala Gly Val Ser Val Lys
          355          360          365
Pro Phe Gln Val Lys Asn His Ile Trp Val Phe Ile Asn Cys Leu Ile
          370          375          380
Glu Asn Pro Thr Phe Asp Ser Gln Thr Lys Glu Asn Met Thr Leu Gln
          385          390          395          400
Pro Lys Ser Phe Gly Ser Lys Cys Gln Leu Ser Glu Lys Phe Phe Lys
          405          410          415
Ala Ala Ser Asn Cys Gly Ile Val Glu Ser Ile Leu Asn Trp Val Lys
          420          425          430
Phe Lys Ala Gln Thr Gln Leu Asn Lys Lys Cys Ser Ser Val Lys Tyr
          435          440          445
Ser Lys Ile Lys Gly Ile Pro Lys Leu Asp Asp Ala Asn Asp Ala Gly
          450          455          460
Gly Lys His Ser Leu Glu Cys Thr Leu Ile Leu Thr Glu Gly Asp Ser
          465          470          475          480
Ala Lys Ser Leu Ala Val Ser Gly Leu Gly Val Ile Gly Arg Asp Arg
          485          490          495
Tyr Gly Val Phe Pro Leu Arg Gly Lys Ile Leu Asn Val Arg Glu Ala

```

500					505					510					
Ser	His	Lys	Gln	Ile	Met	Glu	Asn	Ala	Glu	Ile	Asn	Asn	Ile	Ile	Lys
515					520					525					
Ile	Val	Gly	Leu	Gln	Tyr	Lys	Lys	Ser	Tyr	Asp	Asp	Ala	Gln	Ser	Leu
530					535					540					
Lys	Thr	Leu	Arg	Tyr	Gly	Lys	Ile	Met	Ile	Met	Thr	Asp	Gln	Asp	Gln
545					550					555					
Asp	Gly	Ser	His	Ile	Lys	Gly	Leu	Leu	Ile	Asn	Phe	Ile	His	His	Asn
565					570					575					
Trp	Pro	Ser	Leu	Leu	Lys	His	Gly	Phe	Leu	Glu	Glu	Phe	Ile	Thr	Pro
580					585					590					
Ile	Val	Lys	Ala	Ser	Lys	Asn	Lys	Gln	Glu	Leu	Ser	Phe	Tyr	Ser	Ile
595					600					605					
Pro	Glu	Phe	Asp	Glu	Trp	Lys	Lys	His	Ile	Glu	Asn	Gln	Lys	Ala	Trp
610					615					620					
Lys	Ile	Lys	Tyr	Tyr	Lys	Gly	Leu	Gly	Thr	Ser	Thr	Ala	Lys	Glu	Ala
625					630					635					
Lys	Glu	Tyr	Phe	Ala	Asp	Met	Glu	Arg	His	Arg	Ile	Leu	Phe	Arg	Tyr
645					650					655					
Ala	Gly	Pro	Glu	Asp	Asp	Ala	Ala	Ile	Thr	Leu	Ala	Phe	Ser	Lys	Lys
660					665					670					
Lys	Ile	Asp	Asp	Arg	Lys	Glu	Trp	Leu	Thr	Asn	Phe	Met	Glu	Asp	Arg
675					680					685					
Arg	Gln	Arg	Arg	Leu	His	Gly	Leu	Pro	Glu	Gln	Phe	Leu	Tyr	Gly	Thr
690					695					700					
Ala	Thr	Lys	His	Leu	Thr	Tyr	Asn	Asp	Phe	Ile	Asn	Lys	Glu	Leu	Ile
705					710					715					
Leu	Phe	Ser	Asn	Ser	Asp	Asn	Glu	Arg	Ser	Ile	Pro	Ser	Leu	Val	Asp
725					730					735					
Gly	Phe	Lys	Pro	Gly	Gln	Arg	Lys	Val	Leu	Phe	Thr	Cys	Phe	Lys	Arg
740					745					750					
Asn	Asp	Lys	Arg	Glu	Val	Lys	Val	Ala	Gln	Leu	Ala	Gly	Ser	Val	Ala
755					760					765					
Glu	Met	Ser	Ala	Tyr	His	His	Gly	Glu	Gln	Ala	Leu	Met	Met	Thr	Ile
770					775					780					
Val	Asn	Leu	Ala	Gln	Asn	Phe	Val	Gly	Ser	Asn	Asn	Ile	Asn	Leu	Leu
785					790					795					
Gln	Pro	Ile	Gly	Gln	Phe	Gly	Thr	Arg	Leu	His	Gly	Gly	Lys	Asp	Ala
805					810					815					
Ala	Ser	Pro	Arg	Tyr	Ile	Phe	Thr	Met	Leu	Ser	Thr	Leu	Ala	Arg	Leu
820					825					830					
Leu	Phe	Pro	Ala	Val	Asp	Asp	Asn	Leu	Leu	Lys	Phe	Leu	Tyr	Asp	Asp
835					840					845					
Asn	Gln	Arg	Val	Glu	Pro	Glu	Trp	Tyr	Ile	Pro	Ile	Ile	Pro	Met	Val
850					855					860					
Leu	Ile	Asn	Gly	Ala	Glu	Gly	Ile	Gly	Thr	Gly	Trp	Ala	Cys	Lys	Leu
865					870					875					
Pro	Asn	Tyr	Asp	Ala	Arg	Glu	Ile	Val	Asn	Asn	Val	Arg	Arg	Met	Leu
885					890					895					
Asp	Gly	Leu	Asp	Pro	His	Pro	Met	Leu	Pro	Asn	Tyr	Lys	Asn	Phe	Lys
900					905					910					
Gly	Thr	Ile	Gln	Glu	Leu	Gly	Gln	Asn	Gln	Tyr	Ala	Val	Ser	Gly	Glu
915					920					925					
Ile	Phe	Val	Val	Asp	Arg	Asn	Thr	Val	Glu	Ile	Thr	Glu	Leu	Pro	Val
930					935					940					
Arg	Thr	Trp	Thr	Gln	Val	Tyr	Lys	Glu	Gln	Val	Leu	Glu	Pro	Met	Leu
945					950					955					
Asn	Gly	Thr	Asp	Lys	Thr	Pro	Ala	Leu	Ile	Ser	Asp	Tyr	Lys	Glu	Tyr
965					970					975					
His	Thr	Asp	Thr	Thr	Val	Lys	Phe	Val	Val	Lys	Met	Thr	Glu	Glu	Lys
980					985					990					
Leu	Ala	Gln	Ala	Glu	Ala	Ala	Gly	Leu	His	Lys	Val	Phe	Lys	Leu	Gln
995					1000					1005					
Thr	Thr	Leu	Thr	Cys	Asn	Ser	Met	Val	Leu	Phe	Asp	His	Met	Gly	Cys

1010	1015	1020
Leu Lys Lys Tyr Glu Thr Val Gln Asp Ile Leu Lys Glu Phe Phe Asp		
1025	1030	1035
Leu Arg Leu Ser Tyr Tyr Gly Leu Arg Lys Glu Trp Leu Val Gly Met		1040
	1045	1050
Leu Gly Ala Glu Phe Thr Lys Leu Asn Asn Gln Ala Arg Phe Ile Leu		1055
	1060	1065
Glu Lys Ile Gln Gly Lys Ile Thr Ile Xaa Asn Arg Ser Lys Lys Asp		1070
	1075	1080
Leu Ile Gln Met Leu Val Gln Arg Gly Tyr Glu Ser Asp Pro Val Lys		1085
	1090	1095
Ala Trp Lys Glu Ala Gln Glu Lys Ala Ala Glu Glu Asp Glu Thr Gln		1100
1105	1110	1115
Asn Gln His Asp Asp Ser Ser Ser Asp Ser Gly Thr Pro Ser Gly Pro		1120
	1125	1130
Asp Phe Asn Tyr Ile Leu Asn Met Ser Leu Trp Ser Leu Thr Lys Glu		1135
	1140	1145
Lys Val Glu Glu Leu Ile Lys Gln Arg Asp Ala Lys Gly Arg Glu Val		1150
	1155	1160
Asn Asp Leu Lys Arg Lys Ser Pro Ser Asp Leu Trp Lys Glu Asp Leu		1165
	1170	1175
Ala Ala Phe Val Glu Glu Leu Asp Lys Val Glu Ser Gln Glu Arg Glu		1180
1185	1190	1195
Asp Val Leu Ala Gly Met Ser Gly Lys Ala Ile Lys Gly Lys Val Gly		1200
	1205	1210
Lys Pro Lys Val Lys Lys Leu Gln Leu Glu Glu Thr Met Pro Ser Pro		1215
	1220	1225
Tyr Gly Arg Arg Ile Ile Pro Glu Ile Thr Ala Met Lys Ala Asp Ala		1230
	1235	1240
Ser Lys Lys Leu Leu Lys Lys Lys Gly Asp Leu Asp Thr Ala Ala		1245
	1250	1255
Val Lys Val Glu Phe Asp Glu Glu Phe Ser Gly Ala Pro Val Glu Gly		1260
1265	1270	1275
Ala Gly Glu Glu Ala Leu Thr Pro Ser Val Pro Ile Asn Lys Gly Pro		1280
	1285	1290
Lys Pro Lys Arg Glu Lys Lys Glu Pro Gly Thr Arg Val Arg Lys Thr		1295
	1300	1305
Pro Thr Ser Ser Gly Lys Pro Ser Ala Lys Lys Val Lys Lys Arg Asn		1310
	1315	1320
Pro Trp Ser Asp Asp Glu Ser Lys Ser Glu Ser Asp Leu Glu Glu Thr		1325
	1330	1335
Glu Pro Val Val Ile Pro Arg Asp Ser Leu Leu Arg Arg Ala Ala Ala		1340
1345	1350	1355
Glu Arg Pro Lys Tyr Thr Phe Asp Phe Ser Glu Glu Glu Asp Asp Asp		1360
	1365	1370
Ala Asp Asp Asp Asp Asp Asp Asn Asn Asp Leu Glu Glu Leu Lys Val		1375
	1380	1385
Lys Ala Ser Pro Ile Thr Asn Asp Gly Glu Asp Glu Phe Val Pro Ser		1390
	1395	1400
Asp Gly Leu Asp Lys Asp Glu Tyr Thr Phe Ser Pro Gly Lys Ser Lys		1405
	1410	1415
Ala Thr Pro Glu Lys Ser Leu His Asp Lys Lys Ser Gln Asp Phe Gly		1420
1425	1430	1435
Asn Leu Phe Ser Phe Pro Ser Tyr Ser Gln Lys Ser Glu Asp Asp Ser		1440
	1445	1450
Ala Lys Phe Asp Ser Asn Glu Glu Asp Ser Ala Ser Val Phe Ser Pro		1455
	1460	1465
Ser Phe Gly Leu Lys Gln Thr Asp Lys Val Pro Ser Lys Thr Val Ala		1470
	1475	1480
Ala Lys Lys Gly Lys Pro Ser Ser Asp Thr Val Pro Lys Pro Lys Arg		1485
	1490	1495
Ala Pro Lys Gln Lys Lys Val Val Glu Ala Val Asn Ser Asp Ser Asp		1500
1505	1510	1515
Ser Glu Phe Gly Ile Pro Lys Lys Thr Thr Thr Pro Lys Gly Lys Gly		1520

```

          1525          1530          1535
Arg Gly Ala Lys Lys Arg Lys Ala Ser Gly Ser Glu Asn Glu Gly Asp
          1540          1545          1550
Tyr Asn Pro Gly Arg Lys Thr Ser Lys Thr Thr Ser Lys Lys Pro Lys
          1555          1560          1565
Lys Thr Ser Phe Asp Gln Asp Ser Asp Val Asp Ile Phe Pro Ser Asp
          1570          1575          1580
Phe Pro Thr Glu Pro Pro Ser Leu Pro Arg Thr Gly Arg Ala Arg Lys
1585          1590          1595          1600
Glu Val Lys Tyr Phe Ala Glu Ser Asp Glu Glu Glu Asp Asp Val Asp
          1605          1610          1615
Phe Ala Met Phe Asn
          1620 1621

```

```

<210> 1162
<211> 73
<212> Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(73)
<223> X = any amino acid or stop code

```

```

<400> 1162
Lys Gly Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe Leu Tyr Thr Gly
 1          5          10          15
Glu Leu Tyr Pro Thr Met Ile Arg Xaa Val Glu Ala Xaa Trp Glu Asn
          20          25          30
Asp Ser Leu Phe Leu Gly Lys Asp Ile Leu Leu Cys Thr Gly Gln Thr
          35          40          45
Pro Glu Leu Asn Gln Val His Pro Ser Pro Lys Ala Pro Pro Asn Thr
          50          55          60
His His Cys Lys Ala His Ser Ser His
          65          70          73

```

```

<210> 1163
<211> 336
<212> Amino acid
<213> Homo sapiens

```

```

<400> 1163
Glu Asn Ser Phe Glu Cys Lys Asp Cys Gly Lys Ala Phe Ser Arg Gly
 1          5          10          15
Tyr Gln Leu Ser His His Gln Lys Ile His Thr Gly Glu Lys Pro Tyr
          20          25          30
Glu Cys Lys Glu Cys Lys Lys Ala Phe Arg Trp Gly Asn Gln Leu Thr
          35          40          45
Gln His Gln Lys Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Asp
          50          55          60
Cys Gly Lys Ala Phe Arg Trp Gly Ser Ser Leu Val Ile His Lys Arg
          65          70          75          80
Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Asp Cys Gly Lys Ala
          85          90          95

```

```

Phe Arg Arg Gly Asp Glu Leu Thr Gln His Gln Arg Phe His Thr Gly
      100                      105                      110
Glu Lys Asp Tyr Glu Cys Lys Asp Cys Gly Lys Thr Phe Ser Arg Val
      115                      120                      125
Tyr Lys Leu Ile Gln His Lys Arg Ile His Ser Gly Glu Lys Pro Tyr
      130                      135                      140
Glu Cys Lys Asp Cys Gly Lys Ala Phe Ile Cys Gly Ser Ser Leu Ile
145                      150                      155                      160
Gln His Lys Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Gln Glu
      165                      170                      175
Cys Gly Lys Ala Phe Thr Arg Val Asn Tyr Leu Thr Gln His Gln Lys
      180                      185                      190
Ile His Thr Gly Glu Lys Pro His Glu Cys Lys Glu Cys Gly Lys Ala
      195                      200                      205
Phe Arg Trp Gly Ser Ser Leu Val Lys His Glu Arg Ile His Thr Gly
      210                      215                      220
Glu Lys Pro Tyr Lys Cys Thr Glu Cys Gly Lys Ala Phe Asn Cys Gly
225                      230                      235                      240
Tyr His Leu Thr Gln His Glu Arg Ile His Thr Gly Glu Thr Pro Tyr
      245                      250                      255
Lys Cys Lys Glu Cys Gly Lys Ala Phe Ile Tyr Gly Ser Ser Leu Val
      260                      265                      270
Lys His Glu Arg Ile His Thr Gly Val Lys Pro Tyr Gly Cys Thr Glu
      275                      280                      285
Cys Gly Lys Ser Phe Ser His Gly His Gln Leu Thr Gln His Gln Lys
      290                      295                      300
Thr His Ser Gly Ala Lys Ser Tyr Glu Cys Lys Glu Cys Gly Lys Ala
305                      310                      315                      320
Cys Asn His Leu Asn His Leu Arg Glu His Gln Arg Ile His Asn Ser
      325                      330                      335 336

```

<210> 1164

<211> 118

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(118)

<223> X = any amino acid or stop code

<400> 1164

```

His Gln Tyr Leu Asp Asp Leu Tyr Pro Leu His Val Met Thr Ile Leu
 1                      5                      10                      15
Leu Lys Ser His Phe Phe Thr Met Leu Lys Arg Pro Val Gly Ser Ser
      20                      25                      30
Ser Phe Ala Ser Leu Pro Phe Tyr His Gln Ser Ile Leu Leu Arg Lys
      35                      40                      45
Asn Gln Met Lys Arg Lys Lys Thr Gln Gln Asp Leu Thr His Ile Asn
      50                      55                      60
Trp Thr Leu Gln Ala Val Ser Ile Gln Thr Cys Ile Trp Leu Gln Lys
      65                      70                      75                      80
Lys Pro Ser Ser Tyr Phe His Gln Leu Pro Asn Gln Val Leu Xaa Pro
      85                      90                      95
Glu Asn Ser Gly Pro Glu Ser Cys Leu Tyr Asp Leu Ala Ala Val Val
      100                      105                      110
Val His His Gly Ser Gly

```

115

118

<210> 1165

<211> 146

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(146)

<223> X = any amino acid or stop code

<400> 1165

```

Xaa Leu Asp Pro Asp Thr Leu Pro Ala Val Ala Thr Leu Leu Met Asp
 1           5           10           15
Val Met Phe Tyr Ser Asn Gly Val Lys Asp Pro Met Ala Thr Gly Asp
           20           25           30
Asp Cys Gly His Ile Arg Phe Phe Ser Phe Ser Leu Ile Glu Gly Tyr
           35           40           45
Ile Ser Leu Val Met Asp Val Gln Thr Gln Gln Arg Phe Pro Ser Asn
           50           55           60
Leu Leu Phe Thr Ser Ala Ser Gly Glu Leu Trp Lys Met Val Arg Ile
           65           70           75           80
Gly Gly Gln Pro Leu Gly Phe Gly Pro Val Trp Glu Ser Gly Pro Thr
           85           90           95
Gly Pro Thr Ser Pro Leu Ile Leu Pro Val Thr Pro Ser Ser Ser His
           100          105          110
Arg Gln Ala Ala Ser Gln Val Thr Thr Thr Lys Gln Gly Gln Trp Leu
           115          120          125
Cys Leu Lys Arg Pro Ser Ala Arg Ser Pro Asp His Thr Ala Cys Leu
           130          135          140
Gly *
145

```

<210> 1166

<211> 84

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(84)

<223> X = any amino acid or stop code

<400> 1166

```

Glu Ala Pro Leu Thr Ser Val Cys Phe Ser Leu Glu Arg Arg Phe Gly
 1           5           10           15
Ser Ser Ser Asn Thr Thr Ser Phe Gly Thr Leu Ala Ser Gln Asn Ala
           20           25           30
Pro Thr Phe Gly Ser Leu Ser Gln Gln Thr Ser Gly Phe Gly Thr Gln
           35           40           45
Ser Ser Gly Phe Ser Gly Phe Gly Ser Gly Thr Gly Gly Phe Ser Phe
           50           55           60
Gly Ser Asn Asn Ser Xaa Val Ser Pro Phe Leu Ser Leu Thr Leu Ile

```


65
Lys Ser Ile Lys
84

70

75

80

<210> 1167

<211> 112

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(112)

<223> X = any amino acid or stop code

<400> 1167

Glu	Glu	Pro	Gln	Gly	Ser	Pro	Ile	Trp	Val	Trp	Leu	Ala	Gly	Ser	Leu
1				5				10						15	
Thr	Ser	Val	Ser	Cys	Phe	Leu	Pro	Phe	Gln	Arg	Met	Arg	Ile	Lys	Pro
			20					25					30		
His	Gln	Gly	Gln	Tyr	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	His	Lys
		35				40						45			
Gly	Glu	Cys	Arg	Pro	Gln	Lys	Asp	Xaa	Ala	Arg	Gln	Glu	Asn	Pro	Cys
	50					55				60					
Gly	Pro	Cys	Ser	Glu	Arg	Lys	His	Leu	Leu	Gly	Gln	Asp	Pro	Lys	
	65				70				75					80	
Thr	Cys	Lys	Cys	Ser	Cys	Lys	Asn	Thr	Asp	Ser	Arg	Cys	Lys	Ala	Arg
				85				90						95	
Pro	Leu	Glu	Leu	Asn	Glu	Arg	Thr	Cys	Arg	Cys	Asp	Lys	Pro	Arg	Arg
			100					105					110		112

<210> 1168

<211> 319

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(319)

<223> X = any amino acid or stop code

<400> 1168

Thr	Leu	Trp	Ala	Gly	Pro	Gly	Leu	Cys	Pro	Gln	Ser	His	Ser	Ser	Ser
1				5				10						15	
Ser	Val	Pro	Ala	Pro	Trp	Glu	Pro	His	Val	Glu	Arg	Ala	Leu	Arg	Thr
			20					25					30		
Asp	Arg	Asn	Gln	Gly	Gln	Arg	Pro	Leu	Leu	Ser	Ala	Ser	Trp	Ala	Pro
		35				40						45			
Ala	Pro	Ala	Arg	Pro	Leu	Phe	Leu	Thr	Ser	Pro	Val	Leu	Leu	Pro	Lys
	50					55				60					
Ser	Arg	Ala	Ile	Pro	Ala	Ala	Arg	Asp	Pro	Ser	Xaa	Ala	Gly	Ile	Phe
	65				70					75				80	
Cys	Leu	Leu	Glu	Met	Ala	Gly	Gly	Gln	Ala	Ser	Val	Val	Ile	Ile	Gly

										85					90					95				
Ser	Ala	Gly	Val	Leu	Gly	Cys	Arg	Trp	Gly	Ser	Ser	Gly	Lys	Ser	His									
				100					105					110										
Ser	Leu	Ser	Pro	Ser	Arg	Lys	Gly	Asn	Leu	His	Leu	Leu	Ser	Gln	Glu									
				115					120					125										
Pro	Gln	Thr	Thr	Val	Val	His	Asn	Ala	Thr	Asp	Gly	Ile	Lys	Gly	Ser									
				130					135					140										
Thr	Glu	Ser	Cys	Asn	Thr	Thr	Thr	Glu	Asp	Glu	Asp	Leu	Lys	Val	Arg									
				145					150					155										
Lys	Gln	Glu	Ile	Ile	Lys	Ile	Thr	Glu	Gln	Leu	Ile	Glu	Ala	Ile	Asn									
				165					170					175										
Asn	Gly	Asp	Phe	Glu	Ala	Tyr	Thr	Lys	Ile	Cys	Asp	Pro	Gly	Leu	Thr									
				180					185					190										
Ser	Phe	Glu	Pro	Glu	Ala	Leu	Gly	Asn	Leu	Val	Glu	Gly	Met	Asp	Phe									
				195					200					205										
His	Lys	Phe	Tyr	Phe	Glu	Asn	Arg	Glu	Trp	Val	Arg	Ala	Ala	Asp	Ile									
				210					215					220										
Leu	Leu	Pro	Ala	Pro	Leu	Pro	Leu	Cys	Leu	Cys	Leu	Leu	Leu	Thr	Phe									
				225					230					235										
Ser	Ser	Gln	Leu	Pro	Thr	Phe	Pro	Leu	Phe	Asp	Leu	Arg	Ala	Ala	Leu									
				245					250					255										
Leu	Leu	Cys	Met	Leu	Val	Pro	Leu	Cys	Pro	Asp	Gly	Cys	Arg	Gln	Ala									
				260					265					270										
Pro	Leu	Lys	Ala	Leu	Leu	Leu	Ser	Ser	Lys	Cys	His	Ser	Phe	Cys	Ser									
				275					280					285										
Cys	Phe	Val	Ala	Val	Pro	Val	Thr	Thr	Ile	Lys	Leu	Thr	Tyr	Phe	Leu									
				290					295					300										
Pro	Gly	Ala	Val	Ala	Tyr	Ala	Cys	Asn	Pro	Asn	Thr	Leu	Gly	Gly										
				305					310					315										
														319										

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<210> 1169
<211> 96
<212> Amino acid
<213> Homo sapiens
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	<400> 1169															
Glu	Arg	Ala	Gly	Ala	Gly	Gly	Ala	Ala	Ala	Cys	Arg	Ala	Gly	Thr	Arg	
1				5					10					15		
Ser	Gly	Ala	Thr	Ser	Arg	Thr	Pro	Trp	Pro	Leu	His	Arg	Gln	Leu	Ser	
			20					25					30			
Met	Met	Leu	Met	Leu	Ala	Gln	Ser	Asn	Pro	Gln	Leu	Phe	Ala	Leu	Met	
		35					40					45				
Gly	Thr	Arg	Ala	Gly	Ile	Ala	Arg	Glu	Leu	Glu	Arg	Val	Glu	Gln	Gln	
	50					55					60					
Ser	Arg	Leu	Glu	Gln	Leu	Ser	Ala	Ala	Glu	Leu	Gln	Ser	Arg	Asn	Gln	
	65				70						75			80		
Gly	His	Trp	Ala	Asp	Trp	Leu	Gln	Ala	Tyr	Arg	Ala	Arg	Leu	Gly	Gln	
				85					90					95	96	

```
<210> 1170
<211> 145
<212> Amino acid
<213> Homo sapiens
```

```
<220>  
<221> misc feature
```

<222> (1)...(145)

<223> X = any amino acid or stop code

<400> 1170

```

Asn Gly Thr Leu Phe Ile Met Val Met His Ile Lys Asp Leu Val Ser
 1           5           10           15
Asp Tyr Lys Glu Xaa Trp Leu Xaa Arg Lys Pro Leu Pro Trp Xaa Glu
          20           25           30
Ala Leu Leu Leu Arg Asp Cys Phe Phe Phe Xaa Val Thr Glu Asn Gly
          35           40           45
Ala Asp Pro Asn Pro Tyr Val Lys Thr Tyr Leu Leu Pro Asp Asn His
          50           55           60
Lys Thr Ser Lys Arg Lys Thr Lys Ile Ser Arg Lys Thr Arg Asn Pro
          65           70           75           80
Thr Phe Asn Glu Met Leu Val Tyr Ser Gly Tyr Ser Lys Glu Thr Leu
          85           90           95
Arg Gln Arg Glu Leu Gln Leu Ser Val Leu Ser Ala Glu Ser Leu Arg
          100          105          110
Glu Asn Phe Phe Leu Gly Gly Val Thr Leu Pro Leu Lys Asp Phe Asn
          115          120          125
Leu Ser Lys Glu Thr Val Lys Trp Tyr Gln Leu Thr Ala Ala Thr Tyr
          130          135          140
Leu
145

```

<210> 1171

<211> 464

<212> Amino acid

<213> Homo sapiens

<400> 1171

```

Leu His Arg Ile Met Gln Leu Ala Val Val Val Ser Gln Val Leu Glu
 1           5           10           15
Asn Gly Ser Ser Val Leu Val Cys Leu Glu Glu Gly Trp Asp Ile Thr
          20           25           30
Ala Gln Val Thr Ser Leu Val Gln Leu Leu Ser Asp Pro Phe Tyr Arg
          35           40           45
Thr Leu Glu Gly Phe Gln Met Leu Val Glu Lys Glu Trp Leu Ser Phe
          50           55           60
Gly His Lys Phe Ser Gln Arg Ser Ser Leu Thr Leu Asn Cys Gln Gly
          65           70           75           80
Ser Gly Phe Ala Pro Val Phe Leu Gln Phe Leu Asp Cys Val His Gln
          85           90           95
Val His Asn Gln Tyr Pro Thr Glu Phe Glu Phe Asn Leu Tyr Tyr Leu
          100          105          110
Lys Phe Leu Ala Phe His Tyr Val Ser Asn Arg Phe Lys Thr Phe Leu
          115          120          125
Leu Asp Ser Asp Tyr Glu Arg Leu Glu His Gly Thr Leu Phe Asp Asp
          130          135          140
Lys Gly Glu Lys His Ala Lys Lys Gly Val Cys Ile Trp Glu Cys Ile
          145          150          155          160
Asp Arg Met His Lys Arg Ser Pro Ile Phe Phe Asn Tyr Leu Tyr Ser
          165          170          175
Pro Leu Glu Ile Glu Ala Leu Lys Pro Asn Val Asn Val Ser Ser Leu
          180          185          190

```

Lys Lys Trp Asp Tyr Tyr Ile Glu Glu Thr Leu Ser Thr Gly Pro Ser
 195 200 205
 Tyr Asp Trp Met Met Leu Thr Pro Lys His Phe Pro Ser Glu Asp Ser
 210 215 220
 Asp Leu Ala Gly Glu Ala Gly Pro Arg Ser Gln Arg Arg Thr Val Trp
 225 230 235 240
 Pro Cys Tyr Asp Asp Val Ser Cys Thr Gln Pro Asp Ala Leu Thr Ser
 245 250 255
 Leu Phe Ser Glu Ile Glu Lys Leu Glu His Lys Leu Asn Gln Ala Pro
 260 265 270
 Glu Lys Trp Gln Gln Leu Trp Glu Arg Val Thr Val Asp Leu Lys Glu
 275 280 285
 Glu Pro Arg Thr Asp Arg Ser Gln Arg His Leu Ser Arg Ser Pro Gly
 290 295 300
 Ile Val Ser Thr Asn Leu Pro Ser Tyr Gln Lys Arg Ser Leu Leu His
 305 310 315 320
 Leu Pro Asp Ser Ser Met Gly Glu Glu Gln Asn Ser Ser Ile Ser Pro
 325 330 335
 Ser Asn Gly Val Glu Arg Arg Ala Ala Thr Leu Tyr Ser Gln Tyr Thr
 340 345 350
 Ser Lys Asn Asp Glu Asn Arg Ser Phe Glu Gly Thr Leu Tyr Lys Arg
 355 360 365
 Gly Ala Leu Leu Lys Gly Trp Lys Pro Arg Trp Phe Val Leu Asp Val
 370 375 380
 Thr Lys His Gln Leu Arg Tyr Tyr Asp Ser Gly Glu Asp Thr Ser Cys
 385 390 395 400
 Lys Gly His Ile Asp Leu Ala Glu Val Glu Met Val Ile Pro Ala Gly
 405 410 415
 Pro Ser Met Gly Ala Pro Lys His Thr Ser Asp Lys Ala Phe Phe Asp
 420 425 430
 Leu Lys Thr Ser Lys Arg Val Tyr Asn Phe Cys Ala Gln Asp Gly Gln
 435 440 445
 Ser Ala Gln Gln Trp Met Asp Lys Ile Gln Ser Cys Ile Ser Asp Ala
 450 455 460 464

<210> 1172

<211> 256

<212> Amino acid

<213> Homo sapiens

<400> 1172

Glu Val Glu Gly Pro Arg Arg Val Ser Pro Ala Pro Glu Thr Leu Gly
 1 5 10 15
 Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
 20 25 30
 Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
 35 40 45
 Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly
 50 55 60
 Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
 65 70 75 80
 Leu Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
 85 90 95
 Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
 100 105 110
 His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu
 115 120 125

```

Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr
 130          135          140
His Asp Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr
145          150          155          160
Ser Lys Val Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser
          165          170          175
Thr Ile Thr His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu
          180          185          190
Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser
          195          200          205
Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His
210          215          220
Leu Glu Ala Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu
225          230          235          240
Val Arg Leu Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
          245          250          255 256

```

<210> 1173

<211> 117

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(117)

<223> X = any amino acid or stop code

<400> 1173

```

Gln Ser Ala Glu Leu Gly Pro Arg Arg Arg Glu Gly Ser Arg Arg Pro
 1          5          10          15
Ser Cys Thr Lys Ala Ser Lys Pro Trp Arg Arg Arg Pro Gly Gly Pro
          20          25          30
Thr Ser Gly Leu Gly Xaa Gly Pro Leu Ser Pro Gly Pro Tyr Gln Cys
          35          40          45
Arg Pro Ser Leu Pro Ala Gln Leu Tyr Pro Gln Ser Leu Met Ala Ala
50          55          60
Ala Thr Leu Arg Thr Pro Thr Gln Val Ser Ala Ala Ser Ser Arg Pro
65          70          75          80
His Thr Pro Ser Pro Thr His Val Leu Lys Pro Ser Val Arg Gly Ala
          85          90          95
Cys Ser Ser Pro Arg Cys Pro Gly Ser Gly Thr Leu Arg Arg Ser Trp
          100          105          110
Val Gly Pro Phe Phe
          115          117

```

<210> 1174

<211> 370

<212>Amino acid

<213> Homo sapiens

<400> 1174

```

Leu Trp Trp Pro Pro Leu Ser Arg His Ala Ala His Arg Gln Trp Pro

```

1 5 10 15
 Gly Pro Thr Ala Pro Arg Gly Leu Gly His Lys Val Lys Gly Arg Gly
 20 25 30
 Ala Ser Pro Ala Ala Met Trp Ser Cys Ser Trp Phe Asn Gly Thr Gly
 35 40 45
 Leu Val Glu Glu Leu Pro Ala Cys Gln Asp Leu Gln Leu Gly Leu Ser
 50 55 60
 Leu Leu Ser Leu Leu Gly Leu Val Val Gly Val Pro Val Gly Leu Cys
 65 70 75 80
 Tyr Asn Ala Leu Leu Val Leu Ala Asn Leu His Ser Lys Ala Ser Met
 85 90 95
 Thr Met Pro Asp Val Tyr Phe Val Asn Met Ala Val Ala Gly Leu Val
 100 105 110
 Leu Ser Ala Leu Ala Pro Val His Leu Leu Gly Pro Pro Ser Ser Arg
 115 120 125
 Trp Ala Leu Trp Ser Val Gly Gly Glu Val His Val Ala Leu Gln Ile
 130 135 140
 Pro Phe Asn Val Ser Ser Leu Val Ala Met Tyr Ser Thr Ala Leu Leu
 145 150 155 160
 Ser Leu Asp His Tyr Ile Glu Arg Ala Leu Pro Arg Thr Tyr Met Ala
 165 170 175
 Ser Val Tyr Asn Thr Arg His Val Cys Gly Phe Val Trp Gly Gly Ala
 180 185 190
 Leu Leu Thr Ser Phe Ser Ser Leu Leu Phe Tyr Ile Cys Ser His Val
 195 200 205
 Ser Thr Arg Ala Leu Glu Cys Ala Lys Met Gln Asn Ala Glu Ala Ala
 210 215 220
 Asp Ala Thr Leu Val Phe Ile Gly Tyr Val Val Pro Ala Leu Ala Thr
 225 230 235 240
 Leu Tyr Ala Leu Val Leu Leu Ser Arg Val Arg Arg Glu Asp Thr Pro
 245 250 255
 Leu Asp Arg Asp Thr Gly Arg Leu Glu Pro Ser Ala His Arg Leu Leu
 260 265 270
 Val Ala Thr Val Cys Thr Gln Phe Gly Leu Trp Thr Pro His Tyr Leu
 275 280 285
 Ile Leu Leu Gly His Thr Val Ile Ile Ser Arg Gly Lys Pro Val Asp
 290 295 300
 Ala His Tyr Leu Gly Leu Leu His Phe Val Lys Asp Phe Ser Lys Leu
 305 310 315 320
 Leu Ala Phe Ser Ser Ser Phe Val Thr Pro Leu Leu Tyr Arg Tyr Met
 325 330 335
 Asn Gln Ser Phe Pro Ser Lys Leu Gln Arg Leu Met Lys Lys Leu Pro
 340 345 350
 Cys Gly Asp Arg His Cys Ser Pro Asp His Met Gly Val Gln Gln Val
 355 360 365
 Leu Ala
 370

<210> 1175

<211> 145

<212> Amino acid

<213> Homo sapiens

<400> 1175

Ser Glu Ser Glu Leu Phe Thr Leu Met Pro Ser Leu Pro Thr Thr Asn
 1 5 10 15
 Cys Val His Ser Leu Gln Met Ile Pro Pro Leu Ser Pro Ala Pro Asn
 20 25 30
 Gln Glu Leu Val Leu Gly Leu Cys Tyr Met Ser Tyr Leu Ala Phe Leu

```

      35              40              45
Tyr Met Thr Phe Asp Phe Cys Cys Leu Tyr Phe Ser Thr Val Tyr Ala
      50              55              60
Pro Ser Phe Lys Tyr Ile Cys Val His Thr Asp Thr His Ile Cys Val
      65              70              75              80
Cys Val Cys Ile Tyr Leu Ser Ser Val Val Ser Lys Ser Ser Ala Glu
      85              90              95
Ala Asp Gly Val Leu Gln Pro Arg Arg His Pro Ala Ser Leu Leu Ile
      100             105             110
Val Phe Ala Thr Ser Ile Ser Glu Ser Ser Leu Leu Ile Phe Ser Phe
      115             120             125
Gln Lys Thr Glu Ala Lys Leu Ile Val Phe Ala Val Ser Leu Ala Ala
      130             135             140
Lys
145

```

<210> 1176
 <211> 50
 <212>Amino acid
 <213> Homo sapiens

```

    <400> 1176
Phe Phe Phe Leu Arg Gln Ser Leu Thr Leu Ser Pro Arg Leu Glu Cys
  1              5              10              15
Ser Gly Ala Thr Ser Ala Ser Pro Ser Ala Gly Ile Thr Gly Met Ser
      20              25              30
His His Ser Gln Pro Ile Val Asn Phe Leu Arg Ala Cys Ile Pro Ile
      35              40              45
Ser Lys
      50

```

<210> 1177
 <211> 231
 <212>Amino acid
 <213> Homo sapiens

```

    <400> 1177
Arg Gln His Ala Glu Glu Arg Gly Arg Arg Asn Pro Lys Thr Gly Leu
  1              5              10              15
Thr Leu Glu Arg Val Gly Pro Glu Ser Ser Pro Tyr Leu Leu Arg Arg
      20              25              30
His Gln Arg Gln Gly Gln Glu Gly Glu His Tyr His Ser Cys Val Gln
      35              40              45
Leu Ala Pro Thr Arg Gly Leu Glu Glu Ser Gly His Gly Pro Leu Ser
      50              55              60
Leu Ala Gly Gly Pro Arg Val Gly Gly Val Ala Ala Ala Ala Thr Glu
      65              70              75              80
Ala Pro Arg Met Glu Trp Lys Val Lys Val Arg Ser Asp Gly Thr Arg
      85              90              95
Tyr Val Ala Lys Arg Pro Val Arg Asp Arg Leu Leu Lys Ala Arg Ala
      100             105             110
Leu Lys Ile Arg Glu Glu Arg Ser Gly Met Thr Thr Asp Asp Ala
      115             120             125
Val Ser Glu Met Lys Met Gly Arg Tyr Trp Ser Lys Glu Glu Arg Lys

```

```

      130              135              140
Gln His Leu Ile Arg Ala Arg Glu Gln Arg Lys Arg Arg Glu Phe Met
145              150              155              160
Met Gln Ser Arg Leu Glu Cys Leu Arg Glu Gln Gln Asn Gly Asp Ser
      165              170              175
Lys Pro Glu Leu Asn Ile Ile Ala Leu Ser His Arg Lys Thr Met Lys
      180              185              190
Lys Arg Asn Lys Lys Ile Leu Asp Asn Trp Ile Thr Ile Gln Glu Met
      195              200              205
Leu Ala His Gly Ala Arg Ser Ala Asp Gly Lys Arg Val Tyr Asn Pro
      210              215              220
Leu Leu Ser Val Thr Thr Val
225              230 231

```

<210> 1178
 <211> 204
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 1178
Ser Asp Arg Gly Cys Ser Ala Ala Ala Gly Arg Asn Met Thr Ala Val
  1              5              10              15
Gly Val Gln Ala Gln Arg Pro Leu Gly Gln Arg Gln Pro Arg Arg Ser
      20              25              30
Phe Phe Glu Ser Phe Ile Arg Thr Leu Ile Ile Thr Cys Val Ala Leu
      35              40              45
Ala Val Val Leu Ser Ser Val Ser Ile Cys Asp Gly His Trp Leu Leu
      50              55              60
Ala Glu Asp Arg Leu Phe Gly Leu Trp His Phe Cys Thr Thr Thr Asn
      65              70              75              80
Gln Ser Val Pro Ile Cys Phe Arg Asp Leu Gly Gln Ala His Val Pro
      85              90              95
Gly Leu Ala Val Gly Met Gly Leu Val Arg Ser Val Gly Ala Leu Ala
      100              105              110
Val Val Ala Ala Ile Phe Gly Leu Glu Phe Leu Met Val Ser Gln Leu
      115              120              125
Cys Glu Asp Lys His Ser Gln Cys Lys Trp Val Met Gly Ser Ile Leu
      130              135              140
Leu Leu Val Ser Phe Val Leu Ser Ser Gly Gly Leu Leu Gly Phe Val
      145              150              155              160
Ile Leu Leu Arg Asn Gln Val Thr Leu Ile Gly Phe Thr Leu Met Phe
      165              170              175
Trp Cys Glu Phe Thr Ala Ser Phe Leu Leu Phe Leu Asn Ala Ile Ser
      180              185              190
Gly Leu His Ile Asn Ser Ile Thr His Pro Trp Glu
      195              200              204

```

<210> 1179
 <211> 179
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 1179
Gln Ile Leu Pro Asn Leu Tyr Leu Gly Ser Ala Arg Asp Ser Ala Asn

```



```

      1           5           10           15
Leu Glu Ser Leu Ala Lys Leu Gly Ile Arg Tyr Ile Leu Asn Val Thr
      20           25           30
Pro Asn Leu Pro Asn Phe Phe Glu Lys Asn Gly Asp Phe His Tyr Lys
      35           40           45
Gln Ile Pro Ile Ser Asp His Trp Ser Gln Asn Leu Ser Arg Phe Phe
      50           55           60
Pro Glu Ala Ile Glu Phe Ile Asp Glu Ala Leu Ser Gln Asn Cys Gly
      65           70           75           80
Val Leu Val His Cys Leu Ala Gly Val Ser Arg Ser Val Thr Val Thr
      85           90           95
Val Ala Tyr Leu Met Gln Lys Leu His Leu Ser Leu Asn Asp Ala Tyr
      100          105          110
Asp Leu Val Lys Arg Lys Lys Ser Asn Ile Ser Pro Asn Phe Asn Phe
      115          120          125
Met Gly Gln Leu Leu Asp Phe Glu Arg Ser Leu Arg Leu Glu Glu Arg
      130          135          140
His Ser Gln Glu Gln Gly Ser Gly Gly Gln Ala Ser Ala Ala Ser Asn
      145          150          155          160
Pro Pro Ser Phe Phe Thr Thr Pro Thr Ser Asp Gly Ala Phe Glu Leu
      165          170          175
Ala Pro Thr
      179

```

```

<210> 1180
<211> 159
<212>Amino acid
<213> Homo sapiens

```

```

      <400> 1180
Arg Lys Ser Leu His Glu Asn Lys Leu Lys Arg Leu Gln Glu Lys Val
      1           5           10           15
Glu Val Leu Glu Ala Lys Lys Glu Glu Leu Glu Thr Glu Asn Gln Val
      20           25           30
Leu Asn Arg Gln Asn Val Pro Phe Glu Asp Tyr Thr Arg Leu Gln Lys
      35           40           45
Arg Leu Lys Asp Ile Gln Arg Arg His Asn Glu Phe Arg Ser Leu Ile
      50           55           60
Leu Val Pro Asn Met Pro Pro Thr Ala Ser Ile Asn Pro Val Ser Phe
      65           70           75           80
Gln Ser Ser Ala Met Gly Ser Lys His Gly Thr Thr Ile Ser Ser Ser
      85           90           95
Tyr Ala Gly Gly Thr Thr Ser Lys Gly Thr Leu Ser Thr Ser Gln Lys
      100          105          110
Thr Arg Arg Thr Gly Asn Asn Thr Lys Lys Thr Thr Arg Gly Thr Trp
      115          120          125
Ile Phe Arg Arg Met Met Phe Leu Glu Asn Arg Gln Ile Lys Arg Gly
      130          135          140
Glu Val Gly Asp Ser Val Lys Leu Asp Ile Leu Thr Cys Gly Ile
      145          150          155          159

```

```

<210> 1181
<211> 328
<212>Amino acid
<213> Homo sapiens

```

```

<220>
<221> misc_feature

```

<222> (1)...(328)

<223> X = any amino acid or stop code

<400> 1181

```

Gly Arg Pro Gly Ala Gly Ala Ser Glu Leu Phe Pro Ser Val Thr Thr
 1           5           10           15
Asp Leu Ser Val Ser Lys Gln Asn Ala Cys Leu Thr Cys Val Asp Phe
          20           25           30
Val Thr Val His Val Cys Met Gly Phe Trp Gly Ile Gly Pro Gly Ala
          35           40           45
Leu Ser Thr Ser Cys Ile Pro Tyr Pro Leu Ser His Gly Pro Gly Ser
          50           55           60
Val Lys Ala Glu Met Leu His Met Tyr Ser Gln Lys Asp Pro Leu Ile
          65           70           75           80
Leu Cys Val Arg Leu Ala Val Leu Leu Ala Val Thr Leu Thr Val Pro
          85           90           95
Val Val Leu Phe Pro Ile Arg Arg Ala Leu Gln Gln Leu Leu Phe Pro
          100          105          110
Gly Lys Ala Phe Ser Trp Pro Arg His Val Ala Ile Ala Leu Ile Leu
          115          120          125
Leu Val Leu Val Asn Val Leu Val Ile Cys Val Pro Thr Ile Arg Asp
          130          135          140
Ile Phe Gly Val Ile Gly Ser Thr Ser Ala Pro Ser Leu Ile Phe Ile
          145          150          155          160
Leu Pro Ser Ile Phe Tyr Leu Arg Ile Val Pro Ser Glu Val Glu Pro
          165          170          175
Phe Leu Ser Trp Pro Lys Ile Gln Ala Leu Cys Phe Gly Val Leu Gly
          180          185          190
Val Leu Phe Met Ala Val Ser Leu Gly Phe Met Phe Ala Asn Trp Ala
          195          200          205
Thr Gly Gln Ser Arg Met Ser Gly His Xaa Ser Gly Pro Ala Gly Pro
          210          215          220
Gly Pro Cys Ala His Ala His Gly Gly Val Arg Ala Ala Pro Xaa Gly
          225          230          235          240
Pro Ser Cys Pro Thr Cys Gly Gly Gly Trp Phe Pro Xaa Thr Trp Leu
          245          250          255
Ser Glu Ala Gly Asp Ser Arg Gly Cys Arg Leu Ala His Phe Pro Pro
          260          265          270
Pro Gln Gly Cys Gln Ala Trp Ile Met Ala Leu Ile Pro Thr Pro Thr
          275          280          285
Pro Trp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
          290          295          300
Glu Glu Glu Glu Glu Glu Ala Arg Ser Trp Trp Ser Leu Cys Pro Ala
          305          310          315          320
Gln Ser Ser Leu Pro Pro Pro Gly
          325          328

```

<210> 1182

<211> 144

<212> Amino acid

<213> Homo sapiens

<400> 1182

```

Ile Asn Glu Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val
 1           5           10           15

```

```

Leu Leu Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile
      20                25                30
Asp Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val
      35                40                45
Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr
      50                55                60
Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile Ile Phe
      65                70                75                80
Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu Arg Leu Arg
      85                90                95
Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys
      100               105               110
Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn Val Val Leu Thr Glu
      115               120               125
Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr
      130               135               140               144

```

<210> 1183

<211> 484

<212>Amino acid

<213> Homo sapiens

<400> 1183

```

Asp Asp Pro Ile Lys Thr Ser Trp Thr Pro Pro Arg Tyr Val Leu Ser
  1      5                10                15
Met Ser Glu Glu Arg His Glu Arg Val Arg Lys Lys Tyr His Ile Leu
      20                25                30
Val Glu Gly Asp Gly Ile Pro Pro Pro Ile Lys Ser Phe Lys Glu Met
      35                40                45
Lys Phe Pro Ala Ala Ile Leu Arg Gly Leu Lys Lys Lys Gly Ile His
      50                55                60
His Pro Thr Pro Ile Gln Ile Gln Gly Ile Pro Thr Ile Leu Ser Gly
      65                70                75                80
Arg Asp Met Ile Gly Ile Ala Phe Thr Gly Ser Gly Lys Thr Leu Val
      85                90                95
Phe Thr Leu Pro Val Ile Met Phe Cys Leu Glu Gln Glu Lys Arg Leu
      100               105               110
Pro Phe Ser Lys Arg Glu Gly Pro Tyr Gly Leu Ile Ile Cys Pro Ser
      115               120               125
Arg Glu Leu Ala Arg Gln Thr His Gly Ile Leu Glu Tyr Tyr Cys Arg
      130               135               140
Leu Leu Gln Glu Asp Ser Ser Pro Leu Leu Arg Cys Ala Leu Cys Ile
      145               150               155               160
Gly Gly Met Ser Val Lys Glu Gln Met Glu Thr Ile Arg His Gly Val
      165               170               175
His Met Met Val Ala Thr Pro Gly Arg Leu Met Asp Leu Leu Gln Lys
      180               185               190
Lys Met Val Ser Leu Asp Ile Cys Arg Tyr Leu Ala Leu Asp Glu Ala
      195               200               205
Asp Arg Met Ile Asp Met Gly Phe Glu Gly Asp Ile Arg Thr Ile Phe
      210               215               220
Ser Tyr Phe Lys Gly Gln Arg Gln Thr Leu Leu Phe Ser Ala Thr Met
      225               230               235               240
Pro Lys Lys Ile Gln Asn Phe Ala Lys Ser Ala Leu Val Lys Pro Val
      245               250               255
Thr Ile Asn Val Gly Arg Ala Gly Ala Ala Ser Leu Asp Val Ile Gln
      260               265               270

```

Glu Val Glu Tyr Val Lys Glu Glu Ala Lys Met Val Tyr Leu Leu Glu
 275 280 285
 Cys Leu Gln Lys Thr Pro Pro Pro Val Leu Ile Phe Ala Glu Lys Lys
 290 295 300
 Ala Asp Val Asp Ala Ile His Glu Tyr Leu Leu Leu Lys Gly Val Glu
 305 310 315 320
 Ala Val Ala Ile His Gly Gly Lys Asp Gln Glu Glu Arg Thr Lys Ala
 325 330 335
 Ile Glu Ala Phe Arg Glu Gly Lys Lys Asp Val Leu Val Ala Thr Asp
 340 345 350
 Val Ala Ser Lys Gly Leu Asp Phe Pro Ala Ile Gln His Val Ile Asn
 355 360 365
 Tyr Asp Met Pro Glu Glu Ile Glu Asn Tyr Val His Arg Ile Gly Arg
 370 375 380
 Thr Gly Arg Ser Gly Asn Thr Gly Ile Ala Thr Thr Phe Ile Asn Lys
 385 390 395 400
 Ala Cys Asp Glu Ser Val Leu Met Asp Leu Lys Ala Leu Leu Leu Glu
 405 410 415
 Ala Lys Gln Lys Val Pro Pro Val Leu Gln Val Leu His Cys Gly Asp
 420 425 430
 Glu Ser Met Leu Asp Ile Gly Gly Glu Arg Gly Cys Ala Phe Cys Gly
 435 440 445
 Gly Leu Gly His Arg Ile Thr Asp Cys Pro Lys Leu Glu Ala Met Gln
 450 455 460
 Thr Lys Gln Val Ser Asn Ile Gly Arg Lys Asp Tyr Leu Ala His Ser
 465 470 475 480
 Ser Met Asp Phe
 484

<210> 1184

<211> 125

<212>Amino acid

<213> Homo sapiens

<400> 1184

Ile Glu Thr Thr Gln Pro Ser Glu Asp Thr Asn Ala Asn Ser Gln Asp
 1 5 10 15
 Asn Ser Met Gln Pro Glu Thr Ser Ser Gln Gln Gln Leu Leu Ser Pro
 20 25 30
 Thr Leu Ser Asp Arg Gly Gly Ser Arg Gln Asp Ala Ala Asp Ala Gly
 35 40 45
 Lys Pro Gln Arg Lys Phe Gly Gln Trp Arg Leu Pro Ser Ala Pro Lys
 50 55 60
 Pro Ile Ser His Ser Val Ser Ser Val Asn Leu Arg Phe Gly Gly Arg
 65 70 75 80
 Thr Thr Met Lys Ser Val Val Cys Lys Met Asn Pro Met Thr Asp Ala
 85 90 95
 Ala Ser Cys Gly Ser Glu Val Lys Lys Trp Trp Thr Arg Gln Leu Thr
 100 105 110
 Val Glu Ser Asp Glu Ser Gly Asp Asp Leu Leu Asp Ile
 115 120 125

<210> 1185

<211> 73

<212>Amino acid

<213> Homo sapiens

<400> 1185

```

Asn Asp Arg Phe Ser Ala Cys Tyr Phe Thr Leu Lys Leu Lys Glu Ala
 1          5          10          15
Ala Val Arg Gln Arg Glu Ala Leu Lys Lys Leu Thr Lys Asn Ile Ala
          20          25          30
Thr Asp Ser Tyr Ile Ser Val Asn Leu Arg Asp Val Tyr Ala Arg Ser
          35          40          45
Ile Met Glu Met Leu Arg Leu Lys Gly Arg Glu Arg Ala Ser Thr Arg
          50          55          60
Ser Ser Gly Gly Asp Asp Phe Trp Phe
 65          70          73

```

<210> 1186

<211> 343

<212> Amino acid

<213> Homo sapiens

<400> 1186

```

Phe Thr Val Phe Ile Leu Gly Ile Thr Ile Arg Pro Leu Val Glu Phe
 1          5          10          15
Leu Asp Val Lys Arg Ser Asn Lys Lys Gln Gln Ala Val Ser Glu Glu
          20          25          30
Ile Tyr Cys Arg Leu Phe Asp His Val Lys Thr Gly Ile Glu Asp Val
          35          40          45
Cys Gly His Trp Gly His Asn Phe Trp Arg Asp Lys Phe Lys Lys Phe
          50          55          60
Asp Asp Lys Tyr Leu Arg Lys Leu Leu Ile Arg Glu Asn Gln Pro Lys
          65          70          75          80
Ser Ser Ile Val Ser Leu Tyr Lys Lys Leu Glu Ile Lys His Ala Ile
          85          90          95
Glu Met Ala Glu Thr Gly Met Ile Ser Thr Val Pro Thr Phe Ala Ser
          100          105          110
Leu Asn Asp Cys Arg Glu Glu Lys Ile Arg Lys Val Thr Ser Ser Glu
          115          120          125
Thr Asp Glu Ile Arg Glu Leu Leu Ser Arg Asn Leu Tyr Gln Ile Arg
          130          135          140
Gln Arg Thr Leu Ser Tyr Asn Arg His Ser Leu Thr Ala Asp Thr Ser
          145          150          155          160
Glu Arg Gln Ala Lys Glu Ile Leu Ile Arg Arg Arg His Ser Leu Arg
          165          170          175
Glu Ser Ile Arg Lys Asp Ser Ser Leu Asn Arg Glu His Arg Ala Ser
          180          185          190
Thr Ser Thr Ser Arg Tyr Leu Ser Leu Pro Lys Asn Thr Lys Leu Pro
          195          200          205
Glu Lys Leu Gln Lys Arg Arg Thr Ile Ser Ile Ala Asp Gly Asn Ser
          210          215          220
Ser Asp Ser Asp Ala Asp Ala Gly Thr Thr Val Leu Asn Leu Gln Pro
          225          230          235          240
Arg Ala Arg Arg Phe Leu Pro Glu Gln Phe Ser Lys Lys Ser Pro Gln
          245          250          255
Ser Tyr Lys Met Glu Trp Lys Asn Glu Val Asp Val Asp Ser Gly Arg
          260          265          270
Asp Met Pro Ser Thr Pro Pro Thr Pro His Ser Arg Glu Lys Gly Thr
          275          280          285
Gln Thr Ser Gly Leu Leu Gln Gln Pro Leu Leu Ser Lys Asp Gln Ser
          290          295          300

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Gly Ser Glu Arg Glu Asp Ser Leu Thr Glu Gly Ile Pro Pro Lys Pro
 305 310 315 320
 Pro Pro Arg Leu Val Trp Arg Ala Ser Glu Pro Gly Ser Arg Lys Ala
 325 330 335
 Arg Phe Gly Ser Glu Lys Pro
 340 343

<210> 1187
 <211> 146
 <212> Amino acid
 <213> Homo sapiens

<400> 1187
 His Glu Glu Ala Ser Gly Leu Ser Val Trp Met Gly Lys Gln Met Glu
 1 5 10 15
 Pro Leu His Ala Val Pro Pro Ala Ala Ile Thr Leu Ile Leu Ser Leu
 20 25 30
 Leu Val Ala Val Phe Thr Glu Cys Thr Ser Asn Val Ala Thr Thr Thr
 35 40 45
 Leu Phe Leu Pro Ile Phe Ala Ser Met Ser Arg Ser Ile Gly Leu Asn
 50 55 60
 Pro Leu Tyr Ile Met Leu Pro Cys Thr Leu Ser Ala Ser Phe Ala Phe
 65 70 75 80
 Met Leu Pro Val Ala Thr Pro Pro Asn Ala Ile Val Phe Thr Tyr Gly
 85 90 95
 His Leu Lys Val Ala Asp Met Val Lys Thr Gly Val Ile Met Asn Ile
 100 105 110
 Ile Gly Val Phe Cys Val Phe Leu Ala Val Asn Thr Trp Gly Arg Ala
 115 120 125
 Ile Phe Asp Leu Asp His Phe Pro Asp Trp Ala Asn Val Thr His Ile
 130 135 140
 Glu Thr
 145 146

<210> 1188
 <211> 40
 <212> Amino acid
 <213> Homo sapiens

<400> 1188
 His Glu Leu Glu Asn Asn Trp Leu Gln His Glu Lys Ala Pro Thr Glu
 1 5 10 15
 Glu Gly Lys Lys Glu Leu Leu Ala Leu Ser Asn Ala Asn Pro Ser Leu
 20 25 30
 Leu Glu Arg His Cys Ala Tyr Leu
 35 40

<210> 1189
 <211> 62
 <212> Amino acid
 <213> Homo sapiens

<400> 1189

```

Gly Asn Ile Ile Tyr Met Tyr Met Gln Pro Gly Ala Arg Ser Ser Gln
 1           5           10           15
Asp Gln Gly Lys Phe Leu Thr Leu Phe Tyr Asn Ile Val Thr Pro Leu
          20           25           30
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala
          35           40           45
Leu Gly Arg Leu Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu
 50           55           60           62

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<210> 1190

<211> 623

<212> Amino acid

<213> Homo sapiens

<400> 1190

```

Pro Leu Glu Gln Arg Ser Asn Cys Arg Val Asp Pro Arg Val Arg Thr
 1           5           10           15
His Thr Met Ala Ser Asp Thr Ser Ser Leu Val Gln Ser His Thr Tyr
          20           25           30
Lys Lys Arg Glu Pro Ala Asp Val Pro Tyr Gln Thr Gly Gln Leu His
          35           40           45
Pro Ala Ile Arg Val Ala Asp Leu Leu Gln His Ile Thr Gln Met Lys
 50           55           60
Cys Ala Glu Gly Tyr Gly Phe Lys Glu Glu Tyr Glu Ser Phe Phe Glu
 65           70           75           80
Gly Gln Ser Ala Pro Trp Asp Ser Ala Lys Lys Asp Glu Asn Arg Met
          85           90           95
Lys Asn Arg Tyr Gly Asn Ile Ile Ala Tyr Asp His Ser Arg Val Arg
          100          105          110
Leu Gln Thr Ile Glu Gly Asp Thr Asn Ser Asp Tyr Ile Asn Gly Asn
          115          120          125
Tyr Ile Asp Gly Tyr His Arg Pro Asn His Tyr Ile Ala Thr Gln Gly
          130          135          140
Pro Met Gln Glu Thr Ile Tyr Asp Phe Trp Arg Met Val Trp His Glu
          145          150          155          160
Asn Thr Ala Ser Ile Ile Met Val Thr Asn Leu Val Glu Val Gly Arg
          165          170          175
Val Lys Cys Cys Lys Tyr Trp Pro Asp Asp Thr Glu Ile Tyr Lys Asp
          180          185          190
Ile Lys Val Thr Leu Ile Glu Thr Glu Leu Leu Ala Glu Tyr Val Ile
          195          200          205
Arg Thr Phe Ala Val Glu Lys Arg Gly Val His Glu Ile Arg Glu Ile
          210          215          220
Arg Gln Phe His Phe Thr Gly Trp Pro Asp His Gly Val Pro Tyr His
          225          230          235          240
Ala Thr Gly Leu Leu Gly Phe Val Arg Gln Val Lys Ser Lys Ser Pro
          245          250          255
Pro Ser Ala Gly Pro Leu Val Val His Cys Ser Ala Gly Ala Gly Arg
          260          265          270
Thr Gly Cys Phe Ile Val Ile Asp Ile Met Leu Asp Met Ala Glu Arg
          275          280          285
Glu Gly Val Val Asp Ile Tyr Asn Cys Val Arg Glu Leu Arg Ser Arg
          290          295          300
Arg Val Asn Met Val Gln Thr Glu Glu Gln Tyr Val Phe Ile His Asp
          305          310          315          320

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Ala Ile Leu Glu Ala Cys Leu Cys Gly Asp Thr Ser Val Pro Ala Ser
 325 330 335
 Gln Val Arg Ser Leu Tyr Tyr Asp Met Asn Lys Leu Asp Pro Gln Thr
 340 345 350
 Asn Ser Ser Gln Ile Lys Glu Glu Phe Arg Thr Leu Asn Met Val Thr
 355 360 365
 Pro Thr Leu Arg Val Glu Asp Cys Ser Ile Ala Leu Leu Pro Arg Asn
 370 375 380
 His Glu Lys Asn Arg Cys Met Asp Ile Leu Pro Pro Asp Arg Cys Leu
 385 390 395 400
 Pro Phe Leu Ile Thr Ile Asp Gly Glu Ser Ser Asn Tyr Ile Asn Ala
 405 410 415
 Ala Leu Met Asp Ser Tyr Lys Gln Pro Ser Ala Phe Ile Val Thr Gln
 420 425 430
 His Pro Leu Pro Asn Thr Val Lys Asp Phe Trp Arg Leu Val Leu Asp
 435 440 445
 Tyr His Cys Thr Ser Val Val Met Leu Asn Asp Val Asp Pro Ala Gln
 450 455 460
 Leu Cys Pro Gln Tyr Trp Pro Glu Asn Gly Val His Arg His Gly Pro
 465 470 475 480
 Ile Gln Val Glu Phe Val Ser Ala Asp Leu Glu Glu Asp Ile Ile Ser
 485 490 495
 Arg Ile Phe Arg Ile Tyr Asn Ala Ala Arg Pro Gln Asp Gly Tyr Arg
 500 505 510
 Met Val Gln Gln Phe Gln Phe Leu Gly Trp Pro Met Tyr Arg Asp Thr
 515 520 525
 Pro Val Ser Lys Arg Ser Phe Leu Lys Leu Ile Arg Gln Val Asp Lys
 530 535 540
 Trp Gln Glu Glu Tyr Asn Gly Gly Glu Gly Arg Thr Val Val His Cys
 545 550 555 560
 Leu Asn Gly Gly Gly Arg Ser Gly Thr Phe Cys Ala Ile Ser Ile Val
 565 570 575
 Cys Glu Met Leu Arg His Gln Arg Thr Val Asp Val Phe His Ala Val
 580 585 590
 Lys Thr Leu Arg Asn Asn Lys Pro Asn Met Val Asp Leu Leu Asp Gln
 595 600 605
 Tyr Lys Phe Cys Tyr Glu Val Ala Leu Glu Tyr Leu Asn Ser Gly
 610 615 620 623

<210> 1191

<211> 86

<212> Amino acid

<213> Homo sapiens

<400> 1191

Pro Leu Thr Tyr Asn Lys Lys Tyr Thr Tyr Pro Trp Trp Gly Asp Ala
 1 5 10 15
 Leu Gly Trp Leu Leu Ala Leu Ser Ser Met Val Cys Ile Pro Ala Trp
 20 25 30
 Ser Leu Tyr Arg Leu Gly Thr Leu Lys Gly Pro Phe Arg Glu Arg Ile
 35 40 45
 Arg Gln Leu Met Cys Pro Ala Glu Asp Leu Pro Gln Arg Asn Pro Ala
 50 55 60
 Gly Pro Ser Ala Pro Ala Thr Pro Arg Thr Ser Leu Leu Arg Leu Thr
 65 70 75 80
 Glu Leu Glu Ser His Cys
 85 86

<210> 1192
 <211> 109
 <212>Amino acid
 <213> Homo sapiens

<400> 1192
 Thr Leu Ser Glu Ser Gly Ala Leu Phe Ser Leu Gly Pro Pro Pro Leu
 1 5 10 15
 Ser Leu Lys Ser Ser Ser Ala Pro Arg Pro Tyr Ser Thr Leu Arg Asp
 20 25 30
 Cys Leu Glu His Phe Ala Glu Leu Phe Asp Leu Gly Phe Pro Asn Pro
 35 40 45
 Leu Ala Glu Arg Ile Ile Phe Glu Thr His Gln Ile His Phe Ala Asn
 50 55 60
 Cys Ser Leu Gly Gln Pro Thr Phe Ser Asp Pro Pro Glu Asp Val Leu
 65 70 75 80
 Leu Ala Met Ile Ile Ala Pro Ile Cys Leu Ile Pro Phe Leu Ile Thr
 85 90 95
 Leu Val Val Trp Arg Ser Lys Asp Ser Glu Ala Gln Ala
 100 105 109

<210> 1193
 <211> 257
 <212>Amino acid
 <213> Homo sapiens

<400> 1193
 Cys Glu Glu Arg Glu Gln Glu Lys Asp Asp Val Asp Val Ala Leu Leu
 1 5 10 15
 Pro Thr Ile Val Glu Lys Val Ile Leu Pro Lys Leu Thr Val Ile Ala
 20 25 30
 Glu Asn Met Trp Asp Pro Phe Ser Thr Thr Gln Thr Ser Arg Met Val
 35 40 45
 Gly Ile Thr Leu Lys Leu Ile Asn Gly Tyr Pro Ser Val Val Asn Ala
 50 55 60
 Glu Asn Lys Asn Thr Gln Val Tyr Leu Lys Ala Leu Leu Leu Arg Met
 65 70 75 80
 Arg Arg Thr Leu Asp Asp Asp Val Phe Met Pro Leu Tyr Pro Lys Asn
 85 90 95
 Val Leu Glu Asn Lys Asn Ser Gly Pro Tyr Leu Phe Phe Gln Arg Gln
 100 105 110
 Phe Trp Ser Ser Val Lys Leu Leu Gly Asn Phe Leu Gln Trp Tyr Gly
 115 120 125
 Ile Phe Ser Asn Lys Thr Leu Gln Glu Leu Ser Ile Asp Gly Leu Leu
 130 135 140
 Asn Arg Tyr Ile Leu Met Ala Phe Gln Asn Ser Glu Tyr Gly Asp Asp
 145 150 155 160
 Ser Ile Lys Lys Ala Gln Asn Val Ile Asn Cys Phe Pro Lys Gln Trp
 165 170 175
 Phe Met Asn Leu Lys Gly Glu Arg Thr Ile Ser Gln Leu Glu Asn Phe
 180 185 190
 Cys Arg Tyr Leu Val His Leu Ala Asp Thr Ile Tyr Arg Asn Ser Ile
 195 200 205
 Gly Cys Ser Asp Val Glu Lys Arg Asn Ala Arg Glu Asn Ile Lys Gln
 210 215 220

Ile Val Lys Leu Leu Ala Ser Val Arg Ala Leu Asp His Ala Met Ser
 225 230 235 240
 Val Ala Ser Asp His Asn Val Lys Glu Phe Lys Ser Leu Ile Glu Gly
 245 250 255
 Lys
 257

<210> 1194
 <211> 416
 <212> Amino acid
 <213> Homo sapiens

<400> 1194
 Thr Pro Phe Cys Phe Leu Cys Ser Leu Val Phe Arg Ser Arg Val Trp
 1 5 10 15
 Ala Glu Pro Cys Leu Ile Asp Ala Ala Lys Glu Glu Tyr Asn Gly Val
 20 25 30
 Ile Glu Glu Phe Leu Ala Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val
 35 40 45
 Trp Gly Arg Tyr Asp Leu Leu Phe Met Pro Pro Ser Phe Pro Phe Gly
 50 55 60
 Gly Met Glu Asn Pro Cys Leu Thr Phe Val Thr Pro Cys Leu Leu Ala
 65 70 75 80
 Gly Asp Arg Ser Leu Ala Asp Val Ile Ile His Glu Ile Ser His Ser
 85 90 95
 Trp Phe Gly Asn Leu Val Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu
 100 105 110
 Asn Glu Gly Phe Thr Met Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu
 115 120 125
 Phe Gly Ala Ala Tyr Thr Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu
 130 135 140
 Leu Arg Gln His Met Asp Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys
 145 150 155 160
 Leu Arg Val Lys Ile Glu Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn
 165 170 175
 Glu Thr Pro Tyr Glu Lys Gly Phe Cys Phe Val Ser Tyr Leu Ala His
 180 185 190
 Leu Val Gly Asp Gln Asp Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val
 195 200 205
 His Glu Phe Lys Phe Arg Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe
 210 215 220
 Tyr Leu Glu Tyr Phe Pro Glu Leu Lys Lys Lys Arg Val Asp Ile Ile
 225 230 235 240
 Pro Gly Phe Glu Phe Asp Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro
 245 250 255
 Tyr Leu Pro Asp Leu Ser Pro Gly Asp Ser Leu Met Lys Pro Ala Glu
 260 265 270
 Glu Leu Ala Gln Leu Trp Ala Ala Glu Glu Leu Asp Met Lys Ala Ile
 275 280 285
 Glu Ala Val Ala Ile Ser Pro Trp Lys Thr Tyr Gln Leu Val Tyr Phe
 290 295 300
 Leu Asp Lys Ile Leu Gln Lys Ser Pro Leu Pro Pro Gly Asn Val Lys
 305 310 315 320
 Lys Leu Gly Asp Thr Tyr Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu
 325 330 335
 Leu Arg Leu Arg Trp Gly Gln Ile Val Leu Lys Asn Asp His Gln Glu
 340 345 350
 Asp Phe Trp Lys Val Lys Glu Phe Leu His Asn Gln Gly Lys Gln Lys
 355 360 365

Tyr Thr Leu Pro Leu Tyr His Ala Met Met Gly Gly Ser Glu Val Ala
 370 375 380
 Gln Thr Leu Ala Lys Glu Thr Phe Ala Ser Thr Ala Ser Gln Leu His
 385 390 395 400
 Ser Asn Val Val Asn Tyr Val Gln Gln Ile Val Ala Pro Lys Gly Ser
 405 410 415 416

<210> 1195
 <211> 295
 <212> Amino acid
 <213> Homo sapiens

<400> 1195
 Cys Ala Ser Gly Ser Ser Gly Trp Arg Pro Val Leu Trp Ala Gly Ala
 1 5 10 15
 Phe Thr Met Ala Ser Ala Glu Leu Asp Tyr Thr Ile Glu Ile Pro Asp
 20 25 30
 Gln Pro Cys Trp Ser Gln Lys Asn Ser Pro Ser Pro Gly Gly Lys Glu
 35 40 45
 Ala Glu Thr Arg Gln Pro Val Val Ile Leu Leu Gly Trp Gly Gly Cys
 50 55 60
 Lys Asp Lys Asn Leu Ala Lys Tyr Ser Ala Ile Tyr His Lys Arg Gly
 65 70 75 80
 Cys Ile Val Ile Arg Tyr Thr Ala Pro Trp His Met Val Phe Phe Ser
 85 90 95
 Glu Ser Leu Gly Ile Pro Ser Leu Arg Val Leu Ala Gln Lys Leu Leu
 100 105 110
 Glu Leu Leu Phe Asp Tyr Glu Ile Glu Lys Glu Pro Leu Leu Phe His
 115 120 125
 Val Phe Ser Asn Gly Gly Val Met Leu Tyr Arg Tyr Val Leu Glu Leu
 130 135 140
 Leu Gln Thr Arg Arg Phe Cys Arg Leu Arg Val Val Gly Thr Ile Phe
 145 150 155 160
 Asp Ser Ala Pro Gly Asp Ser Asn Leu Val Gly Ala Leu Arg Ala Leu
 165 170 175
 Ala Ala Ile Leu Glu Arg Arg Ala Ala Met Leu Arg Leu Leu Leu
 180 185 190
 Val Ala Phe Ala Leu Val Val Val Leu Phe His Val Leu Leu Ala Pro
 195 200 205
 Ile Thr Ala Leu Phe His Thr His Phe Tyr Asp Arg Leu Gln Asp Ala
 210 215 220
 Gly Ser Arg Trp Pro Glu Leu Tyr Leu Tyr Ser Arg Ala Asp Glu Val
 225 230 235 240
 Val Leu Ala Arg Asp Ile Glu Arg Met Val Glu Ala Arg Leu Ala Arg
 245 250 255
 Arg Val Leu Ala Arg Ser Val Asp Phe Val Ser Ser Ala His Val Ser
 260 265 270
 His Leu Arg Asp Tyr Pro Thr Tyr Tyr Thr Ser Leu Cys Val Asp Phe
 275 280 285
 Met Arg Asn Trp Val Arg Cys
 290 295

<210> 1196
 <211> 97
 <212> Amino acid
 <213> Homo sapiens

<400> 1196

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Pro Arg Val Arg Asp Arg Leu Pro Ser Thr Gly Val Arg Asp Arg Lys
 1           5           10           15
Gly Asp Lys Pro Trp Lys Glu Ser Gly Gly Ser Val Glu Ala Pro Arg
          20           25           30
Met Gly Phe Thr His Pro Pro Gly His Leu Ser Gly Cys Gln Ser Ser
          35           40           45
Leu Ala Ser Gly Glu Thr Gly Thr Gly Ser Ala Asp Pro Pro Gly Gly
          50           55           60
Pro Arg Pro Gly Leu Thr Arg Arg Ala Pro Val Lys Asp Thr Pro Gly
          65           70           75           80
Arg Ala Pro Ala Ala Asp Ala Ala Pro Ala Gly Pro Ser Ser Cys Leu
          85           90           95
Gly
97

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<210> 1197

<211> 204

<212>Amino acid

<213> Homo sapiens

<400> 1197

```

Gln Gly Arg Thr Ser Cys Ile Gly Leu Tyr Thr Tyr Gln Arg Arg Ile
 1           5           10           15
Cys Lys Tyr Arg Asp Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr
          20           25           30
Thr Phe Ala Ile Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp
          35           40           45
Pro Ser Gln Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly Asp Leu
          50           55           60
Glu Tyr Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu Ser Met
          65           70           75           80
Lys Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro Glu Gln
          85           90           95
Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val Cys
          100          105          110
Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala Asp Gly
          115          120          125
Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile Lys Glu Ala
          130          135          140
Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys Cys Ser Asp Met
          145          150          155          160
Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val Met Met
          165          170          175
Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Ile Phe Asn Asp Ala
          180          185          190
Leu Val Phe Leu Pro Pro Asn Gly Ser Asp Asn Asp
          195          200          204

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<210> 1198

<211> 238

<212>Amino acid

<213> Homo sapiens

<400> 1198
 His Glu Gly Lys Pro Thr Arg Gly Arg Gly Arg Gly Gly Ser Leu Ser
 1 5 10 15
 Thr Arg Gly Arg Gly Ser Glu Val Pro Asp Ser Ala His Leu Ala Pro
 20 25 30
 Thr Pro Leu Phe Ser Glu Ser Gly Cys Cys Gly Leu Arg Ser Arg Phe
 35 40 45
 Leu Thr Asp Cys Lys Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile
 50 55 60
 Lys Met Val His Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met
 65 70 75 80
 Trp Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg
 85 90 95
 His Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His
 100 105 110
 Ile Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln
 115 120 125
 His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu
 130 135 140
 Leu Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu
 145 150 155 160
 Pro Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu
 165 170 175
 Arg Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro
 180 185 190
 Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln
 195 200 205
 Asn Phe Phe Arg Tyr His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys
 210 215 220
 Val Leu Ser Asn Gly Leu Cys Leu Ala Ala Leu Pro Trp Lys
 225 230 235 238

<210> 1199

<211> 100

<212> Amino acid

<213> Homo sapiens

<400> 1199
 Lys Gln Leu Asp Lys Gln Leu Arg Ala Asp Pro Ser Gly Ser Leu Pro
 1 5 10 15
 Pro Leu Pro Pro Ser Pro Pro Pro Pro Leu Glu Ala Gly Gly Arg Pro
 20 25 30
 Pro Glu Val Pro Pro Arg Gly Pro Ser Ala Val Pro Ser Phe Pro Ser
 35 40 45
 Val Ser Gly Asp Trp Gly Gly Pro Val Glu Ala Gly Glu Gly Gly Gln
 50 55 60
 Gln Gly Arg Gly Arg Ala Arg Ala Arg Pro Cys Ser Leu Pro Pro Leu
 65 70 75 80
 Leu Pro Pro Ser Pro Val Cys Arg Leu Ser Gly Ser Arg Ala Pro Leu
 85 90 95
 Gly Cys Asp Gly
 100

<210> 1200
 <211> 194
 <212>Amino acid
 <213> Homo sapiens

<400> 1200
 Arg Asn Gln Leu Ser Ser Gln Lys Ser Val Pro Trp Val Pro Ile Leu
 1 5 10 15
 Lys Ser Leu Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn
 20 25 30
 Trp Thr Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu
 35 40 45
 Ile Leu Arg Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro
 50 55 60
 Tyr Leu Gly Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp
 65 70 75 80
 Asn Leu Arg Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile
 85 90 95
 Phe Ser Leu Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala
 100 105 110
 Gly Phe Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile
 115 120 125
 Ser Thr Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His
 130 135 140
 Leu Asp Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn
 145 150 155 160
 Thr Phe Ala Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser
 165 170 175
 Leu Thr Pro Asp Met Gly Ile Ser Leu His Arg Pro Gly Trp Ser Ala
 180 185 190
 Val Ala
 194

<210> 1201
 <211> 119
 <212>Amino acid
 <213> Homo sapiens

<400> 1201
 Gly Pro Ser Gly Thr Thr His Ala Ser Ala His Ser Gly His Pro Gly
 1 5 10 15
 Ser Pro Arg Gly Ser Leu Ser Arg His Pro Ser Ser Gln Leu Ala Gly
 20 25 30
 Pro Gly Val Glu Gly Gly Glu Gly Thr Gln Lys Pro Arg Asp Tyr Ile
 35 40 45
 Ile Leu Ala Ile Leu Ser Cys Phe Cys Pro Met Trp Pro Val Asn Ile
 50 55 60
 Val Ala Phe Ala Tyr Ala Val Met Ser Arg Asn Ser Leu Gln Gln Gly
 65 70 75 80
 Asp Val Asp Gly Ala Gln Arg Leu Gly Arg Val Ala Lys Leu Leu Ser
 85 90 95
 Ile Val Ala Leu Val Gly Gly Val Leu Ile Ile Ile Ala Ser Cys Val
 100 105 110
 Ile Asn Leu Gly Val Tyr Lys
 115 119

<210> 1202
 <211> 66
 <212>Amino acid
 <213> Homo sapiens

<400> 1202
 Ser Leu Phe Leu Ser Phe Pro Pro Leu Ser Phe Lys Met Thr Leu Asn
 1 5 10 15
 Asp Ala Met Arg Asn Lys Ala Arg Leu Ser Ile Thr Gly Ser Thr Gly
 20 25 30
 Glu Asn Gly Arg Val Met Thr Pro Glu Phe Pro Lys Ala Val His Ala
 35 40 45
 Val Pro Tyr Val Ser Pro Gly Met Gly Met Asn Val Ser Val Thr Asp
 50 55 60
 Leu Ser
 65 66

<210> 1203
 <211> 509
 <212>Amino acid
 <213> Homo sapiens

<400> 1203
 Asp Asp Val Pro Pro Pro Ala Pro Asp Leu Tyr Asp Val Pro Pro Gly
 1 5 10 15
 Leu Arg Arg Pro Gly Pro Gly Thr Leu Tyr Asp Val Pro Arg Glu Arg
 20 25 30
 Val Leu Pro Pro Glu Val Ala Asp Gly Gly Val Val Asp Ser Gly Val
 35 40 45
 Tyr Ala Val Pro Pro Pro Ala Glu Arg Glu Ala Pro Ala Glu Gly Lys
 50 55 60
 Arg Leu Ser Ala Ser Ser Thr Gly Ser Thr Arg Ser Ser Gln Ser Ala
 65 70 75 80
 Ser Ser Leu Glu Val Ala Gly Pro Gly Arg Glu Pro Leu Glu Leu Glu
 85 90 95
 Val Ala Val Glu Ala Leu Ala Arg Leu Gln Gln Gly Val Ser Ala Thr
 100 105 110
 Val Ala His Leu Leu Asp Leu Ala Gly Ser Ala Gly Ala Thr Gly Ser
 115 120 125
 Trp Arg Ser Pro Ser Glu Pro Gln Glu Pro Leu Val Gln Asp Leu Gln
 130 135 140
 Ala Ala Val Ala Ala Val Gln Ser Ala Val His Glu Leu Leu Glu Phe
 145 150 155 160
 Ala Arg Ser Ala Val Gly Asn Ala Ala His Thr Ser Asp Arg Ala Leu
 165 170 175
 His Ala Lys Leu Ser Arg Gln Leu Gln Lys Met Glu Asp Val His Gln
 180 185 190
 Thr Leu Val Ala His Gly Gln Ala Leu Asp Ala Gly Arg Gly Gly Ser
 195 200 205
 Gly Ala Thr Leu Glu Asp Leu Asp Arg Leu Val Ala Cys Ser Arg Ala
 210 215 220
 Val Pro Glu Asp Ala Lys Gln Leu Ala Ser Phe Leu His Gly Asn Ala
 225 230 235 240

```

Ser Leu Leu Phe Arg Arg Thr Lys Ala Thr Ala Pro Gly Pro Glu Gly
      245      250      255
Gly Gly Thr Leu His Pro Asn Pro Thr Asp Lys Thr Ser Ser Ile Gln
      260      265      270
Ser Arg Pro Leu Pro Ser Pro Pro Lys Phe Thr Ser Gln Asp Ser Pro
      275      280      285
Asp Gly Gln Tyr Glu Asn Ser Glu Gly Gly Trp Met Glu Asp Tyr Asp
      290      295      300
Tyr Val His Leu Gln Gly Lys Glu Glu Phe Glu Lys Thr Gln Lys Glu
      305      310      315      320
Leu Leu Glu Lys Gly Ser Ile Thr Arg Gln Gly Lys Ser Gln Leu Glu
      325      330      335
Leu Gln Gln Leu Lys Gln Phe Glu Arg Leu Glu Gln Glu Val Ser Arg
      340      345      350
Pro Ile Asp His Asp Leu Ala Asn Trp Thr Pro Ala Gln Pro Leu Ala
      355      360      365
Pro Gly Arg Thr Gly Gly Leu Gly Pro Ser Asp Arg Gln Leu Leu Leu
      370      375      380
Phe Tyr Leu Glu Gln Cys Glu Ala Asn Leu Thr Thr Leu Thr Asn Ala
      385      390      395      400
Val Asp Ala Phe Phe Thr Ala Val Ala Thr Asn Gln Pro Pro Lys Ile
      405      410      415
Phe Val Ala His Ser Lys Phe Val Ile Leu Ser Ala His Lys Leu Val
      420      425      430
Phe Ile Gly Asp Thr Leu Ser Arg Gln Ala Lys Ala Ala Asp Val Arg
      435      440      445
Ser Gln Val Thr His Tyr Ser Asn Leu Leu Cys Asp Leu Leu Arg Gly
      450      455      460
Ile Val Ala Thr Thr Lys Ala Ala Ala Leu Gln Tyr Pro Ser Pro Ser
      465      470      475      480
Ala Ala Gln Asp Met Val Glu Arg Val Lys Glu Leu Gly His Ser Thr
      485      490      495
Gln Gln Phe Arg Arg Val Leu Gly Gln Leu Ala Ala Ala
      500      505      509

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<210> 1204

<211> 453

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(453)

<223> X = any amino acid or stop code

<400> 1204

```

Glu Met Glu Glu Pro Gln Lys Ser Tyr Val Asn Thr Met Asp Leu Glu
  1      5      10      15
Arg Asp Glu Pro Leu Lys Ser Thr Gly Pro Gln Ile Ser Val Ser Glu
      20      25      30
Phe Ser Cys His Cys Cys Tyr Asp Ile Leu Val Asn Pro Thr Thr Leu
      35      40      45
Asn Cys Gly His Ser Phe Cys Arg His Cys Leu Ala Leu Trp Trp Ala
      50      55      60
Ser Ser Lys Lys Thr Glu Cys Pro Glu Cys Arg Glu Lys Trp Glu Gly
      65      70      75      80
Phe Pro Lys Val Ser Ile Leu Leu Arg Asp Ala Ile Glu Lys Leu Phe
      85      90      95
Pro Asp Ala Ile Arg Leu Arg Phe Glu Asp Ile Gln Gln Asn Asn Asp

```


				100						105				110		
Ile	Val	Gln	Ser	Leu	Ala	Ala	Phe	Gln	Lys	Tyr	Gly	Asn	Asp	Gln	Ile	
		115					120					125				
Pro	Leu	Ala	Pro	Asn	Thr	Gly	Arg	Ala	Asn	Gln	Gln	Met	Gly	Gly	Gly	
		130				135					140					
Phe	Phe	Ser	Gly	Val	Leu	Thr	Ala	Leu	Thr	Gly	Val	Ala	Val	Val	Leu	
145					150					155					160	
Leu	Val	Tyr	His	Trp	Ser	Ser	Arg	Glu	Ser	Glu	His	Asp	Leu	Leu	Val	
				165					170						175	
His	Lys	Ala	Val	Ala	Lys	Trp	Thr	Ala	Glu	Glu	Val	Val	Leu	Trp	Leu	
				180				185					190			
Glu	Gln	Leu	Gly	Pro	Trp	Ala	Ser	Leu	Tyr	Arg	Glu	Arg	Phe	Leu	Ser	
		195				200					205					
Glu	Arg	Val	Asn	Gly	Arg	Leu	Leu	Leu	Thr	Leu	Thr	Glu	Glu	Glu	Phe	
		210				215					220					
Ser	Lys	Thr	Pro	Tyr	Thr	Ile	Glu	Asn	Ser	Ser	His	Arg	Arg	Ala	Ile	
225					230					235					240	
Leu	Met	Glu	Leu	Glu	Arg	Val	Lys	Ala	Leu	Gly	Val	Lys	Pro	Pro	Gln	
				245				250							255	
Asn	Leu	Trp	Glu	Tyr	Lys	Ala	Val	Asn	Pro	Gly	Arg	Ser	Leu	Phe	Leu	
			260					265				270				
Leu	Tyr	Ala	Leu	Lys	Ser	Ser	Pro	Arg	Leu	Ser	Leu	Leu	Tyr	Leu	Tyr	
		275					280					285				
Leu	Phe	Asp	Tyr	Thr	Asp	Thr	Phe	Leu	Pro	Phe	Ile	His	Thr	Ile	Cys	
		290				295					300					
Pro	Leu	Gln	Glu	Asp	Ser	Ser	Gly	Glu	Asp	Ile	Val	Thr	Lys	Leu	Leu	
305					310					315					320	
Asp	Leu	Lys	Glu	Pro	Thr	Trp	Lys	Gln	Trp	Arg	Glu	Phe	Leu	Val	Lys	
				325					330						335	
Tyr	Ser	Phe	Leu	Pro	Tyr	Gln	Leu	Ile	Ala	Glu	Phe	Ala	Trp	Asp	Trp	
			340					345					350			
Leu	Glu	Val	His	Tyr	Trp	Thr	Ser	Arg	Phe	Leu	Ile	Ile	Asn	Ala	Met	
		355					360					365				
Leu	Leu	Ser	Val	Leu	Glu	Leu	Phe	Ser	Phe	Trp	Arg	Ile	Trp	Ser	Arg	
		370				375					380					
Ser	Glu	Leu	Lys	Xaa	Val	Gly	Phe	Arg	Phe	Leu	Arg	Leu	Gly	Val	Ala	
385					390					395					400	
Ala	Leu	Gly	Ser	Val	Glu	Val	Ala	Gly	Leu	Arg	Gly	Val	Val	Lys	Gly	
				405					410					415		
Glu	Arg	Pro	Leu	Leu	Tyr	Gly	His	Gly	Ala	Gly	Ala	Arg	Phe	Pro	His	
			420					425					430			
Ser	Val	Leu	Leu	Leu	Pro	Val	Ala	Lys	Pro	Leu	Pro	Leu				

<210> 1205

<211> 80

<212>Amino acid

<213> Homo sapiens

<400> 1205

Glu	Lys	Ala	Arg	Met	Ile	Tyr	Glu	Asp	Tyr	Ile	Ser	Ile	Leu	Ser	Pro
1				5					10					15	
Lys	Glu	Val	Ser	Leu	Asp	Ser	Arg	Val	Arg	Glu	Val	Ile	Asn	Arg	Asn
			20					25					30		
Leu	Leu	Asp	Pro	Asn	Pro	His	Met	Tyr	Glu	Asp	Ala	Gln	Leu	Gln	Ile
		35					40					45			
Tyr	Thr	Leu	Met	His	Arg	Asp	Ser	Phe	Pro	Arg	Phe	Leu	Asn	Ser	Gln

50 55 60
 Ile Tyr Lys Ser Phe Val Glu Ser Thr Ala Gly Ser Ser Ser Glu Ser
 65 70 75 80

<210> 1206
 <211> 205
 <212>Amino acid
 <213> Homo sapiens

<400> 1206
 Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys Ile Met Ile Ser Asp Phe
 1 5 10 15
 Gly Leu Ser Lys Met Glu Gly Lys Gly Asp Val Met Ser Thr Ala Cys
 20 25 30
 Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu Ala Gln Lys Pro Tyr
 35 40 45
 Ser Lys Ala Val Asp Cys Trp Ser Ile Gly Val Ile Ala Tyr Ile Leu
 50 55 60
 Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu Asn Asp Ser Lys Leu Phe
 65 70 75 80
 Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe Asp Ser Pro Tyr Trp Asp
 85 90 95
 Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile Arg Asn Leu Met Glu Lys
 100 105 110
 Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln Ala Ala Arg His Pro Trp
 115 120 125
 Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn Ile His Glu Ser Val Ser
 130 135 140
 Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser Lys Trp Arg Gln Ala Phe
 145 150 155 160
 Asn Ala Thr Ala Val Val Arg His Met Arg Lys Leu His Leu Gly Ser
 165 170 175
 Ser Leu Asp Ser Ser Asn Ala Ser Val Ser Ser Ser Leu Ser Leu Ala
 180 185 190
 Ser Gln Lys Asp Cys Ala Ser Gly Thr Phe His Ala Leu
 195 200 205

<210> 1207
 <211> 117
 <212>Amino acid
 <213> Homo sapiens

<400> 1207
 Arg Thr Arg Gly Gly Ala Val Ser Phe Glu Asp Phe Ile Lys Gly Leu
 1 5 10 15
 Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys Leu Asn Trp Ala Phe
 20 25 30
 Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met
 35 40 45
 Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly Lys Cys Thr Tyr
 50 55 60
 Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val Glu Thr Phe Phe

65					70					75				80	
Gln	Lys	Met	Asp	Lys	Asn	Lys	Asp	Gly	Val	Val	Thr	Ile	Asp	Glu	Phe
				85					90					95	
Ile	Glu	Ser	Cys	Gln	Lys	Asp	Glu	Asn	Ile	Met	Arg	Ser	Met	Gln	Leu
			100					105						110	
Phe	Glu	Asn	Val	Ile											
		115		117											

<210> 1208

<211> 337

<212> Amino acid

<213> Homo sapiens

<400> 1208

Pro	Arg	Ser	Pro	Glu	His	His	Thr	Pro	Ala	Trp	His	Glu	Gly	Arg	Ser
1				5					10					15	
Leu	Gly	Pro	Ile	Met	Ala	Ser	Met	Ala	Asp	Arg	Asn	Met	Lys	Leu	Phe
			20					25					30		
Ser	Gly	Arg	Val	Val	Pro	Ala	Gln	Gly	Glu	Glu	Thr	Phe	Glu	Asn	Trp
		35					40					45			
Leu	Thr	Gln	Val	Asn	Gly	Val	Leu	Pro	Asp	Trp	Asn	Met	Ser	Glu	Glu
	50				55						60				
Glu	Lys	Leu	Lys	Arg	Leu	Met	Lys	Thr	Leu	Arg	Gly	Pro	Ala	Arg	Glu
65				70					75					80	
Val	Met	Arg	Val	Leu	Gln	Ala	Thr	Asn	Pro	Asn	Leu	Ser	Val	Ala	Asp
			85						90					95	
Phe	Leu	Arg	Ala	Met	Lys	Leu	Val	Phe	Gly	Glu	Ser	Glu	Ser	Ser	Val
		100					105						110		
Thr	Ala	His	Gly	Lys	Phe	Phe	Asn	Thr	Leu	Gln	Ala	Gln	Gly	Glu	Lys
	115						120					125			
Ala	Ser	Leu	Tyr	Val	Ile	Arg	Leu	Glu	Val	Gln	Leu	Gln	Asn	Ala	Ile
	130				135						140				
Gln	Ala	Gly	Ile	Ile	Ala	Glu	Lys	Asp	Ala	Asn	Arg	Thr	Arg	Leu	Gln
145				150					155					160	
Gln	Leu	Leu	Leu	Gly	Gly	Glu	Leu	Ser	Arg	Asp	Leu	Arg	Leu	Arg	Leu
			165					170						175	
Lys	Asp	Phe	Leu	Arg	Met	Tyr	Ala	Asn	Glu	Gln	Glu	Arg	Leu	Pro	Asn
		180					185						190		
Phe	Leu	Glu	Leu	Ile	Lys	Met	Val	Arg	Glu	Glu	Glu	Asp	Trp	Asp	Asp
	195					200						205			
Ala	Phe	Ile	Lys	Arg	Lys	Arg	Pro	Lys	Arg	Ser	Glu	Ser	Met	Val	Glu
	210				215						220				
Arg	Ala	Val	Ser	Pro	Val	Ala	Phe	Gln	Gly	Ser	Pro	Pro	Ile	Val	Ile
225				230						235				240	
Gly	Ser	Ala	Asp	Cys	Asn	Val	Ile	Glu	Ile	Asp	Asp	Thr	Leu	Asp	Asp
			245					250						255	
Ser	Asp	Glu	Asp	Val	Ile	Leu	Val	Glu	Ser	Gln	Asp	Pro	Pro	Leu	Pro
		260					265						270		
Ser	Trp	Gly	Ala	Pro	Pro	Leu	Arg	Asp	Arg	Ala	Arg	Pro	Gln	Asp	Glu
	275					280						285			
Val	Leu	Val	Ile	Asp	Ser	Pro	His	Asn	Ser	Arg	Ala	Gln	Phe	Pro	Ser
	290				295						300				
Thr	Ser	Gly	Gly	Ser	Gly	Tyr	Lys	Asn	Asn	Gly	Pro	Gly	Glu	Met	Arg
305				310						315				320	
Arg	Ala	Arg	Lys	Arg	Lys	His	Thr	Ile	Arg	Cys	Ser	Tyr	Cys	Gly	Glu
			325						330					335	
Glu															
337															

<210> 1209
 <211> 64
 <212> Amino acid
 <213> Homo sapiens

<400> 1209
 Ser Val Ala Cys Thr Val Pro Leu Arg Ser Met Ser Asp Pro Asp Gln
 1 5 10 15
 Asp Phe Asp Lys Glu Pro Asp Ser Asp Ser Thr Lys His Ser Thr Pro
 20 25 30
 Ser Asn Ser Ser Asn Pro Ser Gly Pro Pro Ser Pro Asn Ser Pro His
 35 40 45
 Arg Ser Gln Leu Pro Leu Glu Gly Leu Glu Gln Pro Ala Cys Asp Thr
 50 55 60 64

<210> 1210
 <211> 316
 <212> Amino acid
 <213> Homo sapiens

<400> 1210
 Tyr Ser Ala Val Glu Phe Ala Glu Arg Gly Ser Gly Gly Ser Ser Gly
 1 5 10 15
 Asp Glu Leu Arg Glu Asp Asp Glu Pro Val Lys Lys Arg Gly Arg Lys
 20 25 30
 Gly Arg Gly Arg Gly Pro Pro Ser Ser Asp Ser Glu Pro Glu Ala
 35 40 45
 Glu Leu Glu Arg Glu Ala Lys Lys Ser Ala Lys Lys Pro Gln Ser Ser
 50 55 60
 Ser Thr Glu Pro Ala Arg Lys Pro Gly Gln Lys Glu Lys Arg Val Arg
 65 70 75 80
 Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr Arg
 85 90 95
 Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys Lys Lys
 100 105 110
 Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser Glu Ile Lys
 115 120 125
 Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg Cys Leu Asn Ala
 130 135 140
 Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser Gln Ile Leu Gln Lys
 145 150 155 160
 Asn Thr Asp Val Val Ala Thr Leu Lys Lys Ile Arg Arg Tyr Lys Ala
 165 170 175
 Asn Lys Asp Val Met Glu Lys Ala Ala Glu Val Tyr Thr Arg Leu Lys
 180 185 190
 Ser Arg Val Leu Gly Pro Lys Ile Glu Ala Val Gln Lys Val Asn Lys
 195 200 205
 Ala Gly Met Glu Lys Glu Lys Ala Glu Glu Lys Leu Ala Gly Glu Glu
 210 215 220
 Leu Ala Gly Glu Glu Ala Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser
 225 230 235 240
 Thr Asp Leu Ser Ala Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly

245 250 255
 Glu Ser Ala Glu Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu
 260 265 270
 Gly Pro Arg Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu
 275 280 285
 Gly Pro Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg
 290 295 300
 Ala Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser
 305 310 315 316

<210> 1211
 <211> 767
 <212> Amino acid
 <213> Homo sapiens

<400> 1211
 Leu Ala Glu Leu Ser Ser Leu Ser Val Leu Arg Leu Ser His Asn Ser
 1 5 10 15
 Ile Ser His Ile Ala Glu Gly Ala Phe Lys Gly Leu Arg Ser Leu Arg
 20 25 30
 Val Leu Asp Leu Asp His Asn Glu Ile Ser Gly Thr Ile Glu Asp Thr
 35 40 45
 Ser Gly Ala Phe Ser Gly Leu Asp Ser Leu Ser Lys Leu Thr Leu Phe
 50 55 60
 Gly Asn Lys Ile Lys Ser Val Ala Lys Arg Ala Phe Ser Gly Leu Glu
 65 70 75 80
 Gly Leu Glu His Leu Asn Leu Gly Gly Asn Ala Ile Arg Ser Val Gln
 85 90 95
 Phe Asp Ala Phe Val Lys Met Lys Asn Leu Lys Glu Leu His Ile Ser
 100 105 110
 Ser Asp Ser Phe Leu Cys Asp Cys Gln Leu Lys Trp Leu Pro Pro Trp
 115 120 125
 Leu Ile Gly Arg Met Leu Gln Ala Phe Val Thr Ala Thr Cys Ala His
 130 135 140
 Pro Glu Ser Leu Lys Gly Gln Ser Ile Phe Ser Val Pro Pro Glu Ser
 145 150 155 160
 Phe Val Cys Asp Asp Phe Leu Lys Pro Gln Ile Ile Thr Gln Pro Glu
 165 170 175
 Thr Thr Met Ala Met Val Gly Lys Asp Ile Arg Phe Thr Cys Ser Ala
 180 185 190
 Ala Ser Ser Ser Ser Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn
 195 200 205
 Glu Val Leu Thr Asn Ala Asp Met Glu Asn Phe Val His Val His Ala
 210 215 220
 Gln Asp Gly Glu Val Met Glu Tyr Thr Thr Ile Leu His Leu Arg Gln
 225 230 235 240
 Val Thr Phe Gly His Glu Gly Arg Tyr Gln Cys Val Ile Thr Asn His
 245 250 255
 Phe Gly Ser Thr Tyr Ser His Lys Ala Arg Leu Thr Val Asn Val Leu
 260 265 270
 Pro Ser Phe Thr Lys Thr Pro His Asp Ile Thr Ile Arg Thr Thr Thr
 275 280 285
 Met Ala Arg Leu Glu Cys Ala Ala Thr Gly His Pro Asn Pro Gln Ile
 290 295 300
 Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro Ala Ala Arg Glu Arg
 305 310 315 320
 Arg Met His Val Met Pro Asp Asp Asp Val Phe Phe Ile Thr Asp Val
 325 330 335
 Lys Ile Asp Asp Ala Gly Val Tyr Ser Cys Thr Ala Gln Asn Ser Ala

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      340      345      350
Gly Ser Ile Ser Ala Asn Ala Thr Leu Thr Val Leu Glu Thr Pro Ser
      355      360      365
Leu Val Val Pro Leu Glu Asp Arg Val Val Ser Val Gly Glu Thr Val
      370      375      380
Ala Leu Gln Cys Lys Ala Thr Gly Asn Pro Pro Pro Arg Ile Thr Trp
385      390      395      400
Phe Lys Gly Asp Arg Pro Leu Ser Leu Thr Glu Arg His His Leu Thr
      405      410      415
Pro Asp Asn Gln Leu Leu Val Val Gln Asn Val Val Ala Glu Asp Ala
      420      425      430
Gly Arg Tyr Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Ala
      435      440      445
His Ser Gln Leu Ser Val Leu Pro Ala Ala Gly Cys Arg Lys Asp Gly
450      455      460
Thr Thr Val Gly Ile Phe Thr Ile Ala Val Val Ser Ser Ile Val Leu
465      470      475      480
Thr Ser Leu Val Trp Val Cys Ile Ile Tyr Gln Thr Arg Lys Lys Ser
      485      490      495
Glu Glu Tyr Ser Val Thr Asn Thr Asp Glu Thr Val Val Pro Pro Asp
      500      505      510
Val Pro Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ser Asp Arg Gln Glu
      515      520      525
Thr Val Val Arg Thr Glu Gly Gly Pro Gln Ala Asn Gly His Ile Glu
530      535      540
Ser Asn Gly Val Cys Pro Arg Asp Ala Ser His Phe Pro Glu Pro Asp
545      550      555      560
Thr His Ser Val Ala Cys Arg Gln Pro Lys Leu Cys Ala Gly Ser Ala
      565      570      575
Tyr His Lys Lys Pro Trp Lys Ala Met Glu Lys Ala Glu Gly Thr Pro
580      585      590
Gly Pro His Lys Met Glu His Gly Gly Arg Val Val Cys Ser Asp Cys
      595      600      605
Asn Thr Glu Val Asp Cys Tyr Ser Arg Gly Gln Ala Phe His Pro Gln
610      615      620
Pro Val Ser Arg Asp Ser Ala Gln Pro Ser Ala Pro Asn Gly Pro Glu
625      630      635      640
Pro Gly Gly Ser Asp Gln Glu His Ser Pro His His Gln Cys Ser Arg
      645      650      655
Thr Ala Ala Gly Ser Cys Pro Glu Cys Gln Gly Ser Leu Tyr Pro Ser
      660      665      670
Asn His Asp Arg Met Leu Thr Ala Val Lys Lys Lys Pro Met Ala Ser
675      680      685
Leu Asp Gly Lys Gly Asp Ser Ser Trp Thr Leu Ala Arg Leu Tyr His
690      695      700
Pro Asp Ser Thr Glu Leu Gln Pro Ala Ser Ser Leu Thr Ser Gly Ser
705      710      715      720
Pro Glu Arg Ala Glu Ala Gln Tyr Leu Leu Val Ser Asn Gly His Leu
      725      730      735
Pro Lys Ala Cys Asp Ala Ser Pro Glu Ser Thr Pro Leu Thr Gly Gln
740      745      750
Leu Pro Gly Lys Gln Arg Val Pro Leu Leu Leu Ala Pro Lys Ser
755      760      765      767

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<210> 1212

<211> 821

<212> Amino acid

<213> Homo sapiens

<400> 1212

Ala Ala Ala Gly Ala Ala Arg Arg Val Ser Val Arg Cys Gly Arg Ser
 1 5 10 15
 Gly Pro Gly Pro Gly Arg Gly Ala Ala Gly Leu Ser Pro Ala Asp Ile
 20 25 30
 Ala Leu Ala Ser Glu Gln Gly Ala Ser Cys Ser Val Arg Ala Pro Glu
 35 40 45
 Arg Lys Leu Arg Met Lys Leu Leu Trp Gln Ala Lys Met Ser Ser Ile
 50 55 60
 Gln Asp Trp Gly Glu Glu Val Glu Glu Gly Ala Val Tyr His Val Thr
 65 70 75 80
 Leu Lys Arg Val Gln Ile Gln Gln Ala Ala Asn Lys Gly Ala Arg Trp
 85 90 95
 Leu Gly Val Glu Gly Asp Gln Leu Pro Pro Gly His Thr Val Ser Gln
 100 105 110
 Tyr Glu Thr Cys Lys Ile Arg Thr Ile Lys Ala Gly Thr Leu Glu Lys
 115 120 125
 Leu Val Glu Asn Leu Leu Thr Ala Phe Gly Asp Asn Asp Phe Thr Tyr
 130 135 140
 Ile Ser Ile Phe Leu Ser Thr Tyr Arg Gly Phe Ala Ser Thr Lys Glu
 145 150 155 160
 Val Leu Glu Leu Leu Leu Asp Arg Tyr Gly Asn Leu Thr Ser Pro Asn
 165 170 175
 Cys Glu Glu Asp Gly Ser Gln Ser Ser Ser Glu Ser Lys Met Val Ile
 180 185 190
 Arg Asn Ala Ile Ala Ser Ile Leu Arg Ala Trp Leu Asp Gln Cys Ala
 195 200 205
 Glu Asp Phe Arg Glu Pro Pro His Phe Pro Cys Leu Gln Lys Leu Leu
 210 215 220
 Asp Tyr Leu Thr Arg Met Met Pro Gly Ser Asp Pro Glu Arg Arg Ala
 225 230 235 240
 Gln Asn Leu Leu Glu Gln Phe Gln Lys Gln Glu Val Glu Thr Asp Asn
 245 250 255
 Gly Leu Pro Asn Thr Ile Ser Phe Ser Leu Glu Glu Glu Glu Glu Leu
 260 265 270
 Glu Gly Gly Glu Ser Ala Glu Phe Thr Cys Phe Ser Glu Asp Leu Val
 275 280 285
 Ala Glu Gln Leu Thr Tyr Met Asp Ala Gln Leu Phe Lys Lys Val Val
 290 295 300
 Pro His His Cys Leu Gly Cys Ile Trp Ser Arg Arg Asp Lys Lys Glu
 305 310 315 320
 Asn Lys His Leu Ala Pro Thr Ile Arg Ala Thr Ile Ser Gln Phe Asn
 325 330 335
 Thr Leu Thr Lys Cys Val Val Ser Thr Ile Leu Gly Gly Lys Glu Leu
 340 345 350
 Lys Thr Gln Gln Arg Ala Lys Ile Ile Glu Lys Trp Ile Asn Ile Ala
 355 360 365
 His Glu Cys Arg Leu Leu Lys Asn Phe Ser Ser Leu Arg Ala Ile Val
 370 375 380
 Ser Ala Leu Gln Ser Asn Ser Ile Tyr Arg Leu Lys Lys Thr Trp Ala
 385 390 395 400
 Ala Val Pro Arg Asp Arg Met Leu Met Phe Glu Glu Leu Ser Asp Ile
 405 410 415
 Phe Ser Asp His Asn Asn His Leu Thr Ser Arg Glu Leu Leu Met Lys
 420 425 430
 Glu Gly Thr Ser Lys Phe Ala Asn Leu Asp Ser Ser Val Lys Glu Asn
 435 440 445
 Gln Lys Arg Thr Gln Arg Arg Leu Gln Leu Gln Lys Asp Met Gly Val
 450 455 460
 Met Gln Gly Thr Val Pro Tyr Leu Gly Thr Phe Leu Thr Asp Leu Thr
 465 470 475 480
 Met Leu Asp Thr Ala Leu Gln Asp Tyr Ile Glu Gly Gly Leu Ile Asn
 485 490 495
 Phe Glu Lys Arg Arg Arg Glu Phe Glu Val Ile Ala Gln Ile Lys Leu

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      500      505      510
Leu Gln Ser Ala Cys Asn Ser Tyr Cys Met Thr Pro Asp Gln Lys Phe
      515      520      525
Ile Gln Trp Phe Gln Arg Gln Gln Leu Leu Thr Glu Glu Glu Ser Tyr
      530      535      540
Ala Leu Ser Cys Glu Ile Glu Ala Ala Ala Asp Ala Ser Thr Thr Ser
      545      550      555      560
Pro Lys Pro Trp Lys Ser Met Val Lys Arg Leu Asn Leu Leu Phe Leu
      565      570      575
Gly Ala Asp Met Ile Thr Ser Pro Thr Pro Thr Lys Glu Gln Pro Lys
      580      585      590
Ser Thr Ala Ser Gly Ser Ser Gly Glu Ser Met Asp Ser Val Ser Val
      595      600      605
Ser Ser Cys Glu Ser Asn His Ser Glu Ala Glu Glu Gly Tyr Ile Thr
      610      615      620
Pro Met Asp Thr Pro Asp Glu Pro Gln Lys Lys Leu Ser Glu Ser Ser
      625      630      635      640
Ser Tyr Cys Ser Ser Ile His Ser Met Asp Thr Asn Phe Leu Gln Gly
      645      650      655
Met Ser Ser Leu Ile Asn Pro Leu Ser Ser Pro Pro Ser Cys Asn Asn
      660      665      670
Asn Pro Lys Ile His Lys Arg Ser Val Ser Val Thr Ser Ile Thr Ser
      675      680      685
Thr Val Leu Pro Pro Val Tyr Asn Gln Gln Asn Glu Asp Thr Cys Ile
      690      695      700
Ile Arg Ile Ser Val Glu Asp Asn Asn Gly Asn Met Tyr Lys Ser Ile
      705      710      715      720
Met Leu Thr Ser Gln Asp Lys Thr Pro Ala Val Ile Gln Arg Ala Met
      725      730      735
Leu Lys His Asn Leu Asp Ser Asp Pro Ala Glu Glu Tyr Glu Leu Val
      740      745      750
Gln Val Ile Ser Glu Asp Lys Glu Leu Val Ile Pro Asp Ser Ala Asn
      755      760      765
Val Phe Tyr Ala Met Asn Ser Gln Val Asn Phe Asp Phe Ile Leu Arg
      770      775      780
Lys Lys Asn Ser Met Glu Glu Gln Val Lys Leu Arg Ser Arg Thr Ser
      785      790      795      800
Leu Thr Leu Pro Arg Thr Ala Lys Arg Gly Cys Trp Ser Asn Arg His
      805      810      815
Ser Lys Ile Thr Leu
      820 821

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<210> 1213

<211> 289

<212> Amino acid

<213> Homo sapiens

<400> 1213

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Ala Arg Glu Lys Met Asp Ser Cys Ile Glu Ala Phe Gly Thr Thr Lys
  1      5      10      15
Gln Lys Arg Ala Leu Asn Thr Arg Arg Met Asn Arg Val Gly Asn Glu
      20      25      30
Ser Leu Asn Arg Ala Val Ala Lys Ala Ala Glu Thr Ile Ile Asp Thr
      35      40      45
Lys Gly Val Thr Ala Leu Val Ser Asp Ala Ile His Asn Asp Leu Gln
      50      55      60
Asp Asp Ser Leu Tyr Leu Pro Pro Cys Tyr Asp Asp Ala Ala Lys Pro
      65      70      75      80
Glu Asp Val Tyr Lys Phe Glu Asp Leu Leu Ser Pro Ala Glu Tyr Glu

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```
<210> 1214
<211> 873
<212> Amino acid
<213> Homo sapiens
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727

195 200 205
 Ile Glu Glu Leu Ile Ala Lys Ser Lys Gln Glu Lys Arg Glu Arg Gln
 210 215 220
 Ala Gln Arg Glu Asp Ala Leu Glu Leu Thr Glu Lys Leu Asp Gln Asp
 225 230 235 240
 Trp Lys Glu Ile Gln Thr Leu Leu Ser His Lys Thr Pro Lys Ser Glu
 245 250 255
 Asn Arg Asp Lys Lys Glu Lys Pro Lys Pro Asp Ala Tyr Asp Met Met
 260 265 270
 Val Arg Glu Leu Gly Phe Glu Met Lys Ala Gln Pro Ser Asn Arg Met
 275 280 285
 Lys Thr Glu Ala Glu Leu Ala Lys Glu Glu Gln Glu His Leu Arg Lys
 290 295 300
 Leu Glu Ala Glu Arg Leu Arg Arg Met Leu Gly Lys Asp Glu Asp Glu
 305 310 315 320
 Asn Val Lys Lys Pro Lys His Met Ser Ala Asp Asp Leu Asn Asp Gly
 325 330 335
 Phe Val Leu Asp Lys Asp Asp Arg Arg Leu Leu Ser Tyr Lys Asp Gly
 340 345 350
 Lys Met Asn Val Glu Glu Asp Val Gln Glu Glu Gln Ser Lys Glu Ala
 355 360 365
 Ser Asp Pro Glu Ser Asn Glu Glu Glu Gly Asp Ser Ser Gly Gly Glu
 370 375 380
 Asp Thr Glu Glu Ser Asp Ser Pro Asp Ser His Leu Asp Leu Glu Ser
 385 390 395 400
 Asn Val Glu Ser Glu Glu Glu Asn Glu Lys Pro Ala Lys Glu Gln Arg
 405 410 415
 Gln Thr Pro Gly Lys Gly Leu Ile Ser Gly Lys Glu Arg Ala Gly Lys
 420 425 430
 Ala Thr Arg Asp Glu Leu Pro Tyr Thr Phe Ala Ala Pro Glu Ser Tyr
 435 440 445
 Glu Glu Leu Arg Ser Leu Leu Leu Gly Arg Ser Met Glu Glu Gln Leu
 450 455 460
 Leu Val Val Glu Arg Ile Gln Lys Cys Asn His Pro Ser Leu Ala Glu
 465 470 475 480
 Gly Asn Lys Ala Lys Leu Glu Lys Leu Phe Gly Phe Leu Leu Glu Tyr
 485 490 495
 Val Gly Asp Leu Ala Thr Asp Asp Pro Pro Asp Leu Thr Val Ile Asp
 500 505 510
 Lys Leu Val Val His Leu Tyr His Leu Cys Gln Met Phe Pro Glu Ser
 515 520 525
 Ala Ser Asp Ala Ile Lys Phe Val Leu Arg Asp Ala Met His Glu Met
 530 535 540
 Glu Glu Met Ile Glu Thr Lys Gly Arg Ala Ala Leu Pro Gly Leu Asp
 545 550 555 560
 Val Leu Ile Tyr Leu Lys Ile Thr Gly Leu Leu Phe Pro Thr Ser Asp
 565 570 575
 Phe Trp His Pro Val Val Thr Pro Ala Leu Val Cys Leu Ser Gln Leu
 580 585 590
 Leu Thr Lys Cys Pro Ile Leu Ser Leu Gln Asp Val Val Lys Gly Leu
 595 600 605
 Phe Val Cys Cys Leu Phe Leu Glu Tyr Val Ala Leu Ser Gln Arg Phe
 610 615 620
 Ile Pro Glu Leu Ile Asn Phe Leu Leu Gly Ile Leu Tyr Ile Ala Thr
 625 630 635 640
 Pro Asn Lys Ala Ser Gln Gly Ser Thr Leu Val His Pro Phe Arg Ala
 645 650 655
 Leu Gly Lys Asn Ser Glu Leu Leu Val Ser Ala Arg Glu Asp Val
 660 665 670
 Ala Thr Trp Gln Gln Ser Ser Leu Ser Leu Arg Trp Ala Ser Arg Leu
 675 680 685
 Arg Ala Pro Thr Ser Thr Glu Ala Asn His Ile Arg Leu Ser Cys Leu
 690 695 700
 Ala Val Gly Leu Ala Leu Leu Lys Arg Cys Val Leu Met Tyr Gly Ser

```

705              710              715              720
Leu Pro Ser Phe His Ala Ile Met Gly Pro Leu Arg Ala Leu Leu Thr
              725              730              735
Asp His Leu Ala Asp Cys Ser His Pro Gln Glu Leu Gln Glu Leu Cys
              740              745              750
Gln Ser Thr Leu Thr Glu Met Glu Ser Gln Lys Gln Leu Cys Arg Pro
              755              760              765
Leu Thr Cys Glu Lys Ser Lys Pro Val Pro Leu Lys Leu Phe Thr Pro
              770              775              780
Arg Leu Val Lys Val Leu Glu Phe Gly Arg Lys Gln Gly Ser Ser Lys
785              790              795              800
Glu Glu Gln Glu Arg Lys Arg Leu Ile His Lys His Lys Arg Glu Phe
              805              810              815
Lys Gly Ala Val Arg Glu Ile Arg Lys Asp Asn Gln Phe Leu Ala Arg
              820              825              830
Met Gln Leu Ser Glu Ile Met Glu Arg Asp Ala Glu Arg Lys Arg Lys
              835              840              845
Val Lys Gln Leu Phe Asn Ser Leu Ala Thr Gln Glu Gly Glu Trp Lys
850              855              860
Ala Leu Lys Arg Lys Lys Phe Lys Lys
865              870              873

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<210> 1215

<211> 319

<212> Amino acid

<213> Homo sapiens

<400> 1215

```

Leu Thr Lys Gln Glu Asp Cys Cys Gly Ser Ile Gly Thr Ala Trp Gly
 1              5              10              15
Gln Ser Lys Cys His Lys Cys Pro Gln Leu Gln Tyr Thr Gly Val Gln
              20              25              30
Lys Pro Gly Pro Val Arg Gly Glu Val Gly Ala Asp Cys Pro Gln Gly
              35              40              45
Tyr Lys Arg Leu Asn Ser Thr His Cys Gln Asp Ile Asn Glu Cys Ala
              50              55              60
Met Pro Gly Val Cys Arg His Gly Asp Cys Leu Asn Asn Pro Gly Ser
65              70              75              80
Tyr Arg Cys Val Cys Pro Pro Gly His Ser Leu Gly Pro Ser Arg Thr
              85              90              95
Gln Cys Ile Ala Asp Lys Pro Glu Glu Lys Ser Leu Cys Phe Arg Leu
              100              105              110
Val Ser Pro Glu His Gln Cys Gln His Pro Leu Thr Thr Arg Leu Thr
              115              120              125
Arg Gln Leu Cys Cys Cys Ser Val Gly Lys Ala Trp Gly Ala Arg Cys
130              135              140
Gln Arg Cys Pro Thr Asp Gly Thr Ala Ala Phe Lys Glu Ile Cys Pro
145              150              155              160
Ala Gly Lys Gly Tyr His Ile Leu Thr Ser His Gln Thr Leu Thr Ile
              165              170              175
Gln Gly Glu Ser Asp Phe Ser Leu Phe Leu His Pro Asp Gly Pro Pro
              180              185              190
Lys Pro Gln Gln Leu Pro Glu Ser Pro Ser Gln Ala Pro Pro Pro Glu
              195              200              205
Asp Thr Glu Glu Glu Arg Gly Val Thr Thr Asp Ser Pro Val Ser Glu
210              215              220
Glu Arg Ser Val Gln Gln Ser His Pro Thr Ala Thr Thr Thr Pro Ala
225              230              235              240
Arg Pro Tyr Pro Glu Leu Ile Ser Arg Pro Ser Pro Pro Thr Met Arg

```

245 250 255
 Trp Phe Leu Pro Asp Leu Pro Pro Ser Arg Ser Ala Val Glu Ile Ala
 260 265 270
 Pro Thr Gln Val Thr Glu Thr Asp Glu Cys Arg Leu Asn Gln Asn Ile
 275 280 285
 Cys Gly His Gly Glu Cys Val Pro Gly Pro Pro Asp Tyr Ser Cys His
 290 295 300
 Cys Asn Pro Gly Tyr Arg Ser His Pro Gln His Arg Tyr Cys Val
 305 310 315 319

<210> 1216
 <211> 815
 <212> Amino acid
 <213> Homo sapiens

<400> 1216
 Met Ala Gly Gly His Cys Gly Ser Phe Pro Ala Ala Ala Ala Gly Ser
 1 5 10 15
 Gly Glu Ile Val Gln Leu Asn Val Gly Gly Thr Arg Phe Ser Thr Ser
 20 25 30
 Arg Gln Thr Leu Met Trp Ile Pro Asp Ser Phe Phe Ser Ser Leu Leu
 35 40 45
 Ser Gly Arg Ile Ser Thr Leu Arg Asp Glu Thr Gly Ala Ile Phe Ile
 50 55 60
 Asp Arg Asp Pro Ala Ala Phe Ala Pro Ile Leu Asn Phe Leu Arg Thr
 65 70 75 80
 Lys Glu Leu Asp Leu Arg Gly Val Ser Ile Asn Val Leu Arg His Glu
 85 90 95
 Ala Glu Phe Tyr Gly Ile Thr Pro Leu Val Arg Arg Leu Leu Leu Cys
 100 105 110
 Glu Glu Leu Glu Arg Ser Ser Cys Gly Ser Val Leu Phe His Gly Tyr
 115 120 125
 Leu Pro Pro Pro Gly Ile Pro Ser Arg Lys Ile Asn Asn Thr Val Arg
 130 135 140
 Ser Ala Asp Ser Arg Asn Gly Leu Asn Ser Thr Glu Gly Glu Ala Arg
 145 150 155 160
 Gly Asn Gly Thr Gln Pro Val Leu Ser Gly Thr Gly Glu Glu Thr Val
 165 170 175
 Arg Leu Gly Phe Pro Val Asp Pro Arg Lys Val Leu Ile Val Ala Gly
 180 185 190
 His His Asn Trp Ile Val Ala Ala Tyr Ala His Phe Ala Val Trp Tyr
 195 200 205
 Arg Ile Lys Glu Ser Ser Gly Trp Gln Gln Val Phe Thr Ser Pro Tyr
 210 215 220
 Leu Asp Trp Thr Ile Glu Arg Val Ala Leu Asn Ala Lys Val Val Gly
 225 230 235 240
 Gly Pro His Gly Asp Lys Asp Lys Met Val Ala Val Ala Ser Glu Ser
 245 250 255
 Ser Ile Ile Leu Trp Ser Val Gln Asp Gly Gly Ser Gly Ser Glu Ile
 260 265 270
 Gly Val Phe Ser Leu Gly Val Pro Val Asp Ala Leu Phe Phe Ile Gly
 275 280 285
 Asn Gln Leu Val Ala Thr Ser His Thr Gly Lys Val Gly Val Trp Asn
 290 295 300
 Ala Val Thr Gln His Trp Gln Val Gln Asp Val Val Pro Ile Thr Ser
 305 310 315 320
 Tyr Asp Thr Ala Gly Ser Phe Leu Leu Leu Gly Cys Asn Asn Gly Ser
 325 330 335
 Ile Tyr Tyr Ile Asp Met Gln Lys Phe Pro Leu Arg Met Lys Asp Asn

340	345	350
Asp Leu Leu Val Thr Glu Leu Tyr His Asp Pro Ser Asn Asp Ala Ile		
355	360	365
Thr Ala Leu Ser Val Tyr Leu Thr Pro Lys Thr Ser Val Ser Gly Asn		
370	375	380
Trp Ile Glu Ile Ala Tyr Gly Thr Ser Ser Gly Ala Val Arg Val Ile		
385	390	395
Val Gln His Pro Glu Thr Val Gly Ser Gly Pro Gln Leu Phe Gln Thr		400
405	410	415
Phe Thr Val His Arg Ser Pro Val Thr Lys Ile Met Leu Ser Glu Lys		
420	425	430
His Leu Val Ser Val Cys Ala Asp Asn Asn His Val Arg Thr Trp Thr		
435	440	445
Val Thr Arg Phe Arg Gly Met Ile Ser Thr Gln Pro Gly Ser Thr Pro		
450	455	460
Leu Ala Ser Phe Lys Ile Leu Ser Leu Glu Glu Thr Glu Ser His Gly		
465	470	475
Ser Tyr Ser Ser Gly Asn Asp Ile Gly Pro Phe Gly Glu Arg Asp Asp		480
485	490	495
Gln Gln Val Phe Ile Gln Lys Val Val Pro Ile Thr Asn Lys Leu Phe		
500	505	510
Val Arg Leu Ser Ser Thr Gly Lys Arg Ile Cys Glu Ile Gln Ala Val		
515	520	525
Asp Cys Thr Thr Ile Ser Ser Phe Thr Gly Arg Glu Cys Glu Gly Ser		
530	535	540
Ser Arg Met Gly Ser Arg Pro Arg Arg Tyr Leu Phe Thr Gly His Thr		
545	550	555
Asn Gly Ser Ile Gln Met Trp Asp Leu Thr Thr Ala Met Asp Met Val		560
565	570	575
Asn Lys Ser Glu Asp Lys Asp Val Gly Gly Pro Thr Glu Glu Glu Leu		
580	585	590
Leu Lys Leu Leu Asp Gln Cys Asp Leu Ser Thr Ser Arg Cys Ala Thr		
595	600	605
Pro Asn Ile Ser Pro Ala Thr Ser Val Val Gln His Ser His Leu Arg		
610	615	620
Glu Ser Asn Ser Ser Leu Gln Leu Gln His His Asp Thr Thr His Glu		
625	630	635
Ala Ala Thr Tyr Gly Ser Met Arg Pro Tyr Arg Glu Ser Pro Leu Leu		640
645	650	655
Ala Arg Ala Arg Arg Thr Glu Ser Phe His Ser Tyr Arg Asp Phe Gln		
660	665	670
Thr Ile Asn Leu Asn Arg Asn Val Glu Arg Ala Val Pro Glu Asn Gly		
675	680	685
Asn Leu Gly Pro Ile Gln Ala Glu Val Lys Gly Ala Thr Gly Glu Cys		
690	695	700
Asn Ile Ser Glu Arg Lys Ser Pro Gly Val Glu Ile Lys Ser Leu Arg		
705	710	715
Glu Leu Asp Ser Gly Leu Glu Val His Lys Ile Ala Glu Gly Phe Ser		720
725	730	735
Glu Ser Lys Lys Arg Ser Ser Glu Asp Glu Asn Glu Asn Lys Ile Glu		
740	745	750
Phe Arg Lys Lys Gly Gly Phe Glu Gly Gly Gly Phe Leu Gly Arg Lys		
755	760	765
Lys Val Pro Tyr Leu Ala Ser Ser Pro Ser Thr Ser Asp Gly Gly Thr		
770	775	780
Asp Ser Pro Gly Thr Ala Ser Pro Ser Pro Thr Lys Thr Thr Pro Ser		
785	790	795
Pro Arg His Lys Lys Ser Asp Ser Ser Gly Gln Glu Tyr Ser Leu		800
805	810	815

<210> 1217

<211> 459

<212> Amino acid

<213> Homo sapiens

<400> 1217

```

Arg Arg Pro Thr Arg Pro Ile Leu Thr Asp Glu Leu Phe Lys Arg Thr
 1           5           10           15
Ile Gln Leu Pro His Leu Lys Thr Leu Ile Leu Asn Gly Asn Lys Leu
      20           25           30
Glu Thr Leu Ser Leu Val Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu
      35           40           45
His Leu Asp Leu Ser Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn
      50           55           60
Cys Ser Trp Pro Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys
      65           70           75           80
Leu Ser Asp Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu
      85           90           95
Asp Leu Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His
      100          105          110
Leu Met Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp
      115          120          125
Leu Pro Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile Glu
      130          135          140
Met Asn Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser Cys Gln
      145          150          155          160
Glu Val Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg Cys Thr Cys
      165          170          175
Glu Leu Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser Glu Val Met Met
      180          185          190
Val Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg
      195          200          205
Gly Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr
      210          215          220
Ala Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu
      225          230          235          240
Ala Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg
      245          250          255
Met Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr
      260          265          270
Gln Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr
      275          280          285
Ser Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu
      290          295          300
Glu Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe
      305          310          315          320
Asp Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys
      325          330          335
Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu
      340          345          350
Trp Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu
      355          360          365
Asn Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe Tyr
      370          375          380
Cys Ile Pro Thr Arg Tyr His Lys Leu Lys Ala Leu Leu Glu Lys Lys
      385          390          395          400
Ala Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Phe Trp
      405          410          415
Ala Asn Leu Arg Ala Ala Ile Asn Val Asn Val Leu Ala Thr Arg Glu
      420          425          430
Met Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly
      435          440          445
Ser Thr Ile Ser Leu Met Arg Thr Asp Cys Leu

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450

455

459

<210> 1218
 <211> 366
 <212> Amino acid
 <213> Homo sapiens

<400> 1218
 Pro Thr Arg Pro Pro Thr Arg Pro Pro Thr Arg Pro Leu Leu Thr Pro
 1 5 10 15
 Ser Trp Thr Ser Thr Gly Arg Met Trp Ser His Leu Asn Arg Leu Leu
 20 25 30
 Phe Trp Ser Ile Phe Ser Ser Val Thr Cys Arg Lys Ala Val Leu Asp
 35 40 45
 Cys Glu Ala Met Lys Thr Asn Glu Phe Pro Ser Pro Cys Leu Asp Ser
 50 55 60
 Lys Thr Lys Val Val Met Lys Gly Gln Asn Val Ser Met Phe Cys Ser
 65 70 75 80
 His Lys Asn Lys Ser Leu Gln Ile Thr Tyr Ser Leu Phe Arg Arg Lys
 85 90 95
 Thr His Leu Gly Thr Gln Asp Gly Lys Gly Glu Pro Ala Ile Phe Asn
 100 105 110
 Leu Ser Ile Thr Glu Ala His Glu Ser Gly Pro Tyr Lys Cys Lys Ala
 115 120 125
 Gln Val Thr Ser Cys Ser Lys Tyr Ser Arg Asp Phe Ser Phe Thr Ile
 130 135 140
 Val Asp Pro Val Thr Ser Pro Val Leu Asn Ile Met Val Ile Gln Thr
 145 150 155 160
 Glu Thr Asp Arg His Ile Thr Leu His Cys Leu Ser Val Asn Gly Ser
 165 170 175
 Leu Pro Ile Asn Tyr Thr Phe Phe Glu Asn His Val Ala Ile Ser Pro
 180 185 190
 Ala Ile Ser Lys Tyr Asp Arg Glu Pro Ala Glu Phe Asn Leu Thr Lys
 195 200 205
 Lys Asn Pro Gly Glu Glu Glu Tyr Arg Cys Glu Ala Lys Asn Arg
 210 215 220
 Leu Pro Asn Tyr Ala Thr Tyr Ser His Pro Val Thr Met Pro Ser Thr
 225 230 235 240
 Gly Gly Asp Ser Cys Pro Phe Cys Leu Lys Leu Leu Leu Pro Gly Leu
 245 250 255
 Leu Leu Leu Leu Val Val Ile Ile Leu Ile Leu Ala Phe Trp Val Leu
 260 265 270
 Pro Lys Tyr Lys Thr Arg Lys Ala Met Arg Asn Asn Val Pro Arg Asp
 275 280 285
 Arg Gly Asp Thr Ala Met Glu Val Gly Ile Tyr Ala Asn Ile Leu Glu
 290 295 300
 Lys Gln Ala Lys Glu Glu Ser Val Pro Glu Val Gly Ser Arg Pro Cys
 305 310 315 320
 Val Ser Thr Ala Gln Asp Glu Ala Lys His Ser Gln Glu Leu Gln Tyr
 325 330 335
 Ala Thr Pro Val Phe Gln Glu Val Ala Pro Arg Glu Gln Glu Ala Cys
 340 345 350
 Asp Ser Tyr Lys Ser Gly Tyr Val Tyr Ser Glu Leu Asn Phe
 355 360 365 366

<210> 1219
 <211> 97
 <212> Amino acid

<213> Homo sapiens

<400> 1219

```

Phe Phe Phe Phe Glu Glu Arg Arg Thr Gly Ser His Ser Val Gly His
 1           5           10           15
Pro Arg Met Glu Tyr Ser Gly Val Ser Met Ala His Cys Ser Leu Asn
          20           25           30
Leu Leu Gly Ser Ser Asn Ser Pro Ser Ser Ala Ser Gln Asp Ala Arg
          35           40           45
Thr Thr Gly Ala Cys Gln His Ala Gln Leu Ile Gly Phe Phe Phe Phe
          50           55           60
Val Glu Thr Ala Ser Pro Gln Val Thr His Ala Gly Leu Lys His Leu
          65           70           75           80
Val Ser Arg Asn Pro Ser Ala Val Thr Ser Gln Ser Ala Arg Ile Lys
          85           90           95
Thr
          97

```

<210> 1220

<211> 242

<212> Amino acid

<213> Homo sapiens

<400> 1220

```

Asn Arg Glu Gly Ala Arg Lys Ile Gln Asn Lys Trp Leu Arg Pro Ser
 1           5           10           15
Pro Arg Ser His Arg Thr Pro Glu Ser Val Ser Pro Glu Arg Tyr Ser
          20           25           30
Tyr Gly Thr Ser Ser Ser Ser Lys Arg Thr Glu Gly Ser Cys Arg Arg
          35           40           45
Arg Arg Gln Ser Ser Ser Ser Ala Asn Ser Gln Gln Gly Gln Trp Glu
          50           55           60
Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg Ser Arg Gly Arg Pro
          65           70           75           80
Ser Gly Gly Ala Lys Arg Arg Arg Arg Gly Ala Pro Ala Ala Pro Gln
          85           90           95
Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu Gly Lys Val Thr Cys
          100           105           110
Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys Glu His Gly Pro Ala
          115           120           125
Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln Ala Leu Ala Arg Gln
          130           135           140
Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu Arg Ser Arg Asp Leu
          145           150           155           160
Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu Leu Ser Tyr Leu Asp
          165           170           175
Ala Phe Trp Gly Asp Tyr Leu Ser Gly Ala Leu Leu Gln Ala Leu Arg
          180           185           190
Gly Val Phe Leu Thr Glu Ala Leu Arg Glu Ala Val Gly Arg Glu Ala
          195           200           205
Val Arg Leu Leu Val Ser Val Asp Glu Ala Asp Tyr Glu Ala Gly Arg
          210           215           220
Arg Arg Leu Leu Leu Met Glu Glu Glu Gly Gly Arg Arg Pro Thr Glu
          225           230           235           240
Ala Ser

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242

<210> 1221
 <211> 440
 <212> Amino acid
 <213> Homo sapiens

<400> 1221
 Ala Pro Asn Thr Ala Glu Leu Arg Ile Cys Arg Val Asn Lys Asn Cys
 1 5 10 15
 Gly Ser Val Arg Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val
 20 25 30
 Gln Lys Asp Asp Ile Glu Val Arg Phe Val Leu Asn Asp Trp Glu Ala
 35 40 45
 Lys Gly Ile Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile Val
 50 55 60
 Phe Lys Thr Pro Pro Tyr Cys Lys Ala Ile Thr Glu Pro Val Thr Val
 65 70 75 80
 Lys Met Gln Leu Arg Arg Pro Ser Asp Gln Glu Val Ser Glu Ser Met
 85 90 95
 Asp Phe Arg Tyr Leu Pro Asp Glu Lys Asp Thr Tyr Gly Asn Lys Ala
 100 105 110
 Lys Lys Gln Lys Thr Thr Leu Leu Phe Gln Lys Leu Cys Gln Asp His
 115 120 125
 Val Glu Thr Gly Phe Arg His Val Asp Gln Asp Gly Leu Glu Leu Leu
 130 135 140
 Thr Ser Gly Asp Pro Pro Thr Leu Ala Ser Gln Ser Ala Gly Ile Thr
 145 150 155 160
 Val Asn Phe Pro Glu Arg Pro Arg Pro Gly Leu Leu Gly Ser Ile Gly
 165 170 175
 Glu Gly Arg Tyr Phe Lys Lys Glu Pro Asn Leu Phe Ser His Asp Ala
 180 185 190
 Val Val Arg Glu Met Pro Thr Gly Val Ser Ser Gln Ala Glu Ser Tyr
 195 200 205
 Tyr Pro Ser Pro Gly Pro Ile Ser Ser Gly Leu Ser His His Ala Ser
 210 215 220
 Met Ala Pro Leu Pro Ser Ser Trp Ser Ser Val Ala His Pro Thr
 225 230 235 240
 Pro Arg Ser Gly Asn Thr Asn Pro Leu Ser Ser Phe Ser Thr Arg Thr
 245 250 255
 Leu Pro Ser Asn Ser Gln Gly Ile Pro Pro Phe Leu Arg Ile Pro Val
 260 265 270
 Gly Asn Asp Leu Asn Ala Ser Asn Ala Cys Ile Tyr Asn Asn Ala Asp
 275 280 285
 Asp Ile Val Gly Met Glu Ala Ser Ser Met Pro Ser Ala Asp Leu Tyr
 290 295 300
 Gly Ile Ser Asp Pro Asn Met Leu Ser Asn Cys Ser Val Asn Met Met
 305 310 315 320
 Thr Thr Ser Ser Asp Ser Met Gly Glu Thr Asp Asn Pro Arg Leu Leu
 325 330 335
 Ser Met Asn Leu Glu Asn Pro Ser Cys Asn Ser Val Leu Asp Pro Arg
 340 345 350
 Asp Leu Arg Gln Leu His Gln Met Ser Ser Ser Ser Met Ser Ala Gly
 355 360 365
 Ala Asn Ser Asn Thr Thr Val Phe Val Ser Gln Ser Asp Ala Phe Glu
 370 375 380
 Gly Ser Asp Phe Ser Cys Ala Asp Asn Ser Met Ile Asn Glu Ser Gly
 385 390 395 400
 Pro Ser Asn Ser Thr Asn Pro Asn Ser His Gly Phe Val Gln Asp Ser

				405					410				415				
Gln	Tyr	Ser	Gly	Ile	Gly	Ser	Met	Gln	Asn	Glu	Gln	Leu	Ser	Asp	Ser		
			420					425					430				
Phe	Pro	Tyr	Glu	Phe	Phe	Gln	Val										
			435				440										

<210> 1222
 <211> 437
 <212> Amino acid
 <213> Homo sapiens

<400> 1222

Arg	Arg	Leu	Ser	Leu	Leu	Asp	Leu	Gln	Leu	Gly	Pro	Leu	Gly	Arg	Asp		
1				5					10					15			
Pro	Pro	Gln	Glu	Cys	Ser	Thr	Phe	Ser	Pro	Thr	Asp	Ser	Gly	Glu	Glu		
			20					25					30				
Pro	Gly	Gln	Leu	Ser	Pro	Gly	Val	Gln	Phe	Gln	Arg	Arg	Gln	Asn	Gln		
		35					40					45					
Arg	Arg	Phe	Ser	Met	Glu	Asp	Val	Ser	Lys	Arg	Leu	Ser	Leu	Pro	Met		
	50					55					60						
Asp	Ile	Arg	Leu	Pro	Gln	Glu	Phe	Leu	Gln	Lys	Leu	Gln	Met	Glu	Ser		
	65				70					75					80		
Pro	Asp	Leu	Pro	Lys	Pro	Leu	Ser	Arg	Met	Ser	Arg	Arg	Ala	Ser	Leu		
				85					90					95			
Ser	Asp	Ile	Gly	Phe	Gly	Lys	Leu	Glu	Thr	Tyr	Val	Lys	Leu	Asp	Lys		
			100					105					110				
Leu	Gly	Glu	Gly	Thr	Tyr	Ala	Thr	Val	Phe	Lys	Gly	Arg	Ser	Lys	Leu		
		115					120					125					
Thr	Glu	Asn	Leu	Val	Ala	Leu	Lys	Glu	Ile	Arg	Leu	Glu	His	Glu	Glu		
	130					135					140						
Gly	Ala	Pro	Cys	Thr	Ala	Ile	Arg	Glu	Val	Ser	Leu	Leu	Lys	Asn	Leu		
	145				150					155					160		
Lys	His	Ala	Asn	Ile	Val	Thr	Leu	His	Asp	Leu	Ile	His	Thr	Asp	Arg		
			165						170					175			
Ser	Leu	Thr	Leu	Val	Phe	Glu	Tyr	Leu	Asp	Ser	Asp	Leu	Lys	Gln	Tyr		
			180					185					190				
Leu	Asp	His	Cys	Gly	Asn	Leu	Met	Ser	Met	His	Asn	Val	Lys	Ile	Phe		
		195				200						205					
Met	Phe	Gln	Leu	Leu	Arg	Gly	Leu	Ala	Tyr	Cys	His	His	Arg	Lys	Ile		
	210					215					220						
Leu	His	Arg	Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	Ile	Asn	Glu	Arg	Gly		
	225				230					235				240			
Glu	Leu	Lys	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Lys	Ser	Val	Pro		
			245						250					255			
Thr	Lys	Thr	Tyr	Ser	Asn	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Pro	Pro		
			260					265					270				
Asp	Val	Leu	Leu	Gly	Ser	Thr	Glu	Tyr	Ser	Thr	Pro	Ile	Asp	Met	Trp		
		275					280					285					
Gly	Val	Gly	Cys	Ile	His	Tyr	Glu	Met	Ala	Thr	Gly	Arg	Pro	Leu	Phe		
	290					295					300						
Pro	Gly	Ser	Thr	Val	Lys	Glu	Glu	Leu	His	Lys	Ile	Asn	Arg	Leu	Leu		
	305				310					315					320		
Gly	Thr	Pro	Thr	Glu	Glu	Thr	Trp	Pro	Gly	Val	Thr	Ala	Phe	Ser	Glu		
			325						330					335			
Phe	Arg	Thr	Tyr	Ser	Phe	Pro	Cys	Tyr	Leu	Pro	Gln	Pro	Leu	Ile	Asn		
			340					345					350				
His	Ala	Pro	Arg	Leu	Asp	Thr	Asp	Gly	Ile	His	Leu	Leu	Ser	Ser	Leu		
		355				360						365					
Leu	Leu	Tyr	Glu	Ser	Lys	Ser	Arg	Met	Ser	Ala	Glu	Ala	Ala	Leu	Ser		

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      370              375              380
His Ser Tyr Phe Arg Ser Leu Gly Glu Arg Val His Gln Leu Glu Asp
385              390              395              400
Thr Ala Ser Ile Phe Ser Leu Lys Glu Ile Gln Leu Gln Lys Asp Pro
      405              410              415
Gly Tyr Arg Gly Leu Ala Phe Gln Gln Pro Gly Arg Gly Lys Asn Arg
      420              425              430
Arg Gln Ser Ile Phe
      435              437

```

<210> 1223
 <211> 150
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 1223
Cys Thr Pro His Gly Ser Ser Ser Ser Trp Lys Ile Pro Leu Trp Pro
  1              5              10              15
Arg His Met Ser Pro Leu His Ser Cys Leu Pro Val Gly Thr Ser Thr
      20              25              30
Ser Ser Gly Pro Leu Ala Val Pro Arg Asp Cys Phe His Leu Cys Cys
      35              40              45
Leu Trp Gly Gln Leu Leu Leu Ile Ser Cys Pro Leu Ala Cys Gly Gln
      50              55              60
Gly Cys Arg Val Ala Gly Gln Gln His Val Pro Gly Gln Ala Leu
      65              70              75              80
Gly Thr Leu Ser Pro Leu Val Ser Leu Leu Thr Trp Ala Gly Pro Ser
      85              90              95
Leu Asp Trp Pro His Pro Gly Ser Leu Val Thr Pro Arg Cys Pro Ile
      100              105              110
Leu Pro Ala Val Pro Val Leu Val Lys Gly Leu Gly Gly Trp Pro Pro
      115              120              125
Thr Arg Pro Ser Arg Ala Ala Pro Val Ser Gly Pro Trp Asp Gln Leu
      130              135              140
Pro Tyr Phe Pro Gly Leu
      145              150

```

<210> 1224
 <211> 276
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 1224
Leu Ile Ser Pro Val Trp Gly Asn Ile Gln Arg Ser Arg Ser Val Pro
  1              5              10              15
Leu Phe Pro Ser Gly Leu Val Leu Gly Gly Ile Trp Ala Arg Gly Pro
      20              25              30
Leu Leu Ala Leu Leu Ala Ser Phe Asn Ile Ile Ser Val Leu Asn Ala
      35              40              45
Glu Cys Tyr Leu Lys Gln Ile Leu His Pro Thr Ser His Phe Thr Val
      50              55              60
Ser Glu Thr Pro Pro Leu Ser Gly Asn Asp Thr Asp Ser Leu Ser Cys
      65              70              75              80
Asp Ser Gly Ser Ser Ala Thr Ser Thr Pro Cys Val Ser Arg Leu Val

```

```
<210> 1225
<211> 270
<212>Amino acid
<213> Homo sapiens
```

738

210		215		220
Gly Thr Lys Gly Leu Lys Lys Val Val His Glu Thr Pro Ala Ala Ser				
225		230		235
Lys Thr Val Phe Phe Phe Phe Ser Ser Pro Gly Asn Asn Asn Gly Thr				240
	245		250	255
Ser Ile Glu Asp Gly Gln Ile Pro Glu Ile Ile Phe Tyr Thr				
	260		265	270

<210> 1226

<211> 273

<212>Amino acid

<213> Homo sapiens

<400> 1226

Ser Val Trp Trp Asn Ser Glu Val Lys Asp Trp Met Gln Lys Lys Arg				
1	5	10	15	
Arg Gly Leu Arg Asn Ser Arg Ala Thr Ala Gly Asp Ile Ala His Tyr				
	20	25	30	
Tyr Arg Asp Tyr Val Val Lys Lys Gly Leu Gly His Asn Phe Val Ser				
	35	40	45	
Gly Ala Val Val Thr Ala Val Glu Trp Gly Thr Pro Asp Pro Ser Ser				
	50	55	60	
Cys Gly Ala Gln Asp Ser Ser Pro Leu Phe Gln Val Ser Gly Phe Leu				
	65	70	75	80
Thr Arg Asn Gln Ala Gln Gln Pro Phe Ser Leu Trp Ala Arg Asn Val				
	85	90	95	
Val Leu Ala Thr Gly Thr Phe Asp Ser Pro Ala Arg Leu Gly Ile Pro				
	100	105	110	
Gly Glu Ala Leu Pro Phe Ile His His Glu Leu Ser Ala Leu Glu Ala				
	115	120	125	
Ala Thr Arg Val Gly Ala Val Thr Pro Ala Ser Asp Pro Val Leu Ile				
	130	135	140	
Ile Gly Ala Gly Leu Ser Ala Ala Asp Ala Val Leu Tyr Ala Arg His				
	145	150	155	160
Tyr Asn Ile Pro Val Ile His Ala Phe Arg Arg Ala Val Asp Asp Pro				
	165	170	175	
Gly Leu Val Phe Asn Gln Leu Pro Lys Met Leu Tyr Pro Glu Tyr His				
	180	185	190	
Lys Val His Gln Met Met Arg Glu Gln Ser Ile Leu Ser Pro Ser Pro				
	195	200	205	
Tyr Glu Gly Tyr Arg Ser Leu Pro Arg His Gln Leu Leu Cys Phe Lys				
	210	215	220	
Glu Asp Cys Gln Ala Val Phe Gln Asp Leu Glu Gly Val Glu Lys Val				
	225	230	235	240
Phe Gly Val Ser Leu Val Leu Val Leu Ile Gly Ser His Pro Asp Leu				
	245	250	255	
Ser Phe Leu Pro Gly Ala Gly Leu Thr Leu Gln Trp Ile Leu Thr Ser				
	260	265	270	

Arg
273

<210> 1227

<211> 86

<212>Amino acid

<213> Homo sapiens

<400> 1227

```

Lys Leu Arg Pro Phe Ile Phe Ser Asn Gln Ser Leu Trp Leu His Ser
 1           5           10           15
Tyr Glu Gly Ala Glu Leu Glu Lys Thr Phe Ile Lys Gly Ser Trp Ala
          20           25           30
Thr Phe Trp Val Lys Val Ala Ser Cys Trp Ala Cys Val Leu Leu Tyr
          35           40           45
Leu Gly Leu Leu Leu Ala Pro Leu Cys Trp Pro Pro Thr Gln Lys Pro
          50           55           60
Gln Pro Leu Ile Leu Arg Arg Arg Arg His Arg Ile Ile Ser Pro Asp
          65           70           75           80
Asn Lys Tyr Pro Pro Val
                  85 86

```

<210> 1228

<211> 249

<212>Amino acid

<213> Homo sapiens

<400> 1228

```

Gln Leu Ile His Leu Ser His Gly Tyr Gln Ile His Trp Thr Asp Tyr
 1           5           10           15
Tyr Asn Val Gly Thr Gly Arg Pro Glu Phe Gly Thr Arg Ala Ala His
          20           25           30
Lys Ser Leu Ala Gly Ala Glu Leu Lys Thr Leu Lys Asp Phe Val Thr
          35           40           45
Val Leu Ala Lys Leu Phe Pro Gly Arg Pro Pro Val Lys Lys Leu Leu
          50           55           60
Glu Met Leu Gln Glu Trp Leu Ala Ser Leu Pro Leu Asp Arg Ile Pro
          65           70           75           80
Tyr Asn Ala Val Leu Asp Leu Val Asn Asn Lys Met Arg Ile Ser Gly
          85           90           95
Ile Phe Leu Thr Asn His Ile Lys Trp Val Gly Cys Gln Gly Ser Arg
          100          105          110
Ser Glu Leu Arg Gly Tyr Pro Cys Ser Leu Trp Lys Leu Phe His Thr
          115          120          125
Leu Thr Val Glu Ala Ser Thr His Pro Asp Ala Leu Val Gly Thr Gly
          130          135          140
Phe Glu Asp Asp Pro Gln Ala Val Leu Gln Thr Met Arg Arg Tyr Val
          145          150          155          160
His Thr Phe Phe Gly Cys Lys Glu Cys Gly Glu His Phe Glu Glu Met
          165          170          175
Ala Lys Glu Ser Met Asp Ser Val Lys Thr Pro Asp Gln Ala Ile Leu
          180          185          190
Trp Leu Trp Lys Lys His Asn Met Val Asn Gly Arg Leu Ala Gly Glu
          195          200          205
Lys Pro Leu Gly Met Gly Gly Ser Ala Arg Ala Glu Gly Gly Pro Gly
          210          215          220
Pro Gly Thr Ala Arg Thr Ala Arg Leu Pro Trp Gly Leu Ser Leu Ser
          225          230          235          240
Phe Ala Ala Ser Cys His Pro Leu Cys
                  245          249

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<210> 1229

<211> 800

<212>Amino acid

<213> Homo sapiens

<400> 1229

His Gly Gly Ala Thr Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys
 1 5 10 15
 Cys Pro Ser Arg Ser Ser Met Leu Thr Gly Lys Tyr Val His Asn His
 20 25 30
 Asn Val Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala
 35 40 45
 Met His Glu Pro Arg Thr Phe Ala Val Tyr Leu Asn Asn Thr Gly Tyr
 50 55 60
 Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly Ser Tyr
 65 70 75 80
 Ile Pro Pro Gly Trp Arg Glu Trp Leu Gly Leu Ile Lys Asn Ser Arg
 85 90 95
 Phe Tyr Asn Tyr Thr Val Cys Arg Asn Gly Ile Lys Glu Lys His Gly
 100 105 110
 Phe Asp Tyr Ala Lys Asp Tyr Phe Thr Asp Leu Ile Thr Asn Glu Ser
 115 120 125
 Ile Asn Tyr Phe Lys Met Ser Lys Arg Met Tyr Pro His Arg Pro Val
 130 135 140
 Met Met Val Ile Ser His Ala Glu Pro His Gly Pro Glu Asp Ser Ala
 145 150 155 160
 Pro Gln Phe Ser Lys Leu Tyr Pro Asn Ala Ser Gln His Ile Thr Pro
 165 170 175
 Ser Tyr Asn Tyr Ala Pro Asn Met Asp Lys His Trp Ile Met Gln Tyr
 180 185 190
 Thr Gly Pro Met Leu Pro Ile His Met Glu Phe Thr Asn Ile Leu Gln
 195 200 205
 Arg Lys Arg Leu Gln Thr Leu Met Ser Val Asp Asp Ser Val Glu Arg
 210 215 220
 Leu Tyr Asn Met Leu Val Glu Thr Gly Glu Leu Glu Asn Thr Tyr Ile
 225 230 235 240
 Ile Tyr Thr Ala Asp His Gly Tyr His Ile Gly Gln Phe Gly Leu Val
 245 250 255
 Lys Gly Lys Ser Met Pro Tyr Asp Phe Asp Ile Arg Val Pro Phe Phe
 260 265 270
 Ile Arg Gly Pro Ser Val Glu Pro Gly Ser Ile Val Pro Gln Ile Val
 275 280 285
 Leu Asn Ile Asp Leu Ala Pro Thr Ile Leu Asp Ile Ala Gly Leu Asp
 290 295 300
 Thr Pro Pro Asp Val Asp Gly Lys Ser Val Leu Lys Leu Leu Asp Pro
 305 310 315 320
 Glu Lys Pro Gly Asn Arg Phe Arg Thr Asn Lys Lys Ala Lys Ile Trp
 325 330 335
 Arg Asp Thr Phe Leu Val Glu Arg Gly Lys Phe Leu Arg Lys Lys Glu
 340 345 350
 Glu Ser Ser Lys Asn Ile Gln Gln Ser Asn His Leu Pro Lys Tyr Glu
 355 360 365
 Arg Val Lys Glu Leu Cys Gln Gln Ala Arg Tyr Gln Thr Ala Cys Glu
 370 375 380
 Gln Pro Gly Gln Lys Trp Gln Cys Ile Glu Asp Thr Ser Gly Lys Leu
 385 390 395 400
 Arg Ile His Lys Cys Lys Gly Pro Ser Asp Leu Leu Thr Val Arg Gln
 405 410 415
 Ser Thr Arg Asn Leu Tyr Ala Arg Gly Phe His Asp Lys Asp Lys Glu
 420 425 430
 Cys Ser Cys Arg Glu Ser Gly Tyr Arg Ala Ser Arg Ser Gln Arg Lys
 435 440 445
 Ser Gln Arg Gln Phe Leu Arg Asn Gln Gly Thr Pro Lys Tyr Lys Pro

450 455 460
 Arg Phe Val His Thr Arg Gln Thr Arg Ser Leu Ser Val Glu Phe Glu
 465 470 475 480
 Gly Glu Ile Tyr Asp Ile Asn Leu Glu Glu Glu Glu Leu Gln Val
 485 490 495
 Leu Gln Pro Arg Asn Ile Ala Lys Arg His Asp Glu Gly His Lys Gly
 500 505 510
 Pro Arg Asp Leu Gln Ala Ser Ser Gly Gly Asn Arg Gly Arg Met Leu
 515 520 525
 Ala Asp Ser Ser Asn Ala Val Gly Pro Pro Thr Thr Val Arg Val Thr
 530 535 540
 His Lys Cys Phe Ile Leu Pro Asn Asp Ser Ile His Cys Glu Arg Glu
 545 550 555 560
 Leu Tyr Gln Ser Ala Arg Ala Trp Lys Asp His Lys Ala Tyr Ile Asp
 565 570 575
 Glu Glu Ile Glu Ala Leu Gln Asp Lys Ile Lys Asn Leu Arg Glu Val
 580 585 590
 Arg Gly His Leu Lys Arg Arg Lys Pro Glu Glu Cys Ser Cys Ser Lys
 595 600 605
 Gln Ser Tyr Tyr Asn Lys Glu Lys Gly Val Lys Lys Gln Glu Lys Leu
 610 615 620
 Lys Ser His Leu His Pro Phe Lys Glu Ala Ala Gln Glu Val Asp Ser
 625 630 635 640
 Lys Leu Gln Leu Phe Lys Glu Asn Asn Arg Arg Arg Lys Lys Glu Arg
 645 650 655
 Lys Glu Lys Arg Arg Gln Arg Lys Gly Glu Glu Cys Ser Leu Pro Gly
 660 665 670
 Leu Thr Cys Phe Thr His Asp Asn Asn His Trp Gln Thr Ala Pro Phe
 675 680 685
 Trp Asn Leu Gly Ser Phe Cys Ala Cys Thr Ser Ser Asn Asn Asn Thr
 690 695 700
 Tyr Trp Cys Leu Arg Thr Val Asn Glu Thr His Asn Phe Leu Phe Cys
 705 710 715 720
 Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Met Asn Thr Asp Pro
 725 730 735
 Tyr Gln Leu Thr Asn Thr Val His Thr Val Glu Arg Gly Ile Leu Asn
 740 745 750
 Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys Gln Gly Tyr Lys
 755 760 765
 Gln Cys Asn Pro Arg Pro Lys Asn Leu Asp Val Gly Asn Lys Asp Gly
 770 775 780
 Gly Ser Tyr Asp Leu His Arg Gly Gln Leu Trp Asp Gly Trp Glu Gly
 785 790 795 800

<210> 1230

<211> 698

<212> Amino acid

<213> Homo sapiens

<400> 1230

His Leu Leu Ile Ala Gln Glu Leu Ala Asp Arg Val Gly Glu Gly Arg
 1 5 10 15
 Ala Cys Trp Ser Leu Gly Asn Ala Tyr Val Ser Met Gly Arg Pro Ala
 20 25 30
 Gln Ala Leu Thr Phe Ala Lys Lys His Leu Gln Ile Ser Gln Glu Ile
 35 40 45
 Gly Asp Arg His Gly Glu Leu Thr Ala Arg Met Asn Val Ala Gln Leu

743

565 570 575
 Gly Pro Ile Ser Lys Ala Glu Gly Met Ala Gly His Glu Leu Arg His
 580 585 590
 Ser Lys Thr Pro Ser Gln Glu Lys Gly Gln Gly Leu Val Leu Gly Met
 595 600 605
 Leu Thr Gly Ser Lys Ser Ser Ala Gln Ser Gly Trp Glu Val Ala Pro
 610 615 620
 Gly Ser Val Thr Leu Thr Gln Val Gly Gly Trp Ser Val Glu Ala Gly
 625 630 635 640
 Glu Ala Ser Leu Ser Ser Thr Leu Gln Thr Pro His Met Arg Thr Pro
 645 650 655
 Leu Leu Pro Pro Ala Gly Gly Asp Asp Ile Thr Ala Leu Ser Met Gly
 660 665 670
 Arg Gly Leu Thr Gly His Gln Val Arg Asp Pro Arg Thr Gly Arg Thr
 675 680 685
 Cys Trp Ser Leu Arg Trp Ala Pro Gly Ala
 690 695 698

<210> 1231
 <211> 131
 <212> Amino acid
 <213> Homo sapiens

<400> 1231
 Asn Ser Ala Ala Asp Leu Ala Ile Phe Ala Leu Trp Gly Leu Lys Pro
 1 5 10 15
 Val Val Tyr Leu Leu Ala Ser Ser Phe Leu Gly Leu Gly Leu His Pro
 20 25 30
 Ile Ser Gly His Phe Val Ala Glu His Tyr Met Phe Leu Lys Gly His
 35 40 45
 Glu Thr Tyr Ser Tyr Tyr Gly Pro Leu Asn Trp Ile Thr Phe Asn Val
 50 55 60
 Gly Tyr His Val Glu His His Asp Phe Pro Ser Ile Pro Gly Tyr Asn
 65 70 75 80
 Leu Pro Leu Val Arg Lys Ile Ala Pro Glu Tyr Tyr Asp His Leu Pro
 85 90 95
 Gln His His Ser Trp Val Lys Val Leu Trp Asp Phe Val Phe Glu Asp
 100 105 110
 Ser Leu Gly Pro Tyr Ala Arg Val Lys Arg Val Tyr Arg Leu Ala Lys
 115 120 125
 Asp Gly Leu
 130 131

<210> 1232
 <211> 71
 <212> Amino acid
 <213> Homo sapiens

<400> 1232
 Gln Glu Ser Gly Phe Ser Cys Lys Gly Pro Gly Gln Asn Val Ala Val
 1 5 10 15
 Thr Arg Ala His Pro Asp Ser Gln Gly Arg Arg Arg Pro Glu Arg
 20 25 30
 Gly Ala Arg Gly Gly Gln Val Phe Tyr Asn Ser Glu Tyr Gly Glu Leu

35 40 45
 Ser Glu Pro Ser Glu Glu Asp His Cys Ser Pro Ser Ala Arg Val Thr
 50 55 60
 Phe Phe Thr Asp Asn Ser Tyr
 65 70 71

<210> 1233
 <211> 146
 <212> Amino acid
 <213> Homo sapiens

<400> 1233
 Val Ile Val His Ala Arg Pro Ile Arg Thr Arg Ala Ser Lys Tyr Tyr
 1 5 10 15
 Ile Pro Glu Ala Val Tyr Gly Leu Pro Ala Tyr Pro Ala Tyr Ala Gly
 20 25 30
 Gly Gly Gly Phe Val Leu Ser Gly Ala Thr Leu His Arg Leu Ala Gly
 35 40 45
 Ala Cys Ala Gln Val Glu Leu Phe Pro Ile Asp Asp Val Phe Leu Gly
 50 55 60
 Met Cys Leu Gln Arg Leu Arg Leu Thr Pro Glu Pro His Pro Ala Phe
 65 70 75 80
 Arg Thr Phe Gly Ile Pro Gln Pro Ser Ala Ala Pro His Leu Ser Thr
 85 90 95
 Phe Asp Pro Cys Phe Tyr Arg Glu Leu Val Val Val His Gly Leu Ser
 100 105 110
 Ala Ala Asp Ile Trp Leu Met Trp Arg Leu Leu His Gly Pro His Gly
 115 120 125
 Pro Ala Cys Ala His Pro Gln Pro Val Ala Ala Gly Pro Phe Gln Trp
 130 135 140
 Asp Ser
 145 146

<210> 1234
 <211> 299
 <212> Amino acid
 <213> Homo sapiens

<400> 1234
 Met Ala Ser Ala Ala Cys Ser Met Asp Pro Ile Asp Ser Phe Glu Leu
 1 5 10 15
 Leu Asp Leu Leu Phe Asp Arg Gln Asp Gly Ile Leu Arg His Val Glu
 20 25 30
 Leu Gly Glu Gly Trp Gly His Val Lys Asp Gln Val Leu Pro Asn Pro
 35 40 45
 Asp Ser Asp Asp Phe Leu Ser Ser Ile Leu Gly Ser Gly Asp Ser Leu
 50 55 60
 Pro Ser Ser Pro Leu Trp Ser Pro Glu Gly Ser Asp Ser Gly Ile Ser
 65 70 75 80
 Glu Asp Leu Pro Ser Asp Pro Gln Asp Thr Pro Pro Arg Ser Gly Pro
 85 90 95
 Ala Thr Ser Pro Ala Gly Cys His Pro Ala Gln Pro Gly Lys Gly Pro
 100 105 110
 Cys Leu Ser Tyr His Pro Gly Asn Ser Cys Ser Thr Thr Thr Pro Gly

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      115      120      125
Pro Val Ile Gln Gln Gln His His Leu Gly Ala Ser Tyr Leu Leu Arg
      130      135      140
Pro Gly Ala Gly His Cys Gln Glu Leu Val Leu Thr Glu Asp Glu Lys
145      150      155      160
Lys Leu Leu Ala Lys Glu Gly Ile Thr Leu Pro Thr Gln Leu Pro Leu
      165      170      175
Thr Lys Tyr Glu Glu Arg Val Leu Lys Lys Ile Arg Arg Lys Ile Arg
      180      185      190
Asn Lys Gln Ser Ala Gln Glu Ser Arg Lys Lys Lys Lys Glu Tyr Ile
      195      200      205
Asp Gly Leu Glu Thr Arg Ser Cys Cys Cys Pro Leu Pro Ser Ser Ser
      210      215      220
Ser Pro Pro Ser Ala Leu Leu Ala Pro Thr Lys Pro Arg Ala Leu Gly
225      230      235      240
Thr Leu Arg Leu Tyr Glu Cys Ser Pro Glu Leu Cys Thr Thr Met Leu
      245      250      255
Pro Pro Ala Trp Leu Leu Met Leu Cys Gln Ala Pro Arg Pro Gln Asp
      260      265      270
Pro Asp Pro Arg Leu Thr Gln Pro Glu Lys Ser Leu Gln Glu Ala Pro
      275      280      285
Gly Gln Thr Gly Ala Ser Arg Thr Pro Arg Thr
      290      295      299

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<210> 1235
 <211> 1098
 <212> Amino acid
 <213> Homo sapiens

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      <400> 1235
Ala Arg Gly Arg Arg Ser Arg Pro Val Trp Ala Ala Ser Trp Gly Gly
  1      5      10      15
Arg Gly Arg Pro Ala Ala Arg Arg Arg Pro Arg Gly Leu Ala Ala Thr
      20      25      30
Met Gly Phe Glu Leu Asp Arg Phe Asp Gly Asp Val Asp Pro Asp Leu
      35      40      45
Lys Cys Ala Leu Cys His Lys Val Leu Glu Asp Pro Leu Thr Thr Pro
      50      55      60
Cys Gly His Val Phe Cys Ala Gly Cys Val Leu Pro Trp Val Val Gln
      65      70      75      80
Glu Gly Ser Cys Pro Ala Arg Cys Arg Gly Arg Leu Ser Ala Lys Glu
      85      90      95
Leu Asn His Val Leu Pro Leu Lys Arg Leu Ile Leu Lys Leu Asp Ile
      100      105      110
Lys Cys Ala Tyr Ala Thr Arg Gly Cys Gly Arg Val Val Lys Leu Gln
      115      120      125
Gln Leu Pro Glu His Leu Glu Arg Cys Asp Phe Ala Pro Ala Arg Cys
      130      135      140
Arg His Ala Gly Cys Gly Gln Val Leu Leu Arg Arg Asp Val Glu Ala
145      150      155      160
His Met Arg Asp Ala Cys Asp Ala Arg Pro Val Gly Arg Cys Gln Glu
      165      170      175
Gly Cys Gly Leu Pro Leu Thr His Gly Glu Gln Arg Ala Gly Gly His
      180      185      190
Cys Cys Ala Arg Ala Leu Arg Ala His Asn Gly Ala Leu Gln Ala Arg
      195      200      205
Leu Gly Ala Leu His Lys Ala Leu Lys Lys Glu Ala Leu Arg Ala Gly
      210      215      220
Lys Arg Glu Lys Ser Leu Val Ala Gln Leu Ala Ala Ala Gln Leu Glu

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225 230 235 240
 Leu Gln Met Thr Ala Leu Arg Tyr Gln Lys Lys Phe Thr Glu Tyr Ser
 245 250 255
 Ala Arg Leu Asp Ser Leu Ser Arg Cys Val Ala Ala Pro Pro Gly Gly
 260 265 270
 Lys Gly Glu Glu Thr Lys Ser Leu Thr Leu Val Leu His Arg Asp Ser
 275 280 285
 Gly Ser Leu Gly Phe Asn Ile Ile Gly Gly Arg Pro Ser Val Asp Asn
 290 295 300
 His Asp Gly Ser Ser Ser Glu Gly Ile Phe Val Ser Lys Ile Val Asp
 305 310 315 320
 Ser Gly Pro Ala Ala Lys Glu Gly Gly Leu Gln Ile His Asp Arg Ile
 325 330 335
 Ile Glu Val Asn Gly Arg Asp Leu Ser Arg Ala Thr His Asp Gln Ala
 340 345 350
 Val Glu Ala Phe Lys Thr Ala Lys Glu Pro Ile Val Val Gln Val Leu
 355 360 365
 Arg Arg Thr Pro Arg Thr Lys Met Phe Thr Pro Pro Ser Glu Ser Gln
 370 375 380
 Leu Val Asp Thr Gly Thr Gln Thr Asp Ile Thr Phe Glu His Ile Met
 385 390 395 400
 Ala Leu Thr Lys Met Ser Ser Pro Ser Pro Pro Val Leu Asp Pro Tyr
 405 410 415
 Leu Leu Pro Glu Glu His Pro Ser Ala His Glu Tyr Tyr Asp Pro Asn
 420 425 430
 Asp Tyr Ile Gly Asp Ile His Gln Glu Met Asp Arg Glu Glu Leu Glu
 435 440 445
 Leu Glu Glu Val Asp Leu Tyr Arg Met Asn Ser Gln Asp Lys Leu Gly
 450 455 460
 Leu Thr Val Cys Tyr Arg Thr Asp Asp Glu Asp Asp Ile Gly Ile Tyr
 465 470 475 480
 Ile Ser Glu Ile Asp Pro Asn Ser Ile Ala Ala Lys Asp Gly Arg Ile
 485 490 495
 Arg Glu Gly Asp Arg Ile Ile Gln Ile Asn Gly Ile Glu Val Gln Asn
 500 505 510
 Arg Glu Glu Ala Val Ala Leu Leu Thr Ser Glu Glu Asn Lys Asn Phe
 515 520 525
 Ser Leu Leu Ile Ala Arg Ala Glu Leu Gln Leu Asp Glu Gly Trp Met
 530 535 540
 Asp Asp Asp Arg Asn Asp Phe Leu Asp Asp Leu His Met Asp Met Leu
 545 550 555 560
 Glu Glu Gln His His Gln Ala Met Gln Phe Thr Ala Ser Val Leu Gln
 565 570 575
 Gln Lys Lys His Asp Glu Asp Gly Gly Thr Thr Asp Thr Ala Thr Ile
 580 585 590
 Leu Ser Asn Gln His Glu Lys Asp Ser Gly Val Gly Arg Thr Asp Glu
 595 600 605
 Ser Thr Arg Asn Asp Glu Ser Ser Glu Gln Glu Asn Asn Gly Asp Asp
 610 615 620
 Ala Thr Ala Ser Ser Asn Pro Leu Ala Gly Gln Arg Lys Leu Thr Cys
 625 630 635 640
 Ser Gln Asp Thr Leu Gly Ser Gly Asp Leu Pro Phe Ser Asn Lys Ser
 645 650 655
 Phe Ile Ser Pro Glu Cys Thr Gly Ala Ala Tyr Leu Gly Ile Pro Val
 660 665 670
 Asp Glu Cys Glu Arg Phe Arg Glu Leu Leu Glu Leu Lys Cys Gln Val
 675 680 685
 Lys Ser Ala Thr Pro Tyr Gly Leu Tyr Tyr Pro Ser Gly Pro Leu Asp
 690 695 700
 Ala Gly Lys Ser Asp Pro Glu Ser Val Asp Lys Glu Leu Glu Leu Leu
 705 710 715 720
 Asn Glu Glu Leu Arg Ser Ile Glu Leu Glu Cys Leu Ser Ile Val Arg
 725 730 735
 Ala His Lys Met Gln Gln Leu Lys Glu Gln Tyr Arg Glu Ser Trp Met

740 745 750
 Leu His Asn Ser Gly Phe Arg Asn Tyr Asn Thr Ser Ile Asp Val Arg
 755 760 765
 Arg His Glu Leu Ser Asp Ile Thr Glu Leu Pro Glu Lys Ser Asp Lys
 770 775 780
 Asp Ser Ser Ser Ala Tyr Asn Thr Gly Glu Ser Cys Arg Ser Thr Pro
 785 790 795 800
 Leu Thr Leu Glu Ile Ser Pro Asp Asn Ser Leu Arg Arg Ala Ala Glu
 805 810 815
 Gly Ile Ser Cys Pro Ser Ser Glu Gly Ala Val Gly Thr Thr Glu Ala
 820 825 830
 Tyr Gly Pro Ala Ser Lys Asn Leu Leu Ser Ile Thr Glu Asp Pro Glu
 835 840 845
 Val Gly Thr Pro Thr Tyr Ser Pro Ser Leu Lys Glu Leu Asp Pro Asn
 850 855 860
 Gln Pro Leu Glu Ser Lys Glu Arg Arg Ala Ser Asp Gly Ser Arg Ser
 865 870 875 880
 Pro Thr Pro Ser Gln Lys Leu Gly Ser Ala Tyr Leu Pro Ser Tyr His
 885 890 895
 His Ser Pro Tyr Lys His Ala His Ile Pro Ala His Ala Gln His Tyr
 900 905 910
 Gln Ser Tyr Met Gln Leu Ile Gln Gln Lys Ser Ala Val Glu Tyr Ala
 915 920 925
 Gln Ser Gln Met Ser Leu Val Ser Met Cys Lys Asp Leu Ser Ser Pro
 930 935 940
 Thr Pro Ser Glu Pro Arg Met Glu Trp Lys Val Lys Ile Arg Ser Asp
 945 950 955 960
 Gly Thr Arg Tyr Ile Thr Lys Arg Pro Val Arg Asp Arg Leu Leu Arg
 965 970 975
 Glu Arg Ala Leu Lys Ile Arg Glu Glu Arg Ser Gly Met Thr Thr Asp
 980 985 990
 Asp Asp Ala Val Ser Glu Met Lys Met Gly Arg Tyr Trp Ser Lys Glu
 995 1000 1005
 Glu Arg Lys Gln His Leu Val Lys Ala Lys Glu Gln Arg Arg Arg Arg
 1010 1015 1020
 Glu Phe Met Met Gln Ser Arg Leu Asp Cys Leu Lys Glu Gln Gln Ala
 1025 1030 1035 1040
 Ala Asp Asp Arg Lys Glu Met Asn Ile Leu Glu Leu Ser His Lys Lys
 1045 1050 1055
 Met Met Lys Lys Arg Asn Lys Lys Ile Phe Asp Asn Trp Met Thr Ile
 1060 1065 1070
 Gln Glu Leu Leu Thr His Gly Thr Lys Ser Pro Asp Gly Thr Arg Val
 1075 1080 1085
 Tyr Asn Ser Phe Leu Ser Val Thr Thr Val
 1090 1095 1098

<210> 1236

<211> 51

<212> Amino acid

<213> Homo sapiens

<400> 1236

Phe Phe Phe Leu Val Glu Met Gly Phe Cys His Val Gly Gln Gly Gly
 1 5 10 15
 Leu Thr Leu Ile Gly Ser Ser Asn Leu Pro Ala Ser Ala Ser Lys Ser
 20 25 30
 Ala Gly Ile Thr Gly Val Ser His Cys Ala Arg Pro Asp Phe Lys Ser
 35 40 45
 Cys Val Glu

50 51

<210> 1237
 <211> 70
 <212>Amino acid
 <213> Homo sapiens

<400> 1237
 Leu Ala Gly Arg Lys Val Leu Leu Phe Val Ser Gly Tyr Val Val Gly
 1 5 10 15
 Trp Gly Pro Ile Thr Trp Leu Leu Met Ser Glu Val Leu Pro Leu Arg
 20 25 30
 Ala Arg Gly Val Ala Ser Gly Leu Cys Val Leu Ala Ser Trp Leu Thr
 35 40 45
 Ala Phe Val Leu Thr Lys Ser Phe Leu Pro Gly Gly Val Ser Val Gln
 50 55 60
 Pro Gln Ala Pro Gly Pro
 65 70

<210> 1238
 <211> 114
 <212>Amino acid
 <213> Homo sapiens

<400> 1238
 Phe Trp Ala Pro Gly Pro Pro Gly Val Gly Ala Ala Val Gly Asp Ala
 1 5 10 15
 Ser Thr Arg Ser Leu Arg Glu Ser Cys Pro Ser Pro Ser Pro Gly Arg
 20 25 30
 Leu Arg Arg Thr Thr Ala Pro Trp Ser Ser Gln Ala Arg Ala Ala Ala
 35 40 45
 Pro Ala Pro Ser Ser Ser Cys Arg Gly Pro Asp Gly Ala Ser Ser Pro
 50 55 60
 Arg Asp Leu Pro Trp Arg Pro Trp Lys Ile Leu Arg Arg Thr Pro Leu
 65 70 75 80
 Ser Gly Asp Val Glu Leu Ser Gln Val His Pro Asp Gln Arg Ile Leu
 85 90 95
 Arg Arg Phe Ile Leu Ser Arg Thr Cys Gly Asn Thr Ile Pro Gly Met
 100 105 110
 Ala Glu
 114

<210> 1239
 <211> 174
 <212>Amino acid
 <213> Homo sapiens

<400> 1239
 Met Arg Arg Phe Leu Ser Lys Val Tyr Ser Phe Pro Met Arg Lys Leu

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1           5           10           15
Ile Leu Phe Leu Val Phe Pro Val Val Arg Gln Thr Pro Thr Gln His
20           25           30
Phe Lys Asn Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly Leu
35           40           45
Ala Phe Thr Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu Ile
50           55           60
Pro Glu Ser Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg Gly
65           70           75           80
Met Thr Ser Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn Lys
85           90           95
Pro Asp Ser Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr Pro
100          105          110
Glu Pro Thr Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly
115          120          125
Ser Asn Trp Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Gln
130          135          140
Glu Gly Asp Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp
145          150          155          160
Tyr Thr Lys Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
165          170          174

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<210> 1240

<211> 425

<212> Amino acid

<213> Homo sapiens

<400> 1240

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Phe Val Trp Asp Glu Val Ala Gln Arg Ser Gly Cys Glu Glu Arg Trp
1           5           10           15
Leu Val Ile Asp Arg Lys Val Tyr Asn Ile Ser Glu Phe Thr Arg Arg
20           25           30
His Pro Gly Ser Arg Val Ile Ser His Tyr Ala Gly Gln Asp Ala
35           40           45
Thr Asp Pro Phe Val Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys
50           55           60
Tyr Met Asn Ser Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser
65           70           75           80
Phe Glu Pro Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu
85           90           95
Arg Ala Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe
100          105          110
Phe Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
115          120          125
Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu Cys
130          135          140
Ala Val Leu Leu Ser Ala Val Gln Ala Gln Ala Gly Trp Leu Gln His
145          150          155          160
Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp Asn His Leu
165          170          175
Leu His His Phe Val Ile Gly His Leu Lys Gly Ala Pro Ala Ser Trp
180          185          190
Trp Asn His Met His Phe Gln His His Ala Lys Pro Asn Cys Phe Arg
195          200          205
Lys Asp Pro Asp Ile Asn Met His Pro Phe Phe Phe Ala Leu Gly Lys
210          215          220
Ile Leu Ser Val Glu Leu Gly Lys Gln Lys Lys Lys Tyr Met Pro Tyr
225          230          235          240
Asn His Gln His Lys Tyr Phe Phe Leu Ile Gly Pro Pro Ala Leu Leu

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<210> 1241
<211> 152
<212> Amino acid
<213> Homo sapiens'
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```
<210> 1242
<211> 191
<212>Amino acid
<213> Homo sapiens
```

<400> 1242

```

Ser Pro Glu Arg Ser Ser Leu Ser Val Gly Arg Glu Lys Ala Met Glu
 1          5          10          15
Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu Cys Leu
          20          25          30
Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser Glu Val
          35          40          45
Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu Pro Tyr Tyr
          50          55          60
Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly Lys Asp Val
          65          70          75          80
Thr Gly Ser Leu Phe Arg Ile Asn Val Gly Leu Arg Gly Leu Val Ala
          85          90          95
Gly Gly Ile Ile Gly Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu
          100          105          110
Met Ala Phe Gln Lys Tyr Ser Gly Glu Thr Val Gln Glu Arg Lys Gln
          115          120          125
Lys Asp Arg Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly
          130          135          140
Arg Leu Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu
          145          150          155          160
Gln Glu Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu
          165          170          175
Asn Leu Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp
          180          185          190 191

```

<210> 1243

<211> 381

<212>Amino acid

<213> Homo sapiens

<400> 1243

```

Arg Ser Leu Gly Leu Ala Val Thr Glu Met Val Pro Trp Val Arg Thr
 1          5          10          15
Met Gly Gln Lys Leu Lys Gln Arg Leu Arg Leu Asp Val Gly Arg Glu
          20          25          30
Ile Cys Arg Gln Tyr Pro Leu Phe Cys Phe Leu Leu Leu Cys Leu Ser
          35          40          45
Ala Ala Ser Leu Leu Leu Asn Arg Tyr Ile His Ile Leu Met Ile Phe
          50          55          60
Trp Ser Phe Val Ala Gly Val Val Thr Phe Tyr Cys Ser Leu Gly Pro
          65          70          75          80
Asp Ser Leu Leu Pro Asn Ile Phe Phe Thr Ile Lys Tyr Lys Pro Lys
          85          90          95
Gln Leu Gly Leu Gln Glu Leu Phe Pro Gln Gly His Ser Cys Ala Val
          100          105          110
Cys Gly Lys Val Lys Cys Lys Arg His Arg Pro Ser Leu Leu Leu Glu
          115          120          125
Asn Tyr Gln Pro Trp Leu Asp Leu Lys Ile Ser Ser Lys Val Asp Ala
          130          135          140
Ser Leu Ser Glu Val Leu Glu Leu Val Leu Glu Asn Phe Val Tyr Pro
          145          150          155          160
Trp Tyr Arg Asp Val Thr Asp Asp Glu Ser Phe Val Asp Glu Leu Arg
          165          170          175
Ile Thr Leu Arg Phe Phe Ala Ser Val Leu Ile Arg Arg Ile His Lys
          180          185          190
Val Asp Ile Pro Ser Ile Ile Thr Lys Lys Leu Leu Lys Ala Ala Met

```

195 200 205
 Lys His Ile Glu Val Ile Val Lys Ala Arg Gln Lys Val Lys Asn Thr
 210 215 220
 Glu Phe Leu Gln Gln Ala Ala Leu Glu Glu Tyr Gly Pro Glu Leu His
 225 230 235 240
 Val Ala Leu Arg Ser Arg Arg Asp Glu Leu His Tyr Leu Arg Lys Leu
 245 250 255
 Thr Glu Leu Leu Phe Pro Tyr Ile Leu Pro Pro Lys Ala Thr Asp Cys
 260 265 270
 Arg Ser Leu Thr Leu Leu Ile Arg Glu Ile Leu Ser Gly Ser Val Phe
 275 280 285
 Leu Pro Ser Leu Asp Phe Leu Ala Asp Pro Asp Thr Val Asn His Leu
 290 295 300
 Leu Ile Ile Phe Ile Asp Asp Ser Pro Pro Glu Lys Ala Thr Glu Pro
 305 310 315 320
 Ala Ser Pro Leu Val Pro Phe Leu Gln Lys Phe Ala Glu Pro Arg Asn
 325 330 335
 Lys Lys Pro Ser Val Leu Lys Leu Glu Leu Lys Gln Ile Arg Glu Gln
 340 345 350
 Gln Asp Leu Leu Phe Arg Phe Met Asn Phe Leu Lys Gln Glu Gly Ala
 355 360 365
 Val His Val Leu His Val Leu Phe Asp Cys Gly Gly Ile
 370 375 380 381

<210> 1244

<211> 371

<212> Amino acid

<213> Homo sapiens

<400> 1244
 Gln Ser Leu Ala Glu Val Leu Gln Gln Leu Gly Ala Ser Ser Glu Leu
 1 5 10 15
 Gln Ala Val Leu Ser Tyr Ile Phe Pro Thr Tyr Gly Val Thr Pro Asn
 20 25 30
 His Ser Ala Phe Ser Met His Ala Leu Leu Val Asn His Tyr Met Lys
 35 40 45
 Gly Gly Phe Tyr Pro Arg Gly Val Thr Ser Glu Ile Ala Phe His Thr
 50 55 60
 Ile Pro Val Ile Gln Arg Ala Gly Gly Ala Val Leu Thr Lys Ala Thr
 65 70 75 80
 Val Gln Ser Val Leu Leu Asp Ser Ala Gly Lys Ala Cys Gly Val Ser
 85 90 95
 Val Lys Lys Gly His Glu Leu Val Asn Ile Tyr Cys Pro Ile Val Val
 100 105 110
 Ser Asn Ala Gly Leu Phe Asn Thr Tyr Glu His Leu Leu Pro Gly Asn
 115 120 125
 Ala Arg Cys Leu Pro Gly Val Lys Gln Gln Leu Gly Thr Val Arg Pro
 130 135 140
 Gly Leu Gly Met Thr Ser Val Phe Ile Cys Leu Arg Gly Thr Lys Glu
 145 150 155 160
 Asp Leu His Leu Pro Ser Thr Asn Tyr Tyr Val Tyr Tyr Asp Thr Asp
 165 170 175
 Met Asp Gln Ala Met Glu Arg Tyr Val Ser Met Pro Arg Glu Glu Ala
 180 185 190
 Ala Glu His Ile Pro Leu Leu Phe Ala Phe Pro Ser Ala Lys Asp
 195 200 205
 Pro Thr Trp Glu Asp Arg Phe Pro Gly Arg Ser Thr Met Ile Met Leu
 210 215 220
 Ile Pro Thr Ala Tyr Glu Trp Phe Glu Glu Trp Gln Ala Glu Leu Lys

```
<210> 1245
<211> 295
<212>Amino acid
<213> Homo sapiens
```

75A

260 265 270
 Met Pro Gly Glu Pro Val Asp Val Ala Cys Gly Val Asp His Met Val
 275 280 285
 Thr Leu Ala Lys Ser Phe Ile
 290 295

<210> 1246
 <211> 172
 <212> Amino acid
 <213> Homo sapiens

<400> 1246
 Leu Pro Phe Arg Glu Trp Leu Met Ile Val Val Ser Leu Ser Ala Ala
 1 5 10 15
 Ala Val Ala Ala Ala Phe Met Ala Lys Cys Arg Met Val Leu Ser Ser
 20 25 30
 Arg Tyr Phe Cys Ser His Phe Val Met Ser Ala Ser Arg Ala Arg Ile
 35 40 45
 Arg Ser Ser Phe Ser Arg Thr Ser Ser Arg Arg Ala Gly Ala Leu Tyr
 50 55 60
 Ser Gly Met Leu Ala Gly Trp Pro Phe Pro Cys Phe Cys Trp Val Leu
 65 70 75 80
 Ser Ala Ser Ser Ser Leu Ser Ser Gln Val Arg Ser Leu Arg Ser Ile
 85 90 95
 Cys Ser Arg Phe Ser His Ala Asp Cys Ser Trp Val Arg Ala Cys Cys
 100 105 110
 Ser Phe Ser Thr Phe Ser Thr Tyr Ala Cys Phe Ser Arg Asn Ser Ser
 115 120 125
 Ser Ser Leu Met Thr Leu Ala Trp Ala Leu Leu Lys Ala Trp Ser Arg
 130 135 140
 Ile Ser Met Cys Leu Arg Trp Ser Ser Leu Ala Val Arg Thr Ala Ala
 145 150 155 160
 Asn Ser Ile Ser Asn Phe Ser Phe Ser Phe Lys Asn
 165 170 172

<210> 1247
 <211> 361
 <212> Amino acid
 <213> Homo sapiens

<400> 1247
 Met Gln Ala Val Arg Ala Thr Ala Ser Gln Ser Leu Ser Cys Ala Arg
 1 5 10 15
 Ala Pro Arg Glu Pro Thr Gln His Ala Leu Arg Ala His Trp Phe Pro
 20 25 30
 Pro Ala Ala Ala Val Gln Pro Ser Pro His Ser Gly Val Ala Ala Ala
 35 40 45
 Ala Gly Thr Trp Ser Ser Ala Phe Arg Gly Glu His Pro Leu Val Ser
 50 55 60
 Ser Gly Leu Leu Leu Gly Val Arg Glu Gln Ser Phe Arg Leu Leu Arg
 65 70 75 80
 Ser Lys Ala Gly Thr His Met Tyr Leu Glu His Thr Ser His Cys Pro
 85 90 95
 His His Asp Asp Asp Thr Ala Met Asp Thr Pro Leu Pro Arg Pro Arg

```

      100              105              110
Pro Leu Leu Ala Val Glu Arg Thr Gly Gln Arg Pro Leu Trp Ala Pro
      115              120              125
Ser Leu Glu Leu Pro Lys Pro Asp Met Gln Pro Leu Pro Ala Gly Ala
      130              135              140
Phe Leu Glu Glu Val Ala Glu Gly Thr Pro Ala Gln Thr Glu Ser Glu
      145              150              155              160
Pro Lys Val Leu Asp Pro Glu Glu Asp Leu Leu Cys Ile Ala Lys Thr
      165              170              175
Phe Ser Tyr Leu Arg Glu Ser Gly Trp Tyr Trp Gly Ser Ile Thr Ala
      180              185              190
Ser Glu Ala Arg Gln His Leu Gln Lys Met Pro Glu Gly Thr Phe Leu
      195              200              205
Val Arg Asp Ser Thr His Pro Ser Tyr Leu Phe Thr Leu Ser Val Lys
      210              215              220
Thr Thr Arg Gly Pro Thr Asn Val Arg Ile Glu Tyr Ala Asp Ser Ser
      225              230              235              240
Phe Arg Leu Asp Ser Asn Cys Leu Ser Arg Pro Arg Ile Leu Ala Phe
      245              250              255
Pro Asp Val Val Ser Leu Val Gln His Tyr Val Ala Ser Cys Thr Ala
      260              265              270
Asp Thr Arg Ser Asp Ser Pro Asp Pro Ala Pro Thr Pro Ala Leu Pro
      275              280              285
Met Pro Lys Glu Asp Ala Pro Ser Asp Pro Ala Leu Pro Ala Pro Pro
      290              295              300
Pro Ala Thr Ala Val His Leu Lys Leu Val Gln Pro Phe Val Arg Arg
      305              310              315              320
Ser Ser Ala Arg Ser Leu Gln His Leu Cys Arg Leu Val Ile Asn Arg
      325              330              335
Leu Val Ala Asp Val Asp Cys Leu Pro Leu Pro Arg Arg Met Ala Asp
      340              345              350
Tyr Leu Arg Gln Tyr Pro Phe Gln Leu
      355              360 361

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<210> 1248
 <211> 279
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 1248
Phe Val Asp Ile Phe Gln Arg Trp Lys Glu Cys Arg Gly Lys Ser Pro
      1              5              10              15
Ala Gln Ala Glu Leu Ser Tyr Leu Asn Lys Ala Lys Trp Leu Glu Met
      20              25              30
Tyr Gly Val Asp Met His Val Val Arg Gly Arg Asp Gly Cys Glu Tyr
      35              40              45
Ser Leu Gly Leu Thr Pro Thr Gly Ile Leu Ile Phe Glu Gly Ala Asn
      50              55              60
Lys Ile Gly Leu Phe Phe Trp Pro Lys Ile Thr Lys Met Asp Phe Lys
      65              70              75              80
Lys Ser Lys Leu Thr Leu Val Val Val Glu Asp Asp Asp Gln Gly Arg
      85              90              95
Glu Gln Glu His Thr Phe Val Phe Arg Leu Asp Ser Ala Arg Thr Cys
      100              105              110
Lys His Leu Trp Lys Cys Ala Val Glu His His Ala Phe Arg Leu
      115              120              125
Arg Thr Pro Gly Asn Ser Lys Ser Asn Arg Ser Asp Phe Ile Arg Leu
      130              135              140
Gly Ser Arg Phe Arg Phe Ser Gly Arg Thr Glu Tyr Gln Ala Thr His

```

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145          150          155          160
Gly Ser Arg Leu Arg Arg Thr Ser Thr Phe Glu Arg Lys Pro Ser Lys
          165          170          175
Arg Tyr Pro Ser Arg Arg His Ser Thr Phe Lys Ala Ser Asn Pro Val
          180          185          190
Ile Ala Ala Gln Leu Cys Ser Lys Thr Asn Pro Glu Val His Asn Tyr
          195          200          205
Gln Pro Gln Tyr His Pro Asn Ile His Pro Ser Gln Pro Arg Trp His
          210          215          220
Pro His Ser Pro Asn Val Arg Pro Ser Phe Gln Asp Asp Arg Ser His
225          230          235          240
Trp Lys Ala Ser Ala Ser Gly Asp Asp Ser His Phe Asp Tyr Val His
          245          250          255
Asp Gln Asn Gln Lys Asn Leu Gly Gly Met Gln Ser Met Met Tyr Arg
          260          265          270
Asp Lys Leu Met Thr Ala Leu
          275          279

```

<210> 1249

<211> 255

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(255)

<223> X = any amino acid or stop code

<400> 1249

```

Gly Gly Ile Arg Leu Ile Gln Lys Leu Thr Trp Arg Ser Arg Gln Gln
 1          5          10          15
Asp Arg Glu Asn Cys Ala Met Lys Gly Lys His Lys Asp Glu Cys His
          20          25          30
Asn Phe Ile Lys Val Phe Val Pro Arg Asn Asp Glu Met Val Phe Val
          35          40          45
Cys Gly Thr Asn Ala Phe Asn Pro Met Cys Arg Tyr Tyr Arg Val Ser
          50          55          60
Ile Phe Tyr Val Ile Cys Phe Phe Xaa Ser Thr Phe Leu Pro Ser Leu
65          70          75          80
Ile Cys Cys Xaa Ser Xaa Asn Leu Ser Ala Phe Gln Xaa Phe Val Leu
          85          90          95
Ser Leu Val Gln Xaa Lys Asn Lys Asp Arg Ile Leu Gln Met Glu Phe
          100          105          110
Xaa Tyr Lys Xaa Asn Ser Ile Ala Phe Lys Arg Ala Arg Xaa Ile Asp
          115          120          125
Met Thr Leu Ala Ile Tyr Phe Ser Phe Val Leu Ser Thr Leu Xaa Tyr
          130          135          140
Asp Gly Glu Glu Ile Ser Gly Leu Ala Arg Cys Pro Phe Asp Ala Arg
145          150          155          160
Gln Thr Asn Gly Ala Leu Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr
          165          170          175
Val Ala Asp Phe Leu Ala Ser Asp Ala Val Ile Tyr Arg Ser Met Gly
          180          185          190
Asp Gly Ser Ala Leu Arg Thr Ile Lys Tyr Asp Ser Lys Trp Ile Lys
          195          200          205
Glu Pro His Phe Leu Tyr Ala Ile Lys Tyr Gly Asn Tyr Val Tyr Phe
210          215          220
Ser Phe Arg Glu Ile Val Ala Thr Xaa Xaa Leu Gly Lys Ala Val Asp
225          230          235          240

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Ser Arg Val Ala Arg Tyr Glu Lys Gln Leu Val Gly Pro Thr Val
 245 250 255

<210> 1250

<211> 307

<212>Amino acid

<213> Homo sapiens

<400> 1250

Ala Arg Ala Leu Ala Arg Glu Arg Glu Ser Glu Ser Ala Arg Ala Asp
 1 5 10 15
 Asp Val Thr Leu Gly Val Ser Ala Ile Leu Ala Val Asp Arg Gly Gly
 20 25 30
 Asn Leu Gly Ser Ala Asp Gly Trp Ala Tyr Ile Asp Val Glu Val Arg
 35 40 45
 Arg Pro Trp Ala Phe Val Gly Pro Gly Cys Ser Arg Ser Ser Gly Asn
 50 55 60
 Gly Ser Thr Ala Tyr Gly Leu Val Gly Ser Pro Arg Trp Leu Ser Pro
 65 70 75 80
 Phe His Thr Gly Gly Ala Val Ser Leu Pro Arg Arg Pro Arg Gly Pro
 85 90 95
 Gly Pro Val Leu Gly Val Ala Arg Pro Cys Leu Arg Cys Val Leu Arg
 100 105 110
 Pro Glu His Tyr Glu Pro Gly Ser His Tyr Ser Gly Phe Ala Gly Arg
 115 120 125
 Asp Ala Ser Arg Ala Phe Val Thr Gly Asp Cys Ser Glu Ala Gly Leu
 130 135 140
 Val Asp Asp Val Ser Asp Leu Ser Ala Ala Glu Met Leu Thr Leu His
 145 150 155 160
 Asn Trp Leu Ser Phe Tyr Glu Lys Asn Tyr Val Cys Val Gly Arg Val
 165 170 175
 Thr Gly Arg Phe Tyr Gly Glu Asp Gly Leu Pro Thr Pro Ala Leu Thr
 180 185 190
 Gln Val Glu Ala Ala Ile Thr Arg Gly Leu Glu Ala Asn Lys Leu Gln
 195 200 205
 Leu Gln Glu Lys Gln Thr Phe Pro Pro Cys Asn Ala Glu Trp Ser Ser
 210 215 220
 Ala Arg Gly Ser Arg Leu Trp Cys Ser Gln Lys Ser Gly Gly Val Ser
 225 230 235 240
 Arg Asp Trp Ile Gly Val Pro Arg Lys Leu Tyr Lys Pro Gly Ala Lys
 245 250 255
 Glu Pro Arg Cys Val Cys Val Arg Thr Thr Gly Pro Pro Ser Gly Gln
 260 265 270
 Met Pro Asp Asn Pro Pro His Arg Asn Arg Gly Asp Leu Asp His Pro
 275 280 285
 Asn Leu Ala Glu Tyr Thr Gly Cys Pro Pro Leu Ala Ile Thr Cys Ser
 290 295 300
 Phe Pro Leu
 305 307

<210> 1251

<211> 100

<212>Amino acid

<213> Homo sapiens

<400> 1251

Tyr Phe Ile Ile Cys Arg Asp Gly Val Leu Leu Phe Cys Pro Gly Trp
 1 5 10 15
 Ser Gln Thr Pro Gly Ala Gln Ala Ile Leu Leu His Trp Ala Thr Gln
 20 25 30
 Asn Ala Gly Met Thr Asp Met Ser His Ser Ala Gln Pro Ile Tyr Leu
 35 40 45
 Phe Ile Tyr Leu Ile Arg Thr Arg Ser His Tyr Val Ala Gln Ala Gly
 50 55 60
 Gln Leu Leu Asp Ser Asn Asp Ser Pro Asn Val Ala Ser Gln Asn Val
 65 70 75 80
 Gly Ile Thr Gly Met Ser His His Ala Trp Leu Lys Ile Val Leu Tyr
 85 90 95
 Phe Cys Ile Ile
 100

<210> 1252

<211> 464

<212> Amino acid

<213> Homo sapiens

<400> 1252

Pro Ala Ala Arg Pro Pro Ser Leu Val Arg Leu Ser Pro Ser Pro Pro
 1 5 10 15
 Lys Pro Arg Ala Arg Ala Arg Ala Pro Gln Ser Val Glu Pro Ala Ala
 20 25 30
 Pro Leu Val Ala Arg Gly Ser Ser Pro Pro Ala Arg Pro Ala Pro Ala
 35 40 45
 Met Val Arg Pro Arg Arg Ala Pro Tyr Arg Ser Gly Ala Gly Gly Pro
 50 55 60
 Leu Gly Gly Arg Gly Arg Pro Pro Arg Pro Leu Val Val Arg Ala Val
 65 70 75 80
 Arg Ser Arg Ser Trp Pro Ala Ser Pro Arg Gly Pro Gln Pro Pro Arg
 85 90 95
 Ile Arg Ala Arg Ser Ala Pro Pro Met Glu Gly Ala Arg Val Phe Gly
 100 105 110
 Ala Leu Gly Pro Ile Gly Pro Ser Ser Pro Gly Leu Thr Leu Gly Gly
 115 120 125
 Leu Ala Val Ser Glu His Arg Leu Ser Asn Lys Leu Leu Ala Trp Ser
 130 135 140
 Gly Val Leu Glu Trp Gln Glu Lys Arg Arg Pro Tyr Ser Asp Ser Thr
 145 150 155 160
 Ala Lys Leu Lys Arg Thr Leu Pro Cys Gln Ala Tyr Val Asn Gln Gly
 165 170 175
 Glu Asn Leu Glu Thr Asp Gln Trp Pro Gln Lys Leu Ile Met Gln Leu
 180 185 190
 Ile Pro Gln Gln Leu Leu Thr Thr Leu Gly Pro Leu Phe Arg Asn Ser
 195 200 205
 Gln Leu Ala Gln Phe His Phe Thr Asn Arg Asp Cys Asp Ser Leu Lys
 210 215 220
 Gly Leu Cys Arg Ile Met Gly Asn Gly Phe Ala Gly Cys Met Leu Phe
 225 230 235 240
 Pro His Ile Ser Pro Cys Glu Val Arg Val Leu Met Leu Leu Tyr Ser
 245 250 255
 Ser Lys Lys Lys Ile Phe Met Gly Leu Ile Pro Tyr Asp Gln Ser Gly
 260 265 270
 Phe Val Ser Ala Ile Arg Gln Val Ile Thr Thr Arg Lys Gln Ala Val
 275 280 285

Gly Pro Gly Gly Val Asn Ser Gly Pro Val Gln Ile Val Asn Asn Lys
 290 295 300
 Phe Leu Ala Trp Ser Gly Val Met Glu Trp Gln Glu Pro Arg Pro Glu
 305 310 315 320
 Pro Asn Ser Arg Ser Lys Arg Trp Leu Pro Ser His Val Tyr Val Asn
 325 330 335
 Gln Gly Glu Ile Leu Arg Thr Glu Gln Trp Pro Arg Lys Leu Tyr Met
 340 345 350
 Gln Leu Ile Pro Gln Gln Leu Leu Thr Thr Leu Val Pro Leu Phe Arg
 355 360 365
 Asn Ser Arg Leu Val Gln Phe His Phe Thr Lys Asp Leu Glu Thr Leu
 370 375 380
 Lys Ser Leu Cys Arg Ile Met Asp Asn Gly Phe Ala Gly Cys Val His
 385 390 395 400
 Phe Ser Tyr Lys Ala Ser Cys Glu Ile Arg Val Leu Met Leu Leu Tyr
 405 410 415
 Ser Ser Glu Lys Lys Ile Phe Ile Gly Leu Ile Pro His Asp Gln Gly
 420 425 430
 Asn Phe Val Asn Gly Ile Arg Arg Val Ile Ala Asn Gln Gln Val
 435 440 445
 Leu Gln Arg Asn Leu Glu Gln Glu Gln Gln Arg Gly Met Gly Gly
 450 455 460 464

<210> 1253

<211> 214

<212> Amino acid

<213> Homo sapiens

<400> 1253

Gly Arg Pro Ala Leu Gly Arg Glu Ala Pro Pro Gln Ala Gly Leu Ser
 1 5 10 15
 Ser Thr Pro Pro Pro Cys Ser Glu Thr Cys Thr Met Gly Pro His Ser
 20 25 30
 Ile Leu Arg Thr Val His Cys Arg Pro Thr Lys Thr Pro Pro Glu Pro
 35 40 45
 Ser Ala Glu Pro His Pro Leu Ser Leu Leu Thr Ser Ser Asn Thr Ser
 50 55 60
 Leu Ala Gly Thr Ser Leu Gly Arg Asp Leu Thr Pro Gly Gly Gly Lys
 65 70 75 80
 Pro Pro Ser Gly Gln Thr Pro Arg Asn Pro Glu Ser Pro Arg His Arg
 85 90 95
 Leu Gly Ser Pro Arg Gly Arg Arg Trp Leu Ala Ser Pro Thr Pro Thr
 100 105 110
 Gly Ser Gly Arg Ser Gly Pro Ala Ser Arg Gly Gln Arg Arg Leu Ser
 115 120 125
 Cys Ala Ala Gln Asp Pro Thr Ser Glu Gly Ala Ser Val Gly Ala Met
 130 135 140
 Glu Ala Gly Leu Gly Pro Pro Thr Ala Ala Pro Arg Gly Val Val Ser
 145 150 155 160
 Glu Ala Ala Glu Ser Leu Gly Gly Thr Leu Ser Trp Gly Ala Trp Gly
 165 170 175
 Arg Pro Pro Ala Gly Pro Ser Gly Leu Ala Gly Arg Arg Ser Arg Arg
 180 185 190
 Glu Ala Leu Arg Pro Asp Arg Lys Glu Ala Ser Val Met Met Ala Ala
 195 200 205
 Val Ser Ala Ile Gln Pro
 210 214

<210> 1254
 <211> 198
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(198)
 <223> X = any amino acid or stop code

<400> 1254
 Pro Gly Val Pro Thr His Gly Trp Pro Arg Ser Arg Val Leu Thr Arg
 1 5 10 15
 Val Arg Gly Ser Arg Gly Ser Gly Lys Met Ala Ala Ala Val Val Leu
 20 25 30
 Ala Ala Gly Leu Arg Ala Ala Arg Arg Ala Val Ala Ala Thr Gly Val
 35 40 45
 Arg Gly Gly Gln Val Arg Gly Ala Ala Gly Val Thr Asp Gly Asn Glu
 50 55 60
 Val Ala Lys Ala Gln Gln Ala Thr Pro Gly Gly Ala Ala Pro Thr Ile
 65 70 75 80
 Phe Ser Arg Ile Leu Asp Lys Ser Leu Pro Ala Asp Ile Leu Tyr Glu
 85 90 95
 Asp Gln Gln Cys Leu Val Phe Arg Asp Val Ala Pro Gln Ala Pro Val
 100 105 110
 His Phe Leu Val Ile Pro Lys Lys Pro Ile Pro Arg Ile Ser Gln Ala
 115 120 125
 Glu Glu Glu Asp Gln Gln Leu Thr Tyr Val Pro Pro Leu Ser Leu Xaa
 130 135 140
 Leu Leu Gly His Leu Leu Leu Val Ala Lys Gln Thr Ala Lys Ala Glu
 145 150 155 160
 Gly Leu Gly Asp Gly Tyr Arg Leu Val Ile Asn Asp Gly Lys Leu Gly
 165 170 175
 Ala Gln Ser Val Tyr His Leu His Ile His Val Leu Gly Gly Arg Gln
 180 185 190
 Leu Gln Trp Pro Pro Gly
 195 198

<210> 1255
 <211> 458
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(458)
 <223> X = any amino acid or stop code

<400> 1255
 Val Pro Asn Tyr Leu Pro Ser Val Ser Ser Ala Ile Gly Gly Glu Val
 1 5 10 15
 Pro Gln Arg Tyr Val Trp Arg Phe Cys Ile Gly Leu His Ser Ala Pro
 20 25 30

Arg Phe Leu Val Ala Phe Ala Tyr Trp Asn His Tyr Leu Ser Cys Thr
 35 40 45
 Ser Pro Cys Ser Cys Tyr Arg Pro Leu Cys Arg Leu Asn Phe Gly Leu
 50 55 60
 Asn Val Val Glu Asn Leu Ala Leu Leu Val Leu Thr Tyr Val Ser Ser
 65 70 75 80
 Ser Glu Asp Phe Thr Trp Val Pro Gly Xaa Gly Arg Ser Gly Glu Val
 85 90 95
 Phe Pro Glu Gly Thr Gly Leu Pro Leu Pro His Ser Asp Leu Pro Thr
 100 105 110
 Ser Trp Cys Gly His Ser Leu Gln Cys Gly Ser Gln Ser Ser Phe Pro
 115 120 125
 Pro Ala Ile His Glu Asn Ala Phe Ile Val Phe Ile Ala Ser Ser Leu
 130 135 140
 Gly His Met Leu Leu Thr Cys Ile Leu Trp Arg Leu Thr Lys Lys His
 145 150 155 160
 Thr Val Ser Gln Glu Asp Gly Leu Ser Leu Ala Gly Ala Pro Arg Gln
 165 170 175
 Pro Arg Arg Lys Ser Arg Thr Ser Val Leu Arg Ile Arg Val Met Val
 180 185 190
 Arg Trp Glu Leu Ser Ser Asn Gly Asn Pro Gly Arg Gly Val Leu Gly
 195 200 205
 Leu Gly Leu Gly Leu Gly Asn Lys Leu Arg Val Val Gly Gln Asn Leu
 210 215 220
 Gly Leu Xaa His Cys Val Trp Val Val Trp Glu Thr Gly Glu Xaa Lys
 225 230 235 240
 Arg Trp Arg Leu Gln Met Gly Ile Glu Xaa Gly Val Ala Ser Arg Arg
 245 250 255
 Gln Xaa Val Arg Asn Ser Val Arg Gly Leu Val Cys His Asn Ser Ser
 260 265 270
 Ala Pro Pro Met Tyr Met Gly Phe Phe Ser Pro Thr Val Phe Gly Gly
 275 280 285
 Gly Val Gly Gly Xaa Leu His Val Thr Phe Ile Leu His Pro Pro Glu
 290 295 300
 Val Glu Ala Ala Gly Ile Pro Leu Leu Leu Gly Pro Ser Leu Pro Gln
 305 310 315 320
 Arg Gln Gly Arg Glu His Ile Val Val Ile Leu Ala Ala Pro Ala Cys
 325 330 335
 Ala Pro Phe His Asp Arg Xaa Trp Glu Pro Arg Glu Ile Arg Pro Ser
 340 345 350
 Pro Xaa Glu Leu Gly Leu Arg Gly Glu Pro Thr Leu Ser Tyr Pro Ala
 355 360 365
 Ser Cys Arg Val Ile Arg Gln Pro Ile Pro Xaa Asp Arg Lys Ser Tyr
 370 375 380
 Ser Trp Lys Gln Arg Leu Phe Ile Ile Asn Phe Ile Ser Phe Phe Ser
 385 390 395 400
 Ala Leu Ala Val Tyr Phe Arg His Asn Met Tyr Cys Glu Ala Gly Val
 405 410 415
 Tyr Thr Ile Phe Ala Ile Leu Glu Tyr Thr Val Val Leu Thr Asn Met
 420 425 430
 Ala Phe His Met Thr Ala Trp Trp Asp Phe Gly Asn Lys Glu Leu Leu
 435 440 445
 Ile Thr Ser Gln Pro Glu Glu Lys Arg Phe
 450 455 458

<210> 1256

<211> 83

<212> Amino acid

<213> Homo sapiens

<400> 1256

```

Ile Asp Leu Leu Glu Ile Arg Asn Gly Pro Arg Ser His Glu Ser Phe
 1           5           10           15
Gln Glu Met Asp Leu Asn Asp Asp Trp Lys Leu Ser Lys Asp Glu Val
           20           25           30
Lys Ala Tyr Leu Lys Lys Glu Phe Glu Lys His Gly Ala Val Val Asn
           35           40           45
Glu Ser His His Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp
           50           55           60
Glu Asp Lys Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His
           65           70           75           80
Asp Glu Leu
           83

```

<210> 1257

<211> 203

<212>Amino acid

<213> Homo sapiens

<400> 1257

```

Pro Arg Val Arg Gly Arg Val Gly Lys Glu Gly Ala Ala Ala Lys Pro
 1           5           10           15
Arg Ser Leu Leu Arg Arg Phe Gln Leu Ser Trp Ser Val Cys Gly
           20           25           30
Gly Asn Lys Asp Pro Trp Val Gln Glu Leu Met Ser Cys Leu Asp Leu
           35           40           45
Lys Glu Cys Gly His Ala Tyr Ser Gly Ile Val Ala His Gln Lys His
           50           55           60
Leu Leu Pro Thr Ser Pro Pro Ile Ser Gln Ala Ser Glu Gly Ala Ser
           65           70           75           80
Ser Asp Ile His Thr Pro Ala Gln Met Leu Leu Ser Thr Leu Gln Ser
           85           90           95
Thr Gln Arg Pro Thr Leu Pro Val Gly Ser Leu Ser Ser Asp Lys Glu
           100          105          110
Leu Thr Arg Pro Asn Glu Thr Thr Ile His Thr Ala Gly His Ser Leu
           115          120          125
Ala Ala Gly Pro Glu Ala Gly Glu Asn Gln Lys Gln Pro Glu Lys Asn
           130          135          140
Ala Gly Pro Thr Ala Arg Thr Ser Ala Thr Val Pro Val Leu Cys Leu
           145          150          155          160
Leu Ala Ile Ile Phe Ile Leu Thr Ala Ala Leu Ser Tyr Val Leu Cys
           165          170          175
Lys Arg Arg Arg Gly Gln Ser Pro Gln Ser Ser Pro Asp Leu Pro Val
           180          185          190
His Tyr Ile Pro Val Ala Pro Asp Ser Asn Thr
           195          200          203

```

<210> 1258

<211> 195

<212>Amino acid

<213> Homo sapiens

<400> 1258

```

Leu Ile Ile Ser Asn Phe Leu Lys Ala Lys Gln Lys Pro Gly Ser Thr
 1           5           10           15
Pro Asn Leu Gln Lys Lys Ser Gln Ala Arg Leu Ala Pro Asp Ile
      20           25           30
Val Ser Ala Ser Gln Tyr Arg Lys Phe Asp Glu Phe Gln Thr Gly Ile
      35           40           45
Leu Ile Tyr Glu Leu Leu His Gln Pro Asn Pro Phe Glu Val Arg Ala
      50           55           60
Gln Leu Arg Glu Arg Asp Tyr Arg Gln Glu Asp Leu Pro Pro Leu Pro
      65           70           75           80
Ala Leu Ser Leu Tyr Ser Pro Gly Leu Gln Gln Leu Ala His Leu Leu
      85           90           95
Leu Glu Ala Asp Pro Ile Lys Arg Ile Arg Ile Gly Glu Ala Lys Arg
      100          105          110
Val Leu Gln Cys Leu Leu Trp Gly Pro Arg Arg Glu Leu Val Gln Gln
      115          120          125
Pro Gly Thr Ser Glu Glu Ala Leu Cys Gly Thr Leu His Asn Trp Ile
      130          135          140
Asp Met Lys Arg Ala Leu Met Met Met Lys Phe Ala Glu Lys Ala Val
      145          150          155          160
Asp Arg Arg Arg Gly Val Glu Leu Glu Asp Trp Leu Cys Cys Gln Tyr
      165          170          175
Leu Ala Ser Ala Glu Pro Gly Ala Leu Leu Gln Ser Leu Lys Leu Leu
      180          185          190
Gln Leu Leu
      195

```

<210> 1259

<211> 672

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(672)

<223> X = any amino acid or stop code

<400> 1259

```

Lys Arg Gly Leu Ile Val Val Met Ala His Glu Met Ile Gly Thr Gln
 1           5           10           15
Ile Val Thr Glu Arg Gly Val Ala Leu Leu Glu Ser Gly Thr Glu Lys
      20           25           30
Val Leu Leu Ile Asp Ser Arg Pro Phe Val Glu Tyr Asn Thr Ser His
      35           40           45
Ile Leu Glu Ala Ile Asn Ile Asn Cys Ser Lys Leu Met Lys Arg Arg
      50           55           60
Leu Gln Gln Asp Lys Val Leu Ile Thr Glu Leu Ile Gln His Ser Ala
      65           70           75           80
Lys His Lys Val Asp Ile Asp Cys Ser Gln Lys Val Val Val Tyr Asp
      85           90           95
Gln Ser Ser Gln Asp Val Ala Ser Leu Ser Ser Asp Cys Phe Leu Thr
      100          105          110
Val Leu Leu Gly Lys Leu Glu Lys Ser Phe Asn Ser Val His Leu Leu
      115          120          125
Ala Gly Gly Phe Ala Glu Phe Ser Arg Cys Phe Pro Gly Leu Cys Glu
      130          135          140
Gly Lys Ser Thr Leu Val Pro Thr Cys Ile Ser Gln Pro Cys Leu Pro
      145          150          155          160
Val Ala Asn Ile Gly Pro Thr Arg Ile Leu Pro Asn Leu Tyr Leu Gly

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				165					170					175	
Cys	Gln	Arg	Asp	Val	Leu	Asn	Lys	Glu	Leu	Met	Gln	Gln	Asn	Gly	Ile
			180					185					190		
Gly	Tyr	Val	Leu	Asn	Ala	Ser	Asn	Thr	Cys	Pro	Lys	Pro	Asp	Phe	Ile
		195					200					205			
Pro	Glu	Ser	His	Phe	Leu	Arg	Val	Pro	Val	Asn	Asp	Ser	Phe	Cys	Glu
	210					215					220				
Lys	Ile	Leu	Pro	Trp	Leu	Asp	Lys	Ser	Val	Asp	Phe	Ile	Glu	Lys	Ala
225					230					235				240	
Lys	Ala	Ser	Asn	Gly	Cys	Val	Leu	Val	His	Cys	Leu	Ala	Gly	Ile	Ser
			245						250					255	
Arg	Ser	Ala	Thr	Ile	Ala	Ile	Ala	Tyr	Ile	Met	Lys	Arg	Met	Asp	Met
		260						265					270		
Ser	Leu	Asp	Glu	Ala	Tyr	Arg	Phe	Val	Lys	Glu	Lys	Arg	Pro	Thr	Ile
	275						280					285			
Ser	Pro	Asn	Phe	Asn	Phe	Leu	Gly	Gln	Leu	Leu	Asp	Tyr	Glu	Lys	Lys
	290				295						300				
Ile	Lys	Asn	Gln	Thr	Gly	Ala	Ser	Gly	Pro	Lys	Ser	Lys	Leu	Lys	Leu
305					310					315				320	
Leu	His	Leu	Glu	Lys	Pro	Asn	Glu	Pro	Val	Pro	Ala	Val	Ser	Glu	Gly
			325						330					335	
Gly	Gln	Lys	Ser	Glu	Thr	Pro	Leu	Ser	Pro	Pro	Cys	Ala	Asp	Ser	Ala
		340						345					350		
Thr	Ser	Glu	Ala	Ala	Gly	Gln	Arg	Pro	Val	His	Pro	Ala	Ser	Val	Pro
	355						360					365			
Ser	Val	Pro	Ser	Val	Gln	Pro	Ser	Leu	Leu	Glu	Asp	Ser	Pro	Leu	Val
	370				375						380				
Gln	Ala	Leu	Ser	Gly	Leu	His	Leu	Ser	Ala	Asp	Arg	Leu	Glu	Asp	Ser
385					390					395				400	
Asn	Lys	Leu	Lys	Arg	Ser	Phe	Ser	Leu	Asp	Ile	Lys	Ser	Val	Ser	Tyr
			405						410					415	
Ser	Ala	Ser	Met	Ala	Ala	Ser	Leu	His	Gly	Phe	Ser	Ser	Ser	Glu	Asp
		420						425					430		
Ala	Leu	Glu	Tyr	Tyr	Lys	Pro	Ser	Thr	Thr	Leu	Asp	Gly	Thr	Asn	Lys
	435						440					445			
Leu	Cys	Gln	Phe	Ser	Pro	Val	Gln	Glu	Leu	Cys	Gly	Ala	Asp	Ser	Arg
	450					455					460				
Asn	Gln	Ser	Xaa	Xaa	Gly	Gly	Ser	Gln	Pro	Ser	Pro	Arg	Ser	Cys	Arg
465				470						475				480	
Pro	Pro	Gly	Leu	Gln	Thr	Ala	Arg	Ala	Ser	Asp	Cys	Ile	Arg	Ser	Glu
			485						490					495	
Pro	Ala	Ala	Val	Ala	Pro	Pro	Arg	Gly	Pro	Phe	Tyr	Leu	His	Cys	Ile
		500						505					510		
Glu	Val	Gly	Ala	Trp	Arg	Thr	Ile	Thr	Thr	Pro	Ala	Ser	Phe	Ser	Ala
	515						520					525			
Phe	Pro	Pro	Pro	Ala	Ala	Pro	His	Glu	Val	Cys	Trp	Pro	Gly	Pro	Xaa
	530					535					540				
Gly	Leu	Ala	Pro	Asp	Ile	Leu	Ala	Pro	Gln	Thr	Ser	Thr	Pro	Ser	Leu
545				550						555				560	
Thr	Ser	Ser	Trp	Tyr	Phe	Ala	Thr	Glu	Ser	Ser	His	Phe	Tyr	Ser	Ala
			565					570						575	
Ser	Ala	Ile	Tyr	Gly	Gly	Ser	Ala	Ser	Tyr	Ser	Ala	Tyr	Ser	Cys	Ser
		580						585					590		
Gln	Leu	Pro	Thr	Cys	Gly	Asp	Gln	Val	Tyr	Ser	Val	Arg	Arg	Arg	Gln
	595					600						605			
Lys	Pro	Ser	Asp	Arg	Ala	Asp	Ser	Arg	Arg	Ser	Trp	His	Glu	Glu	Ser
	610					615					620				
Pro	Phe	Glu	Lys	Gln	Phe	Lys	Arg	Arg	Ser	Cys	Gln	Met	Glu	Phe	Gly
625					630					635				640	
Glu	Ser	Ile	Met	Ser	Glu	Asn	Arg	Ser	Arg	Glu	Glu	Leu	Gly	Lys	Val
			645					650						655	
Gly	Ser	Gln	Ser	Ser	Phe	Ser	Gly	Ser	Met	Glu	Ile	Ile	Glu	Val	Ser
		660						665					670		672

<210> 1260

<211> 260

<212>Amino acid

<213> Homo sapiens

<400> 1260

Ala Ser Ser Ser Lys Arg Val Ser Arg Gln Lys Met Leu Gln Leu Trp
 1 5 10 15
 Lys Leu Val Leu Leu Cys Gly Val Leu Thr Gly Thr Ser Glu Ser Leu
 20 25 30
 Leu Asp Asn Leu Gly Asn Asp Leu Ser Asn Val Val Asp Lys Leu Glu
 35 40 45
 Pro Val Leu His Glu Gly Leu Glu Thr Val Asp Asn Thr Leu Lys Gly
 50 55 60
 Ile Leu Glu Lys Leu Lys Val Asp Leu Gly Val Leu Gln Lys Ser Ser
 65 70 75 80
 Ala Trp Gln Leu Ala Lys Gln Lys Ala Gln Glu Ala Glu Lys Leu Leu
 85 90 95
 Asn Asn Val Ile Ser Lys Leu Leu Pro Thr Asn Thr Asp Ile Phe Gly
 100 105 110
 Leu Lys Ile Ser Asn Ser Leu Ile Leu Asp Val Lys Ala Glu Pro Ile
 115 120 125
 Asp Asp Gly Lys Gly Leu Asn Leu Ser Phe Pro Val Thr Ala Asn Val
 130 135 140
 Thr Glu Ala Gly Pro Ile Ile Asp Gln Ile Ile Asn Leu Arg Ala Ser
 145 150 155 160
 Leu Asp Leu Leu Thr Ala Val Thr Ile Glu Thr Asp Pro Gln Thr His
 165 170 175
 His Pro Val Ala Gly Leu Gly Glu Cys Ala Arg Asp Pro Thr Ser Ile
 180 185 190
 Ser Leu Cys Leu Leu Asp Lys His Ser Gln Ile Ile Asn Lys Phe Val
 195 200 205
 Asn Ser Val Ile Asn Thr Leu Lys Ser Thr Val Ser Ser Leu Leu Gln
 210 215 220
 Lys Glu Ile Cys Pro Leu Ile Arg Ile Phe Ile His Ser Leu Asp Val
 225 230 235 240
 Asn Val Ile Gln Gln Val Val Asp Asn Pro Gln His Lys Thr Gln Leu
 245 250 255
 Gln Thr Leu Ile
 260

<210> 1261

<211> 278

<212>Amino acid

<213> Homo sapiens

<400> 1261

Cys Ser Leu Arg Arg Pro Arg Ser Ala Ala Glu Pro Asp Ala Asp His
 1 5 10 15
 Val Pro Leu Leu Gly Leu Leu Arg Leu Gln Leu Arg Ala Ala Arg Gln
 20 25 30
 Pro Gly Ala Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu


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      35      40      45
Arg Gly Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser
  50      55      60
Ala Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
  65      70      75      80
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly
      85      90      95
Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr
      100      105      110
Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys
      115      120      125
Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys
      130      135      140
Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu
      145      150      155      160
Cys Thr Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe
      165      170      175
Ser Gly Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp
      180      185      190
Tyr Phe Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu
      195      200      205
Ala Ile Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile
      210      215      220
Asn Ile His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly
      225      230      235      240
Ala Gly Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr
      245      250      255
Pro Lys Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile
      260      265      270
Ile Glu Glu Leu Pro Lys
      275      278

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<210> 1262
 <211> 362
 <212> Amino acid
 <213> Homo sapiens

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      <400> 1262
Met His Ser Ala Met Leu Gly Thr Arg Val Asn Leu Ser Val Ser Asp
  1      5      10      15
Phe Trp Arg Val Met Met Arg Val Cys Trp Leu Val Arg Gln Asp Ser
      20      25      30
Arg His Gln Arg Ile Arg Leu Pro His Leu Glu Ala Val Val Ile Gly
      35      40      45
Arg Gly Pro Glu Thr Lys Ile Thr Asp Lys Lys Cys Ser Arg Gln Gln
      50      55      60
Val Gln Leu Lys Ala Glu Cys Asn Lys Gly Tyr Val Lys Val Lys Gln
      65      70      75      80
Val Gly Val Asn Pro Thr Ser Ile Asp Ser Val Val Ile Gly Lys Asp
      85      90      95
Gln Glu Val Lys Leu Gln Pro Gly Gln Val Leu His Met Val Asn Glu
      100      105      110
Leu Tyr Pro Tyr Ile Val Glu Phe Glu Glu Glu Ala Lys Asn Pro Gly
      115      120      125
Leu Glu Thr His Arg Lys Arg Lys Arg Ser Gly Asn Ser Asp Ser Ile
      130      135      140
Glu Arg Asp Ala Ala Gln Glu Ala Glu Ala Gly Thr Gly Leu Glu Pro
      145      150      155      160
Gly Ser Asn Ser Gly Gln Cys Ser Val Pro Leu Lys Lys Gly Lys Asp

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165      170      175
Ala Pro Ile Lys Lys Glu Ser Leu Gly His Trp Ser Gln Gly Leu Lys
180      185      190
Ile Ser Met Gln Asp Pro Lys Met Gln Val Tyr Lys Asp Glu Gln Val
195      200      205
Val Val Ile Lys Asp Lys Tyr Pro Lys Ala Arg Tyr His Trp Leu Val
210      215      220
Leu Pro Trp Thr Ser Ile Ser Ser Leu Lys Ala Val Ala Arg Glu His
225      230      235      240
Leu Glu Leu Leu Lys His Met His Thr Val Gly Glu Lys Val Ile Val
245      250      255
Asp Phe Ala Gly Ser Ser Lys Leu Arg Phe Arg Leu Gly Tyr His Ala
260      265      270
Ile Pro Ser Met Ser His Val His Leu His Val Ile Ser Gln Asp Phe
275      280      285
Asp Ser Pro Cys Leu Lys Asn Lys Lys His Trp Asn Ser Phe Asn Thr
290      295      300
Glu Tyr Phe Leu Glu Ser Gln Ala Val Ile Glu Met Val Gln Glu Ala
305      310      315      320
Gly Arg Val Thr Val Arg Asp Gly Met Pro Glu Leu Leu Lys Leu Pro
325      330      335
Leu Arg Cys His Glu Cys Gln Gln Leu Leu Pro Ser Ile Pro Gln Leu
340      345      350
Lys Glu His Leu Arg Lys His Trp Thr Gln
355      360      362

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<210> 1263

<211> 618

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(618)

<223> X = any amino acid or stop code

<400> 1263

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Asp Met Ser Asp Thr Ser Glu Ser Gly Ala Gly Leu Thr Arg Phe Gln
1      5      10      15
Ala Glu Ala Ser Glu Lys Asp Ser Ser Ser Met Met Gln Thr Leu Leu
20      25      30
Thr Val Thr Gln Asn Val Glu Val Pro Glu Thr Pro Lys Ala Ser Lys
35      40      45
Ala Leu Glu Val Ser Glu Asp Val Lys Val Ser Lys Ala Ser Gly Val
50      55      60
Ser Lys Ala Thr Glu Val Ser Lys Thr Pro Glu Ala Arg Glu Ala Pro
65      70      75      80
Ala Thr Gln Ala Ser Ser Thr Thr Gln Leu Thr Asp Thr Gln Val Leu
85      90      95
Ala Ala Glu Asn Lys Ser Leu Ala Ala Asp Thr Lys Lys Gln Asn Ala
100      105      110
Asp Pro Gln Ala Val Thr Met Pro Ala Thr Glu Thr Lys Lys Val Ser
115      120      125
His Val Ala Asp Thr Lys Val Asn Thr Lys Ala Gln Glu Thr Glu Ala
130      135      140
Ala Pro Ser Gln Ala Pro Ala Asp Glu Pro Glu Pro Glu Ser Ala Ala
145      150      155      160
Ala Gln Ser Gln Glu Asn Gln Asp Thr Arg Pro Lys Val Lys Ala Lys
165      170      175

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Lys Ala Arg Lys Val Lys His Leu Asp Gly Glu Glu Asp Gly Ser Ser
 180 185 190
 Asp Gln Ser Gln Ala Ser Gly Thr Thr Gly Gly Arg Arg Val Ser Lys
 195 200 205
 Ala Leu Met Ala Ser Met Ala Arg Arg Ala Ser Arg Gly Pro Ile Ala
 210 215 220
 Phe Trp Ala Arg Arg Ala Ser Arg Thr Arg Leu Ala Cys Phe Gly Pro
 225 230 235 240
 Gly Glu Pro Leu Leu Ser Pro Trp Arg Ser Pro Lys Ala Arg Arg Gln
 245 250 255
 Arg Gly Phe Ala Val Arg Val Ala Lys Phe Gln Ser Ser Gln Glu Pro
 260 265 270
 Glu Ala Pro Pro Pro Trp Asp Val Ala Leu Leu Gln Gly Arg Ala Asn
 275 280 285
 Asp Leu Val Lys Tyr Leu Leu Ala Lys Asp Gln Thr Lys Ile Pro Ile
 290 295 300
 Lys Arg Ser Asp Met Leu Lys Asp Ile Ile Lys Glu Tyr Thr Asp Val
 305 310 315 320
 Tyr Pro Glu Ile Ile Glu Arg Ala Gly Tyr Ser Leu Glu Lys Val Phe
 325 330 335
 Gly Ile Gln Leu Lys Glu Ile Asp Lys Asn Asp His Leu Tyr Ile Leu
 340 345 350
 Leu Ser Thr Leu Glu Pro Thr Asp Ala Gly Ile Leu Gly Thr Thr Lys
 355 360 365
 Asp Ser Pro Lys Leu Gly Leu Leu Met Val Leu Leu Ser Ile Ile Phe
 370 375 380
 Met Asn Gly Asn Arg Ser Ser Glu Ala Val Ile Trp Glu Val Leu Arg
 385 390 395 400
 Arg Ser Leu Gly Leu Arg Leu Gly Ile His His Ser Leu Leu Gly Asp
 405 410 415
 Val Lys Lys Leu Ile Thr Asp Glu Val Val Lys Gln Lys Tyr Leu Asp
 420 425 430
 Tyr Ala Arg Val Pro His Ser Asn Ser Pro Glu Tyr Glu Phe Phe Trp
 435 440 445
 Gly Leu Arg Ser Tyr Tyr Glu Asp Gln Gln Arg Xaa Lys Ser Phe Lys
 450 455 460
 Phe Ala Cys Lys Val Gln Lys Lys Asp Pro Lys Glu Trp Ala Ala Gln
 465 470 475 480
 Ser Pro Pro Gly Lys Ala Arg Glu Arg Met Glu Ala Asp Leu Lys Ala
 485 490 495
 Ala Ser Xaa Gly Ser Pro Trp Lys Pro Arg Leu Arg Ala Glu Ile Lys
 500 505 510
 Ala Arg Met Gly Ile Gly Leu Gly Ser Glu Asn Ala Ala Gly Pro Cys
 515 520 525
 Asn Trp Asp Glu Ala Asp Ile Gly Pro Trp Ala Lys Ala Arg Ile Gln
 530 535 540
 Ala Gly Ala Glu Ala Lys Ala Lys Ala Gln Glu Ser Gly Ser Ala Ser
 545 550 555 560
 Thr Gly Ala Ser Thr Ser Thr Asn Asn Ser Ala Ser Ala Ser Ala Ser
 565 570 575
 Thr Ser Gly Gly Phe Ser Ala Gly Ala Ser Leu Thr Ala Thr Leu Thr
 580 585 590
 Phe Gly Leu Phe Ala Gly Leu Gly Gly Ala Gly Ala Ser Thr Ser Gly
 595 600 605
 Ser Ser Gly Ala Cys Gly Phe Ser Tyr Lys
 610 615 618

<210> 1264

<211> 464

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(464)

<223> X = any amino acid or stop code

<400> 1264

Ala Arg Pro Pro Val Cys Thr Gly Ser Thr Met Ser Leu Thr Val Val
 1 5 10 15
 Ser Met Ala Cys Val Gly Phe Phe Leu Leu Gln Gly Ala Trp Pro Leu
 20 25 30
 Met Gly Gly Gln Asp Lys Pro Phe Leu Ser Ala Arg Pro Ser Thr Val
 35 40 45
 Val Pro Arg Gly Gly His Val Ala Leu Gln Cys His Tyr Arg Arg Gly
 50 55 60
 Phe Asn Asn Phe Met Leu Tyr Lys Glu Asp Arg Ser His Val Pro Ile
 65 70 75 80
 Phe His Gly Arg Ile Phe Gln Glu Ser Phe Ile Met Gly Pro Val Thr
 85 90 95
 Pro Ala His Ala Gly Thr Tyr Arg Cys Arg Gly Ser Arg Pro His Ser
 100 105 110
 Leu Thr Gly Trp Ser Ala Pro Ser Asn Pro Leu Val Ile Met Val Thr
 115 120 125
 Gly Asn His Arg Lys Pro Ser Leu Leu Ala His Pro Gly Pro Leu Leu
 130 135 140
 Lys Ser Gly Glu Thr Val Ile Leu Gln Cys Trp Ser Asp Ile Met Phe
 145 150 155 160
 Glu His Phe Phe Leu His Lys Glu Gly Ile Ser Lys Asp Pro Ser Arg
 165 170 175
 Leu Val Gly Gln Ile His Asp Gly Val Ser Lys Ala Asn Phe Ser Ile
 180 185 190
 Gly Pro Met Met Leu Ala Leu Ala Gly Thr Tyr Arg Cys Tyr Gly Ser
 195 200 205
 Val Thr His Thr Pro Tyr Gln Leu Ser Ala Pro Ser Asp Pro Leu Asp
 210 215 220
 Ile Val Val Thr Gly Pro Tyr Glu Lys Pro Ser Leu Ser Ala Gln Pro
 225 230 235 240
 Gly Pro Lys Val Gln Ala Gly Glu Ser Val Thr Leu Ser Cys Ser Ser
 245 250 255
 Arg Ser Ser Tyr Asp Met Tyr His Leu Ser Arg Glu Gly Gly Ala His
 260 265 270
 Glu Arg Arg Leu Pro Ala Val Arg Lys Val Asn Arg Thr Phe Gln Ala
 275 280 285
 Asp Phe Pro Leu Gly Pro Ala Thr His Gly Gly Thr Tyr Arg Cys Phe
 290 295 300
 Gly Ser Phe Arg His Ser Pro Tyr Glu Trp Ser Asp Pro Ser Asp Pro
 305 310 315 320
 Leu Leu Val Ser Val Thr Gly Asn Pro Ser Ser Ser Trp Pro Ser Pro
 325 330 335
 Thr Glu Pro Ser Ser Lys Ser Gly Asn Leu Arg His Leu His Ile Leu
 340 345 350
 Ile Gly Thr Ser Val Val Lys Ile Pro Phe Thr Ile Leu Leu Phe Phe
 355 360 365
 Leu Leu His Arg Trp Cys Ser Asn Lys Lys Asn Ala Ala Val Met Asp
 370 375 380
 Gln Glu Pro Ala Gly Asn Arg Val Asn Ser Glu Asp Ser Asp Glu Gln
 385 390 395 400
 Asp His Gln Glu Val Ser Tyr Pro Xaa Leu Glu His Cys Val Phe Thr
 405 410 415
 Gln Arg Lys Ile Thr Arg Pro Ser Gln Arg Pro Lys Thr Pro Pro Thr
 420 425 430
 Asp Thr Ser Met Tyr Ile Glu Leu Pro Asn Ala Glu Pro Arg Ser Lys

435 440 445
 Val Val Phe Cys Pro Arg Ala Pro Gln Ser Gly Leu Glu Gly Ile Phe
 450 455 460 464

<210> 1265
 <211> 1879
 <212> Amino acid
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(1879)
 <223> X = any amino acid or stop code

<400> 1265
 Leu His Asn Leu Arg Glu Arg Tyr Phe Ser Gly Leu Ile Tyr Thr Tyr
 1 5 10 15
 Ser Gly Leu Phe Cys Val Val Val Asn Pro Tyr Lys His Leu Pro Ile
 20 25 30
 Tyr Ser Glu Lys Ile Val Asp Met Tyr Lys Gly Lys Lys Arg His Glu
 35 40 45
 Met Pro Pro His Ile Tyr Ala Ile Ala Asp Thr Ala Tyr Arg Ser Met
 50 55 60
 Leu Gln Asp Arg Glu Asp Gln Ser Ile Leu Cys Thr Gly Glu Ser Gly
 65 70 75 80
 Ala Gly Lys Thr Glu Asn Thr Lys Lys Val Ile Gln Tyr Leu Ala Val
 85 90 95
 Val Ala Ser Ser His Lys Gly Lys Lys Asp Thr Ser Ile Thr Gly Glu
 100 105 110
 Leu Glu Lys Gln Leu Leu Gln Ala Asn Pro Ile Leu Glu Ala Phe Gly
 115 120 125
 Asn Ala Lys Thr Val Lys Asn Asp Asn Ser Ser Arg Phe Gly Lys Phe
 130 135 140
 Ile Arg Ile Asn Phe Asp Val Thr Gly Tyr Ile Val Gly Ala Asn Ile
 145 150 155 160
 Glu Thr Tyr Leu Leu Glu Lys Ser Arg Ala Ile Arg Gln Ala Arg Asp
 165 170 175
 Glu Arg Thr Phe His Ile Phe Tyr Tyr Met Ile Ala Gly Ala Lys Glu
 180 185 190
 Lys Met Arg Ser Asp Leu Leu Leu Glu Gly Phe Asn Asn Tyr Thr Phe
 195 200 205
 Leu Ser Asn Gly Phe Val Pro Ile Pro Ala Ala Gln Asp Asp Glu Met
 210 215 220
 Phe Gln Glu Thr Val Glu Ala Met Ala Ile Met Gly Phe Ser Glu Glu
 225 230 235 240
 Glu Gln Leu Ser Ile Leu Lys Val Val Ser Ser Val Leu Gln Leu Gly
 245 250 255
 Asn Ile Val Phe Lys Lys Glu Arg Asn Thr Asp Gln Ala Ser Met Pro
 260 265 270
 Asp Asn Thr Ala Ala Gln Lys Val Cys His Leu Met Gly Ile Asn Val
 275 280 285
 Thr Asp Phe Thr Arg Ser Ile Leu Thr Pro Arg Ile Lys Val Gly Arg
 290 295 300
 Asp Val Val Gln Lys Ala Gln Thr Lys Glu Gln Ala Asp Phe Ala Val
 305 310 315 320
 Glu Ala Leu Ala Lys Ala Thr Tyr Glu Arg Leu Phe Arg Trp Ile Leu
 325 330 335

Thr	Arg	Val	Asn	Lys	Ala	Leu	Asp	Lys	Thr	His	Arg	Gln	Gly	Ala	Ser	340	345	350
Phe	Leu	Gly	Ile	Leu	Asp	Ile	Ala	Gly	Phe	Glu	Ile	Phe	Glu	Val	Asn	355	360	365
Ser	Phe	Glu	Gln	Leu	Cys	Ile	Asn	Tyr	Thr	Asn	Glu	Lys	Leu	Gln	Gln	370	375	380
Leu	Phe	Asn	His	Thr	Met	Phe	Ile	Leu	Glu	Gln	Glu	Glu	Tyr	Gln	Arg	385	390	395
Glu	Gly	Ile	Glu	Trp	Asn	Phe	Ile	Asp	Phe	Gly	Leu	Asp	Leu	Gln	Pro	405	410	415
Cys	Ile	Glu	Leu	Ile	Glu	Arg	Pro	Asn	Asn	Pro	Pro	Gly	Val	Leu	Ala	420	425	430
Leu	Leu	Asp	Glu	Glu	Cys	Trp	Phe	Pro	Lys	Ala	Thr	Asp	Lys	Ser	Phe	435	440	445
Val	Glu	Lys	Leu	Cys	Thr	Glu	Gln	Gly	Ser	His	Pro	Lys	Phe	Gln	Lys	450	455	460
Pro	Lys	Gln	Leu	Lys	Asp	Lys	Thr	Glu	Phe	Ser	Ile	Ile	His	Tyr	Ala	465	470	475
Gly	Lys	Val	Asp	Tyr	Asn	Ala	Ser	Ala	Trp	Leu	Thr	Lys	Asn	Met	Asp	485	490	495
Pro	Leu	Asn	Asp	Asn	Val	Thr	Ser	Leu	Leu	Asn	Ala	Ser	Ser	Asp	Lys	500	505	510
Phe	Val	Ala	Asp	Leu	Trp	Lys	Asp	Val	Asp	Arg	Ile	Val	Gly	Leu	Asp	515	520	525
Gln	Met	Ala	Lys	Met	Thr	Glu	Ser	Ser	Leu	Pro	Ser	Ala	Ser	Lys	Thr	530	535	540
Lys	Lys	Gly	Met	Phe	Arg	Thr	Val	Gly	Gln	Leu	Tyr	Lys	Glu	Gln	Leu	545	550	555
Gly	Lys	Leu	Met	Thr	Thr	Leu	Arg	Asn	Thr	Thr	Pro	Asn	Phe	Val	Arg	565	570	575
Cys	Ile	Ile	Pro	Asn	His	Glu	Lys	Arg	Ser	Gly	Lys	Leu	Asp	Ala	Phe	580	585	590
Leu	Val	Leu	Glu	Gln	Leu	Arg	Cys	Asn	Gly	Val	Leu	Glu	Gly	Ile	Arg	595	600	605
Ile	Cys	Arg	Gln	Gly	Phe	Pro	Asn	Arg	Ile	Val	Phe	Gln	Glu	Phe	Arg	610	615	620
Gln	Arg	Tyr	Glu	Ile	Leu	Ala	Ala	Asn	Ala	Ile	Pro	Lys	Gly	Phe	Met	625	630	635
Asp	Gly	Lys	Gln	Ala	Cys	Ile	Leu	Met	Ile	Lys	Ala	Leu	Glu	Leu	Asp	645	650	655
Pro	Asn	Leu	Tyr	Arg	Ile	Gly	Gln	Ser	Lys	Ile	Phe	Phe	Arg	Thr	Gly	660	665	670
Val	Leu	Ala	His	Leu	Glu	Glu	Glu	Arg	Asp	Leu	Lys	Ile	Thr	Asp	Val	675	680	685
Ile	Met	Ala	Phe	Gln	Ala	Met	Cys	Arg	Gly	Tyr	Leu	Ala	Arg	Lys	Ala	690	695	700
Phe	Ala	Lys	Arg	Gln	Gln	Gln	Leu	Thr	Ala	Met	Lys	Val	Ile	Gln	Arg	705	710	715
Asn	Cys	Ala	Ala	Tyr	Ile	Lys	Leu	Arg	Asn	Trp	Gln	Trp	Cys	Arg	Leu	725	730	735
Phe	Thr	Lys	Val	Xaa	Pro	Leu	Leu	Gln	Val	Thr	Arg	Gln	Glu	Xaa	Glu	740	745	750
Met	Gln	Ala	Lys	Glu	Asp	Glu	Leu	Gln	Lys	Thr	Lys	Glu	Arg	Gln	Gln	755	760	765
Lys	Ala	Glu	Asn	Glu	Leu	Lys	Glu	Leu	Glu	Gln	Lys	His	Ser	Gln	Leu	770	775	780
Thr	Glu	Glu	Lys	Asn	Leu	Leu	Gln	Glu	Gln	Leu	Gln	Ala	Glu	Thr	Glu	785	790	795
Leu	Tyr	Ala	Glu	Ala	Glu	Glu	Met	Arg	Val	Arg	Leu	Ala	Ala	Lys	Lys	805	810	815
Gln	Glu	Leu	Glu	Glu	Ile	Leu	His	Glu	Met	Glu	Ala	Arg	Leu	Glu	Glu	820	825	830
Glu	Glu	Asp	Arg	Gly	Gln	Gln	Leu	Gln	Ala	Glu	Arg	Lys	Lys	Met	Ala	835	840	845

Gln Gln Met Leu Asp Leu Glu Glu Gln Leu Glu Glu Glu Glu Ala Ala
 850 855 860
 Arg Gln Lys Leu Gln Leu Glu Lys Val Thr Ala Glu Ala Lys Ile Lys
 865 870 875 880
 Lys Leu Glu Asp Glu Ile Leu Val Met Asp Asp Gln Asn Asn Lys Leu
 885 890 895
 Ser Lys Glu Arg Lys Leu Leu Glu Glu Arg Ile Ser Asp Leu Thr Thr
 900 905 910
 Asn Leu Ala Glu Glu Glu Glu Lys Ala Lys Asn Leu Thr Lys Leu Lys
 915 920 925
 Asn Lys His Glu Ser Met Ile Ser Glu Leu Glu Val Arg Leu Lys Lys
 930 935 940
 Glu Glu Lys Ser Arg Gln Glu Leu Glu Lys Leu Lys Arg Lys Leu Glu
 945 950 955 960
 Gly Asp Ala Ser Asp Phe His Glu Gln Ile Ala Asp Leu Gln Ala Gln
 965 970 975
 Ile Ala Glu Leu Lys Met Gln Leu Ala Lys Lys Glu Glu Glu Leu Gln
 980 985 990
 Ala Ala Leu Ala Arg Leu Asp Asp Glu Ile Ala Gln Lys Asn Asn Ala
 995 1000 1005
 Leu Lys Lys Ile Arg Glu Leu Glu Gly His Ile Ser Asp Leu Gln Glu
 1010 1015 1020
 Asp Leu Asp Ser Glu Arg Ala Ala Arg Asn Lys Ala Glu Lys Gln Lys
 1025 1030 1035 1040
 Arg Asp Leu Gly Glu Glu Leu Glu Ala Leu Lys Thr Glu Leu Glu Asp
 1045 1050 1055
 Thr Leu Asp Ser Thr Ala Thr Gln Gln Glu Leu Arg Ala Lys Arg Glu
 1060 1065 1070
 Gln Glu Val Thr Val Leu Lys Arg Ala Leu Asn Glu Glu Thr Arg Ser
 1075 1080 1085
 His Glu Ala Gln Val Gln Glu Met Arg Gln Lys His Ala Gln Ala Val
 1090 1095 1100
 Gln Ser Leu Thr Glu Gln Leu Glu Gln Xaa Lys Arg Ala Lys Ala Asn
 1105 1110 1115 1120
 Leu Asp Lys Asn Lys Gln Thr Leu Glu Lys Glu Asn Thr Asp Leu Ala
 1125 1130 1135
 Gly Glu Leu Arg Val Leu Gly Gln Ala Lys Gln Glu Val Glu His Arg
 1140 1145 1150
 Met Lys Lys Leu Gln Ala Gln Val Gln Glu Leu Gln Ser Lys Cys Ser
 1155 1160 1165
 Asp Gly Glu Arg Ala Arg Ala Glu Leu Asn Asp Lys Val His Lys Leu
 1170 1175 1180
 Gln Asn Glu Val Glu Ser Val Thr Gly Met Leu Asn Glu Ala Glu Gly
 1185 1190 1195 1200
 Lys Ala Ile Lys Leu Ala Lys Asp Val Ala Ser Leu Ser Ser Gln Leu
 1205 1210 1215
 Gln Asp Thr Gln Glu Leu Leu Gln Glu Ser Arg Gln Lys Leu Asn
 1220 1225 1230
 Val Ser Thr Ser Leu Arg Gln Leu Glu Glu Glu Arg Asn Ser Leu Gln
 1235 1240 1245
 Asp Gln Leu Asp Glu Glu Met Glu Ala Lys Gln Asn Leu Glu Arg His
 1250 1255 1260
 Ile Ser Thr Leu Asn Ile Gln Leu Ser Asp Ser Lys Lys Lys Leu Gln
 1265 1270 1275 1280
 Asp Phe Ala Ser Thr Val Glu Ala Leu Glu Glu Gly Lys Lys Arg Phe
 1285 1290 1295
 Gln Lys Glu Ile Glu Asn Leu Thr Gln Gln Tyr Glu Glu Lys Ala Ala
 1300 1305 1310
 Ala Tyr Asp Lys Leu Glu Lys Thr Lys Asn Arg Leu Gln Glu Leu
 1315 1320 1325
 Asp Asp Leu Val Val Asp Leu Asp Asn Gln Arg Gln Leu Val Ser Asn
 1330 1335 1340
 Leu Glu Lys Lys Gln Arg Lys Phe Asp Gln Leu Leu Ala Glu Glu Lys
 1345 1350 1355 1360

Asn Ile Ser Ser Lys Tyr Ala Asp Glu Arg Asp Arg Val Glu Ala Glu
 1365 1370 1375
 Ala Arg Glu Lys Glu Thr Lys Ala Leu Ser Leu Ala Arg Ala Leu Glu
 1380 1385 1390
 Glu Ala Leu Glu Ala Lys Glu Glu Leu Glu Arg Thr Asn Lys Met Leu
 1395 1400 1405
 Lys Ala Glu Met Gly Arg Pro Gly Ser Ala Ser Lys Asp Asp Val Gly
 1410 1415 1420
 Gln Glu Leu Ser His Asp Leu Glu Lys Ser Lys Arg Ala Leu Gly Asp
 1425 1430 1435 1440
 Pro Arg Leu Glu Glu Met Lys Thr Gln Leu Glu Glu Leu Gly Arg Thr
 1445 1450 1455
 Glu Leu Ala Ser Pro Arg Arg Asp Ala Lys Leu Arg Leu Glu Val Asn
 1460 1465 1470
 Met Gln Ala Pro Ser Arg Ala Ser Phe Glu Arg Asp Leu Gln Ala Arg
 1475 1480 1485
 Thr Glu Gln Asn Glu Glu Ser Arg Arg His Leu Gln Arg Gln Leu His
 1490 1495 1500
 Glu Tyr Glu Thr Glu Leu Glu Asp Glu Arg Lys Gln Arg Ala Leu Ala
 1505 1510 1515 1520
 Ala Ala Ala Lys Ile Lys Leu Gly Trp Asp Pro Val Arg Thr Leu Asp
 1525 1530 1535
 Leu Xaa Ala Asp Ser Ala Ile Lys Gly Arg Gly Gly Lys Ala Ile Lys
 1540 1545 1550
 Gln Leu Arg Lys Leu Gln Ala Gln Met Lys Asp Phe Gln Arg Glu Leu
 1555 1560 1565
 Glu Asp Ala Arg Ala Ser Arg Asp Glu Ile Phe Ala Thr Ala Lys Glu
 1570 1575 1580
 Asn Glu Lys Lys Ala Lys Ser Leu Glu Ala Asp Leu Met Gln Leu Gln
 1585 1590 1595 1600
 Glu Asp Leu Ala Ala Ala Glu Glu Gly Arg Lys Gln Ala Asp Leu Glu
 1605 1610 1615
 Lys Glu Glu Leu Ala Glu Glu Leu Ala Ser Ser Leu Ser Gly Arg Asn
 1620 1625 1630
 Ala Leu Gln Asp Glu Lys Arg Arg Leu Glu Ala Arg Ile Ala Gln Leu
 1635 1640 1645
 Glu Glu Glu Leu Glu Glu Glu Gln Gly Asn Met Glu Ala Met Ser Asp
 1650 1655 1660
 Arg Val Arg Lys Ala Thr Gln Gln Ala Glu Gln Leu Ser Asn Glu Leu
 1665 1670 1675 1680
 Ala Thr Glu Arg Ser Thr Ala Gln Lys Asn Glu Ser Ala Arg Gln Gln
 1685 1690 1695
 Leu Glu Arg Gln Asn Lys Glu Leu Arg Ser Lys Leu His Glu Met Glu
 1700 1705 1710
 Gly Ala Val Lys Ser Lys Phe Lys Ser Thr Ile Ala Ala Leu Glu Ala
 1715 1720 1725
 Lys Ile Ala Gln Leu Glu Glu Gln Val Glu Gln Glu Ala Arg Glu Lys
 1730 1735 1740
 Gln Ala Ala Thr Lys Ser Leu Lys Gln Lys Asp Lys Lys Leu Lys Glu
 1745 1750 1755 1760
 Ile Leu Leu Gln Val Glu Asp Glu Arg Lys Met Ala Glu Gln Tyr Lys
 1765 1770 1775
 Glu Gln Ala Glu Lys Gly Asn Ala Arg Val Lys Gln Leu Lys Arg Gln
 1780 1785 1790
 Leu Glu Glu Ala Glu Glu Glu Ser Gln Arg Ile Asn Ala Asn Arg Arg
 1795 1800 1805
 Lys Leu Gln Arg Glu Leu Asp Glu Ala Thr Glu Ser Asn Glu Ala Met
 1810 1815 1820
 Gly Arg Glu Val Asn Ala Leu Lys Ser Lys Leu Arg Arg Gly Asn Glu
 1825 1830 1835 1840
 Thr Ser Phe Val Pro Ser Arg Arg Ser Gly Gly Arg Arg Val Ile Glu
 1845 1850 1855
 Asn Ala Asp Gly Ser Glu Glu Glu Thr Asp Thr Arg Asp Ala Asp Phe
 1860 1865 1870

Asn Gly Thr Lys Ala Ser Glu
1875 1879

<210> 1266
<211> 257
<212>Amino acid
<213> Homo sapiens

<400> 1266
Lys Leu His Phe Ala Lys Ser Leu Asn Ser Glu Leu Ser Cys Ser Thr
1 5 10 15
Arg Glu Ala Met Gln Asp Glu Asp Gly Tyr Ile Thr Leu Asn Ile Lys
20 25 30
Thr Arg Lys Pro Ala Leu Val Ser Val Gly Pro Ala Ser Ser Trp
35 40 45
Trp Arg Val Met Ala Leu Ile Leu Leu Ile Leu Cys Val Gly Met Val
50 55 60
Val Gly Leu Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn Tyr
65 70 75 80
Leu Gln Asp Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln Leu Ala
85 90 95
Lys Arg Phe Cys Gln Tyr Val Val Lys Gln Ser Glu Leu Lys Gly Thr
100 105 110
Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr Asn Trp Arg Tyr Tyr
115 120 125
Gly Asp Ser Cys Tyr Gly Phe Phe Arg His Asn Leu Thr Trp Glu Glu
130 135 140
Ser Lys Gln Tyr Cys Thr Asp Met Asn Ala Thr Leu Leu Lys Ile Asp
145 150 155 160
Asn Arg Asn Ile Val Glu Tyr Ile Lys Ala Arg Thr His Leu Ile Arg
165 170 175
Trp Val Gly Leu Ser Arg Gln Lys Ser Asn Glu Val Trp Lys Trp Glu
180 185 190
Asp Gly Ser Val Ile Ser Glu Asn Met Phe Glu Phe Leu Glu Asp Gly
195 200 205
Lys Gly Asn Met Asn Cys Ala Tyr Phe His Asn Gly Lys Met His Pro
210 215 220
Thr Phe Cys Glu Asn Lys His Tyr Leu Met Cys Glu Arg Lys Ala Gly
225 230 235 240
His Asp Pro Arg Trp Thr Gln Leu Pro Leu Met Pro Lys Arg Trp Thr
245 250 255
Gly
257

<210> 1267
<211> 208
<212>Amino acid
<213> Homo sapiens

<400> 1267
Asn Gln Gly Leu Arg Asp Val Gly Leu Cys Arg Thr Cys Leu Val Asn
1 5 10 15
Lys Ile Phe Ala Ser Ser Ile Leu Gly Lys Ser His His His Ser Leu
20 25 30

Val Ser Ile Asn Gln Gly His Asn Ala Pro Trp Lys Ala Ala Gly Ser
 35 40 45
 Leu Pro Leu Lys Ala Ala Tyr Cys Gln Gly Phe Ser Pro Cys Asp Cys
 50 55 60
 Leu Lys Tyr Gly Ser Trp Asp Glu Lys Asp Leu Met Val Pro Gln Pro
 65 70 75 80
 Asp Thr His Lys Gly Ser Val Leu Arg Trp Ile Ser Lys Arg Gly Lys
 85 90 95
 Pro Leu Ala Val Glu Met Glu Glu Gly His Cys Leu Cys Leu Pro Leu
 100 105 110
 Gly Thr Glu Cys Leu Gly Val Lys Pro Ile Val His Leu Phe Asn Ser
 115 120 125
 Glu Met Gly Glu Lys Arg Pro Val Ala Gly Ala Arg His Val Gly Ser
 130 135 140
 Ser Ala Ala Leu Leu Phe Phe Thr Pro Leu Arg Cys Leu Gly Gly Glu
 145 150 155 160
 Lys His Lys Ser Gly Leu Arg Ala Arg Pro Gly Ile Val Pro Ser Leu
 165 170 175
 Glu Leu Asn Tyr Asp Ile Asp Ser Phe Ala His Met Phe Phe Ser Val
 180 185 190
 Asp Leu Leu Leu Ile Ile Thr Leu Leu Ser Tyr Tyr Ile Pro Phe Cys
 195 200 205 208

<210> 1268
 <211> 158
 <212> Amino acid
 <213> Homo sapiens

<400> 1268
 Met Trp Trp Arg Leu Ala Pro Thr Gln Ala Ile Trp Arg Ala Ala Gly
 1 5 10 15
 Cys Cys Met Arg Phe Ser Arg Arg Arg Ser Thr Cys Cys Cys Leu Ala
 20 25 30
 Ser Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly Asp Gln Pro Ala
 35 40 45
 Ala Lys Arg Arg Gln Arg Arg Arg Arg Ala Ala Pro Ser Ala Pro Pro
 50 55 60
 Gln Ala Ala Arg Leu His Pro Pro Pro Lys Leu Arg Arg Phe Asp Gly
 65 70 75 80
 Val Gln Asp Pro Ala Pro Tyr Ser Trp Ala Ile Asn Gly Lys Val Phe
 85 90 95
 Asp Val Thr Gln Arg Pro Ala Asn Phe Leu Arg Gly Pro Arg Gly Pro
 100 105 110
 Glu Thr Leu Ser Asp Trp Glu Ser Gln Phe Thr Phe Lys Tyr His His
 115 120 125
 Val Gly Lys Leu Leu Lys Glu Gly Glu Glu Pro Thr Val Tyr Ser Asp
 130 135 140
 Glu Glu Glu Pro Lys Asp Glu Ser Ala Arg Lys Asn Asp *
 145 150 155 157

<210> 1269
 <211> 178
 <212> Amino acid
 <213> Homo sapiens

<400> 1269

Gly Pro Arg Met Ala Lys Phe Leu Ser Gln Asp Gln Ile Asn Glu Tyr
 1 5 10 15
 Lys Glu Cys Phe Ser Leu Tyr Asp Lys Gln Gln Arg Gly Lys Ile Lys
 20 25 30
 Ala Thr Asp Leu Met Val Ala Met Arg Cys Leu Gly Ala Ser Pro Thr
 35 40 45
 Pro Gly Glu Val Gln Arg His Leu Gln Thr His Gly Ile Asp Gly Asn
 50 55 60
 Gly Glu Leu Asp Phe Ser Thr Phe Leu Thr Ile Met His Met Gln Ile
 65 70 75 80
 Lys Gln Glu Asp Pro Lys Lys Glu Ile Leu Leu Ala Met Leu Met Val
 85 90 95
 Asp Lys Glu Lys Lys Gly Tyr Val Met Ala Ser Asp Leu Arg Ser Lys
 100 105 110
 Leu Thr Ser Leu Gly Glu Lys Leu Thr His Lys Glu Val Asp Asp Leu
 115 120 125
 Phe Arg Glu Ala Asp Ile Glu Pro Asn Gly Lys Val Lys Tyr Asp Glu
 130 135 140
 Phe Ile His Lys Ile Thr Leu Leu Pro Gly Arg Asp Leu Leu Lys Glu
 145 150 155 160
 Glu Asn Gly Arg Ala Ser Pro Gly Pro Glu Asn Leu Glu Gln Leu Ile
 165 170 175
 Phe Leu
 178

<210> 1270

<211> 457

<212> Amino acid

<213> Homo sapiens

<400> 1270

Ala Asp Pro His Thr Thr Val Ile Arg Phe Phe Pro Ala Ala Ser Ala
 1 5 10 15
 Thr Lys Arg Val Leu Pro Pro Val Leu Arg Val Ser Ser Pro Arg Thr
 20 25 30
 Trp Asn Pro Asn Val Pro Glu Ser Pro Arg Ile Pro Ala Pro Arg Leu
 35 40 45
 Pro Lys Arg Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu
 50 55 60
 Cys Ala Ala Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln
 65 70 75 80
 Ser Lys Ser Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala
 85 90 95
 His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg
 100 105 110
 Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly
 115 120 125
 Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro
 130 135 140
 Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu
 145 150 155 160
 Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln
 165 170 175
 Gln Gln Arg His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln
 180 185 190

Ser Gln Phe Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala
 195 200 205
 Lys Pro Ala Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp
 210 215 220
 Pro Ala His Asn Val Ser Arg Leu His Arg Leu Pro Arg Asp Cys Gln
 225 230 235 240
 Glu Leu Phe Gln Val Gly Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln
 245 250 255
 Pro Gln Gly Ser Pro Pro Phe Leu Val Asn Cys Lys Met Thr Ser Asp
 260 265 270
 Gly Gly Trp Thr Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe
 275 280 285
 Asn Arg Pro Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly
 290 295 300
 Glu Phe Trp Leu Gly Leu Glu Lys Val His Ser Ile Thr Gly Asp Arg
 305 310 315 320
 Asn Ser Arg Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu
 325 330 335
 Leu Leu Gln Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr Ser
 340 345 350
 Leu Gln Leu Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr Thr Val
 355 360 365
 Pro Pro Ser Gly Leu Ser Val Pro Phe Ser Thr Trp Asp Gln Asp His
 370 375 380
 Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys Ser Leu Ser Gly Gly Trp
 385 390 395 400
 Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn Gly Gln Tyr Phe Arg
 405 410 415
 Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys Lys Gly Ile Phe Trp Lys
 420 425 430
 Thr Trp Arg Gly Arg Tyr Tyr Pro Leu Gln Ala Thr Thr Met Leu Ile
 435 440 445
 Gln Pro Met Ala Ala Glu Ala Ala Ser
 450 455 457

<210> 1271

<211> 394

<212> Amino acid

<213> Homo sapiens

<400> 1271

Ala Leu Asp Phe Gly Asp Ser Cys Gln Trp Pro Arg Pro Gln Asp Thr
 1 5 10 15
 Met Lys Gln Leu Pro Val Leu Glu Pro Gly Asp Lys Pro Arg Lys Ala
 20 25 30
 Thr Trp Tyr Thr Leu Thr Val Pro Gly Asp Ser Pro Cys Ala Arg Val
 35 40 45
 Gly His Ser Cys Ser Tyr Leu Pro Pro Val Gly Asn Ala Lys Arg Gly
 50 55 60
 Lys Val Phe Ile Val Gly Gly Ala Asn Pro Asn Arg Ser Phe Ser Asp
 65 70 75 80
 Val His Thr Met Asp Leu Gly Lys His Gln Trp Asp Leu Asp Thr Cys
 85 90 95
 Lys Gly Leu Leu Pro Arg Tyr Glu His Ala Ser Phe Ile Pro Ser Cys
 100 105 110
 Thr Pro Asp Arg Ile Trp Val Phe Gly Gly Ala Asn Gln Ser Gly Asn
 115 120 125
 Arg Asn Cys Leu Gln Val Leu Asn Pro Glu Thr Arg Thr Trp Thr Thr
 130 135 140

Pro Glu Val Thr Ser Pro Pro Pro Ser Pro Arg Thr Phe His Thr Ser
 145 150 155 160
 Ser Ala Ala Ile Gly Asn Gln Leu Tyr Val Phe Gly Gly Gly Glu Arg
 165 170 175
 Gly Ala Gln Pro Val Gln Asp Thr Lys Leu His Val Phe Asp Ala Asn
 180 185 190
 Thr Leu Thr Trp Ser Gln Pro Glu Thr Leu Gly Asn Pro Pro Ser Pro
 195 200 205
 Arg His Gly His Val Met Val Ala Ala Gly Thr Lys Leu Phe Ile His
 210 215 220
 Gly Gly Leu Ala Gly Asp Arg Phe Tyr Asp Asp Leu His Cys Ile Asp
 225 230 235 240
 Ile Ser Asp Met Lys Trp Gln Lys Leu Asn Pro Thr Gly Ala Ala Pro
 245 250 255
 Ala Gly Cys Ala Ser His Thr Pro Ala Val Ala Met Gly Lys His Val
 260 265 270
 Tyr Ile Phe Gly Gly Met Thr Pro Ala Gly Ala Pro Gly Thr Gln Cys
 275 280 285
 Thr Gln Tyr His Thr Glu Glu Gln His Trp Asp Pro Cys Leu Lys Phe
 290 295 300
 Asp Thr Pro Ser Tyr Pro Pro Gly Thr Ile Gly Thr His Ser His Val
 305 310 315 320
 Val Ser Phe Pro Trp Pro Val Thr Cys Ala Ser Glu Lys Glu Asp Ser
 325 330 335
 Asn Ser Leu Thr Leu Asn His Glu Ala Glu Lys Glu Asp Ser Ala Asp
 340 345 350
 Lys Val Met Ser His Ser Gly Asp Ser His Glu Glu Ser Gln Thr Ala
 355 360 365
 Thr Leu Leu Cys Leu Val Phe Gly Gly Met Asn Thr Glu Gly Glu Ile
 370 375 380
 Tyr Asp Asp Cys Ile Val Thr Val Val Asp
 385 390 394

<210> 1272

<211> 176

<212> Amino acid

<213> Homo sapiens

<400> 1272

Gly Phe Ser Ile Gly Lys Ala Thr Asp Arg Met Asp Ala Phe Arg Lys
 1 5 10 15
 Ala Lys Asn Arg Ala Val His His Leu His Tyr Ile Glu Arg Tyr Glu
 20 25 30
 Asp His Thr Ile Phe His Asp Ile Ser Leu Arg Phe Lys Arg Thr His
 35 40 45
 Ile Lys Met Lys Lys Gln Pro Lys Gly Tyr Gly Leu Arg Cys His Arg
 50 55 60
 Ala Ile Ile Thr Ile Cys Arg Leu Ile Gly Ile Lys Asp Met Tyr Ala
 65 70 75 80
 Lys Val Ser Gly Ser Ile Asn Met Leu Ser Leu Thr Gln Gly Leu Phe
 85 90 95
 Arg Gly Leu Ser Arg Gln Glu Thr His Gln Gln Leu Ala Asp Lys Lys
 100 105 110
 Gly Leu His Val Val Glu Ile Arg Glu Glu Cys Gly Pro Leu Pro Ile
 115 120 125
 Val Val Ala Ser Pro Arg Gly Pro Leu Arg Lys Asp Pro Glu Pro Glu
 130 135 140
 Asp Glu Val Pro Asp Val Lys Leu Asp Trp Glu Asp Val Lys Thr Ala
 145 150 155 160

Gln Gly Met Lys Arg Ser Val Trp Ser Asn Leu Lys Arg Ala Ala Thr
 165 170 175 176

<210> 1273

<211> 457

<212> Amino acid

<213> Homo sapiens

<400> 1273

Ala Asp Pro His Thr Thr Val Ile Arg Phe Phe Pro Ala Ala Ser Ala
 1 5 10 15
 Thr Lys Arg Val Leu Pro Pro Val Leu Arg Val Ser Ser Pro Arg Thr
 20 25 30
 Trp Asn Pro Asn Val Pro Glu Ser Pro Arg Ile Pro Ala Pro Arg Leu
 35 40 45
 Pro Lys Arg Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu
 50 55 60
 Cys Ala Ala Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln
 65 70 75 80
 Ser Lys Ser Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala
 85 90 95
 His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg
 100 105 110
 Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly
 115 120 125
 Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro
 130 135 140
 Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu
 145 150 155 160
 Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln
 165 170 175
 Gln Gln Arg His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln
 180 185 190
 Ser Gln Phe Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala
 195 200 205
 Lys Pro Ala Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp
 210 215 220
 Pro Ala His Asn Val Ser Arg Leu His Arg Leu Pro Arg Asp Cys Gln
 225 230 235 240
 Glu Leu Phe Gln Val Gly Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln
 245 250 255
 Pro Gln Gly Ser Pro Pro Phe Leu Val Asn Cys Lys Met Thr Ser Asp
 260 265 270
 Gly Gly Trp Thr Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe
 275 280 285
 Asn Arg Pro Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly
 290 295 300
 Glu Phe Trp Leu Gly Leu Glu Lys Val His Ser Ile Thr Gly Asp Arg
 305 310 315 320
 Asn Ser Arg Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu
 325 330 335
 Leu Leu Gln Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr Ser
 340 345 350
 Leu Gln Leu Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr Thr Val
 355 360 365
 Pro Pro Ser Gly Leu Ser Val Pro Phe Ser Thr Trp Asp Gln Asp His
 370 375 380

Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys Ser Leu Ser Gly Gly Trp
 385 390 395 400
 Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn Gly Gln Tyr Phe Arg
 405 410 415
 Ser Ile Pro Gln Arg Gln Lys Leu Lys Lys Gly Ile Phe Trp Lys
 420 425 430
 Thr Trp Arg Gly Arg Tyr Tyr Pro Leu Gln Ala Thr Thr Met Leu Ile
 435 440 445
 Gln Pro Met Ala Ala Glu Ala Ala Ser
 450 455 457

<210> 1274
 <211> 359
 <212> Amino acid
 <213> Homo sapiens

<400> 1274
 Thr Leu Arg Ser Arg Pro Ala Gly Glu Ala Gly Tyr Leu Gly Trp Asp
 1 5 10 15
 Pro Glu Gln Ala Gly Glu Gly Ser Ala Leu Ser Arg Pro Gly Ala Met
 20 25 30
 Ala Ala Leu Met Thr Pro Gly Thr Gly Ala Pro Pro Ala Pro Gly Asp
 35 40 45
 Phe Ser Gly Glu Gly Ser Gln Gly Leu Pro Asp Pro Ser Pro Glu Pro
 50 55 60
 Lys Gln Leu Pro Glu Leu Ile Arg Met Lys Arg Asp Gly Gly Arg Leu
 65 70 75 80
 Ser Glu Ala Asp Ile Arg Gly Phe Val Ala Ala Val Val Asn Gly Ser
 85 90 95
 Ala Gln Gly Ala Gln Ile Gly Ala Trp Gly Gly Leu Gly Val Pro Asp
 100 105 110
 Pro Asp Trp Glu Val Ser Pro Arg Asp Phe Gly Ser Leu Gly Val Arg
 115 120 125
 Arg Cys Pro Thr Thr Ser Thr Gly Pro Arg Val Pro His Arg Cys Gly
 130 135 140
 Leu Pro Pro Ser Arg Val Pro Pro His Thr Arg Gly Met Leu Met Ala
 145 150 155 160
 Ile Arg Leu Arg Gly Met Asp Leu Glu Glu Thr Ser Val Leu Thr Gln
 165 170 175
 Ala Leu Ala Gln Ser Gly Gln Gln Leu Glu Trp Pro Glu Ala Trp Arg
 180 185 190
 Gln Gln Leu Val Asp Lys His Ser Thr Gly Gly Val Gly Asp Lys Val
 195 200 205
 Ser Leu Val Leu Ala Pro Ala Leu Ala Cys Gly Cys Lys Val Ile
 210 215 220
 Asn His Leu Leu Ser Arg Arg Glu Pro Ile Pro His Met Gln Gln Pro
 225 230 235 240
 Val His Pro Gln Ala Ala Pro Asn Leu Lys Pro Gly Pro Lys Pro Pro
 245 250 255
 Arg Pro Tyr Gln Gly Phe Ser Pro Pro Cys Ser Pro Ala Gln Phe Ser
 260 265 270
 Pro Pro Arg Ser Pro Ala Gln Arg Leu Gly Pro Leu Trp Leu Gln Thr
 275 280 285
 Arg Pro Leu Gly Ala Gly Lys Arg Ser Thr Asp Gly Ile Gln Thr Pro
 290 295 300
 Phe Pro Leu Gly Pro Gln Thr Ala Pro Pro Arg Glu Glu Leu Arg Thr
 305 310 315 320
 Ser Leu Pro Leu Pro Gln Ala Leu Phe Pro Gln Gly Gln Val Pro Thr
 325 330 335

Ser Ser Pro Thr Asp Thr Ser Gln Pro Arg Lys Leu Pro Phe His Ser
 340 345 350
 Leu Thr Ser Trp Ala Pro Leu
 355 359

<210> 1275

<211> 146

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(146)

<223> X = any amino acid or stop code

<400> 1275

Arg Ala Leu Arg Glu Leu Arg Glu Arg Val Thr His Gly Leu Ala Glu
 1 5 10 15
 Ala Gly Arg Asp Arg Glu Asp Val Ser Thr Glu Leu Tyr Arg Ala Leu
 20 25 30
 Glu Ala Val Arg Leu Gln Asn Ser Glu Gly Ser Cys Glu Pro Cys Pro
 35 40 45
 Thr Ser Trp Leu Pro Phe Gly Gly Ser Cys Tyr Tyr Phe Ser Val Pro
 50 55 60
 Lys Thr Thr Trp Ala Glu Ala Gln Gly His Cys Ala Asp Ala Ser Ala
 65 70 75 80
 His Leu Ala Ile Val Gly Gly Leu Gly Glu Gln Asp Phe Leu Ser Arg
 85 90 95
 Asp Thr Ser Ala Leu Glu Tyr Trp Ile Gly Arg Arg Ala Val Gln His
 100 105 110
 Leu Arg Lys Val Gln Gly Tyr Ser Trp Val Asp Gly Val Pro Leu Ser
 115 120 125
 Phe Arg Xaa Trp Glu Gly His Pro Gly Glu Thr Trp Gly Pro Gln Val
 130 135 140
 Arg Leu
 145 146

<210> 1276

<211> 187

<212>Amino acid

<213> Homo sapiens

<400> 1276

Arg Trp Pro Arg Ser Trp Pro Pro Arg Ala Gly Ala Ala Arg Gly Ala
 1 5 10 15
 Ala Glu Ala Ala Met Val Gly Ala Leu Cys Gly Cys Trp Phe Arg Leu
 20 25 30
 Gly Gly Ala Arg Pro Leu Ile Pro Leu Gly Pro Thr Val Val Gln Thr
 35 40 45
 Ser Met Ser Arg Ser Gln Val Ala Leu Leu Gly Leu Ser Leu Leu Leu
 50 55 60
 Met Leu Leu Leu Tyr Val Gly Leu Pro Gly Pro Pro Glu Gln Thr Ser
 65 70 75 80
 Cys Leu Trp Gly Asp Pro Asn Val Thr Val Leu Ala Gly Leu Thr Pro

				85					90				95				
Gly	Asn	Ser	Pro	Ile	Phe	Tyr	Arg	Glu	Val	Leu	Pro	Leu	Asn	Gln	Ala		
			100					105					110				
His	Arg	Val	Glu	Val	Cys	Cys	Phe	Met	Glu	Arg	Pro	Leu	Thr	Leu	Thr		
		115					120					125					
Arg	Gly	Ser	Ser	Trp	Ala	His	Cys	Ser	Tyr	Cys	His	Arg	Gly	Ala	Thr		
	130					135					140						
Gly	Pro	Trp	Pro	Leu	Thr	Phe	Gln	Val	Leu	Gly	Thr	Arg	His	Leu	Gln		
145				150						155					160		
Arg	Arg	Gln	Ala	Gln	Arg	Gln	Gly	Gly	Gln	Arg	Cys	Trp	Ser	Gly	Arg		
			165						170					175			
Cys	Gly	Thr	Trp	Arg	Tyr	Arg	Met	Pro	Cys	Trp							
		180						185		187							

<210> 1277

<211> 481

<212> Amino acid

<213> Homo sapiens

<400> 1277

Gln	Glu	Asn	Gln	Leu	Glu	Lys	Lys	Met	Lys	Phe	Leu	Ile	Phe	Ala	Phe		
1				5					10					15			
Phe	Gly	Gly	Val	His	Leu	Leu	Ser	Leu	Cys	Ser	Gly	Lys	Ala	Ile	Cys		
			20					25					30				
Lys	Asn	Gly	Ile	Ser	Lys	Arg	Thr	Phe	Glu	Glu	Ile	Lys	Glu	Glu	Ile		
	35					40					45						
Ala	Ser	Cys	Gly	Asp	Val	Ala	Lys	Ala	Ile	Ile	Asn	Leu	Ala	Val	Tyr		
	50					55				60							
Gly	Lys	Ala	Gln	Asn	Arg	Ser	Tyr	Glu	Arg	Leu	Ala	Leu	Leu	Val	Asp		
65				70					75					80			
Thr	Val	Gly	Pro	Arg	Leu	Ser	Gly	Ser	Lys	Asn	Leu	Glu	Lys	Ala	Ile		
				85					90					95			
Gln	Ile	Met	Tyr	Gln	Asn	Leu	Gln	Gln	Asp	Gly	Leu	Glu	Lys	Val	His		
			100					105					110				
Leu	Glu	Pro	Val	Arg	Ile	Pro	His	Trp	Glu	Arg	Gly	Glu	Glu	Ser	Ala		
	115					120						125					
Val	Met	Leu	Glu	Pro	Arg	Ile	His	Lys	Ile	Ala	Ile	Leu	Gly	Leu	Gly		
	130					135					140						
Ser	Ser	Ile	Gly	Thr	Pro	Pro	Glu	Gly	Ile	Thr	Ala	Glu	Val	Leu	Val		
145				150						155				160			
Val	Thr	Ser	Phe	Asp	Glu	Leu	Gln	Arg	Arg	Ala	Ser	Glu	Ala	Arg	Gly		
			165					170						175			
Lys	Ile	Val	Val	Tyr	Asn	Gln	Pro	Tyr	Ile	Asn	Tyr	Ser	Arg	Thr	Val		
		180						185					190				
Gln	Tyr	Arg	Thr	Gln	Gly	Ala	Val	Glu	Ala	Ala	Lys	Val	Gly	Ala	Leu		
	195					200						205					
Ala	Ser	Leu	Ile	Arg	Ser	Val	Ala	Ser	Phe	Ser	Ile	Tyr	Ser	Pro	His		
	210					215					220						
Thr	Gly	Ile	Gln	Glu	Tyr	Gln	Asp	Gly	Val	Pro	Lys	Ile	Pro	Thr	Ala		
225				230						235				240			
Cys	Ile	Thr	Val	Glu	Asp	Ala	Glu	Met	Met	Ser	Arg	Met	Ala	Ser	His		
			245					250						255			
Gly	Ile	Lys	Ile	Val	Ile	Gln	Leu	Lys	Met	Gly	Ala	Lys	Thr	Tyr	Pro		
		260						265					270				
Asp	Thr	Asp	Ser	Phe	Asn	Thr	Val	Ala	Glu	Ile	Thr	Gly	Ser	Lys	Tyr		
	275					280						285					
Pro	Glu	Gln	Val	Val	Leu	Val	Ser	Gly	His	Leu	Asp	Ser	Trp	Asp	Val		
	290					295					300						
Gly	Gln	Gly	Ala	Met	Asp	Asp	Gly	Gly	Gly	Ala	Phe	Ile	Ser	Trp	Glu		

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<210> 1278
<211> 428
<212> Amino acid
<213> Homo sapiens
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784

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225          230          235          240
Arg Met Cys Thr Glu Asp Leu Pro Phe Pro Pro Ala Ala Ser Cys Asp
          245          250          255
Ser Phe Lys Asn Gln Leu Val Thr Arg Glu Gly Asn Glu Leu Tyr His
          260          265          270
Cys Val Ile Tyr Leu Ala Pro Gly Asp Tyr His Cys Phe His Ser Pro
          275          280          285
Thr Asp Trp Thr Val Ser His Arg Arg His Phe Pro Gly Ser Leu Met
          290          295          300
Ser Val Asn Pro Gly Met Ala Arg Trp Ile Lys Glu Leu Phe Cys His
305          310          315          320
Asn Glu Arg Val Val Leu Thr Gly Asp Trp Lys His Gly Phe Phe Ser
          325          330          335
Leu Thr Ala Val Gly Ala Thr Asn Trp Gly Ser Ile Arg Ile Tyr Phe
          340          345          350
Asp Arg Asp Leu His Thr Asn Ser Pro Arg His Ser Lys Gly Ser Tyr
          355          360          365
Asn Asp Phe Ser Phe Val Thr His Thr Asn Arg Glu Gly Val Pro Met
          370          375          380
Arg Lys Gly Glu His Leu Gly Glu Phe Asn Leu Gly Ser Thr Ile Val
385          390          395          400
Leu Ile Phe Glu Ala Pro Lys Asp Phe Asn Phe Gln Leu Lys Thr Gly
          405          410          415
Gln Lys Ile Arg Phe Gly Glu Ala Leu Gly Ser Leu
          420          425          428

```

<210> 1279

<211> 633

<212> Amino acid

<213> Homo sapiens

<400> 1279

```

Leu Pro Glu Arg Ala Phe Gly Pro Arg Thr Pro Arg Ala Pro Arg Arg
1          5          10          15
Arg Arg Arg Arg Leu Leu Leu Ser Pro Pro Pro Arg Pro Pro Pro
          20          25          30
Leu Asp Arg Glu Pro Arg Ala Pro Gly Pro Trp Leu Cys Pro Ser Arg
          35          40          45
Ala Gly Thr Ala Gln Asp Pro Ala Arg Ile Arg Glu Arg Arg Gly Arg
          50          55          60
Val Ala Gly Gly Ala Ala Gly Pro Ala Met Glu Leu Arg Ala Arg Gly
65          70          75          80
Trp Trp Leu Leu Cys Ala Ala Ala Leu Val Ala Cys Ala Arg Gly
          85          90          95
Asp Pro Ala Ser Lys Ser Arg Ser Cys Gly Glu Val Arg Gln Ile Tyr
          100          105          110
Gly Ala Lys Gly Phe Ser Ser Ser Asp Val Pro Gln Ala Glu Ile Ser
          115          120          125
Gly Glu His Leu Arg Ile Cys Pro Gln Gly Tyr Thr Cys Cys Thr Ser
          130          135          140
Glu Met Glu Glu Asn Leu Ala Asn Arg Ser His Ala Glu Leu Glu Thr
145          150          155          160
Ala Leu Arg Asp Ser Ser Arg Val Leu Gln Ala Met Leu Ala Thr Gln
          165          170          175
Leu Arg Ser Phe Asp Asp His Phe Gln His Leu Leu Asn Asp Ser Glu
          180          185          190
Arg Thr Leu Gln Ala Thr Phe Pro Gly Ala Phe Gly Glu Leu Tyr Thr
          195          200          205
Gln Asn Ala Arg Ala Phe Arg Asp Leu Tyr Ser Glu Leu Arg Leu Tyr

```

210 215 220
 Tyr Arg Gly Ala Asn Leu His Leu Glu Glu Thr Leu Ala Glu Phe Trp
 225 230 235 240
 Ala Arg Leu Leu Glu Arg Leu Phe Lys Gln Leu His Pro Gln Leu Leu
 245 250 255
 Leu Pro Asp Asp Tyr Leu Asp Cys Leu Gly Lys Gln Ala Glu Ala Leu
 260 265 270
 Arg Pro Phe Gly Glu Ala Pro Arg Glu Leu Arg Leu Arg Ala Thr Arg
 275 280 285
 Ala Phe Val Ala Ala Arg Ser Phe Val Gln Gly Leu Gly Val Ala Ser
 290 295 300
 Asp Val Val Arg Lys Val Ala Gln Val Pro Leu Gly Pro Glu Cys Ser
 305 310 315 320
 Arg Ala Val Ile Glu Ala Gly Ser Tyr Cys Ala Leu His Cys Val Gly
 325 330 335
 Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys Arg Asn Val Leu Lys
 340 345 350
 Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala Glu Trp Arg Asn Leu
 355 360 365
 Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe Trp Gly Thr Ser Gly
 370 375 380
 Val Glu Ser Val Ile Gly Ser Val His Thr Trp Leu Ala Glu Ala Ile
 385 390 395 400
 Asn Ala Leu Gln Asp Asn Arg Asp Thr Leu Thr Ala Lys Val Ile Gln
 405 410 415
 Gly Cys Gly Asn Pro Lys Val Asn Pro Gln Gly Pro Gly Pro Glu Glu
 420 425 430
 Lys Arg Arg Arg Gly Lys Leu Ala Pro Arg Glu Arg Pro Pro Ser Gly
 435 440 445
 Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala Gln Leu Arg Asp Val
 450 455 460
 Gln Asp Phe Trp Ile Ser Leu Pro Gly Thr Leu Cys Ser Glu Lys Met
 465 470 475 480
 Ala Leu Ser Thr Ala Ser Asp Asp Arg Cys Trp Asn Gly Met Ala Arg
 485 490 495
 Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly Leu Ala Asn Gln Ile
 500 505 510
 Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys Pro Asp Met Thr Ile
 515 520 525
 Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr Asn Arg Leu Arg Ser
 530 535 540
 Ala Tyr Asn Gly Asn Asp Val Asp Phe Gln Asp Ala Ser Asp Asp Gly
 545 550 555 560
 Ser Gly Ser Gly Ser Gly Asp Gly Cys Leu Asp Asp Leu Cys Gly Arg
 565 570 575
 Lys Val Ser Arg Lys Ser Ser Ser Ser Arg Thr Pro Leu Thr His Ala
 580 585 590
 Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys Thr Ser Ala Ala Ser
 595 600 605
 Cys Pro Gln Pro Pro Thr Phe Leu Leu Pro Leu Leu Phe Leu Ala
 610 615 620
 Leu Thr Val Ala Arg Pro Arg Trp Arg
 625 630 633

<210> 1280

<211> 133

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(133)

<223> X = any amino acid or stop code

<400> 1280

```

Ala Thr Glu Leu Thr Arg Ala Gly Met Glu Ala Ser Ala Leu Thr Lys
 1           5           10           15
Ser Ala Val Thr Ser Val Ala Lys Val Val Arg Val Ala Ser Gly Ser
           20           25           30
Ala Val Val Leu Pro Leu Ala Arg Ile Ala Thr Ser Cys Asp Xaa Arg
           35           40           45
Val Gly Gly Pro Val Gln Ala Val Pro Met Val Leu Ser Ala Met Gly
 50           55           60
Leu Gln Leu Arg Ala Gly Ile Ala Ser Ser Ser Ile Ala Ala Lys Met
 65           70           75           80
Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Pro Gly Gln
           85           90           95
Pro Leu Trp Leu Leu Leu Gln Ser Leu Gly Ala Thr Gly Leu Ser Gly
           100           105           110
Leu Thr Lys Phe Ile Leu Gly Ser Ile Gly Ser Ala Ile Ala Ala Val
           115           120           125
Ile Ala Arg Phe Tyr
130           133

```

<210> 1281

<211> 457

<212> Amino acid

<213> Homo sapiens

<400> 1281

```

Thr Asn Gly Arg Asn Leu Leu His His Trp Ile Leu Gly Val Cys Gly
 1           5           10           15
Met His Pro His His Gln Glu Thr Leu Lys Lys Asn Arg Val Val Leu
           20           25           30
Ala Lys Gln Leu Leu Leu Ser Glu Leu Leu Glu His Leu Leu Glu Lys
           35           40           45
Asp Ile Ile Thr Leu Glu Met Arg Glu Leu Ile Gln Ala Lys Val Gly
 50           55           60
Ser Phe Ser Gln Asn Val Glu Leu Leu Asn Leu Leu Pro Lys Arg Gly
 65           70           75           80
Pro Gln Ala Phe Asp Ala Phe Cys Glu Ala Leu Arg Glu Thr Lys Gln
           85           90           95
Gly His Leu Glu Asp Met Leu Leu Thr Thr Leu Ser Gly Leu Gln His
           100           105           110
Val Leu Pro Pro Leu Ser Cys Asp Tyr Asp Leu Ser Leu Pro Phe Pro
           115           120           125
Val Cys Glu Ser Cys Pro Leu Tyr Lys Lys Leu Arg Leu Ser Thr Asp
           130           135           140
Thr Val Glu His Ser Leu Asp Asn Lys Asp Gly Pro Val Cys Leu Gln
 145           150           155           160
Val Lys Pro Cys Thr Pro Glu Phe Tyr Gln Thr His Phe Gln Leu Ala
           165           170           175
Tyr Arg Leu Gln Ser Arg Pro Arg Gly Leu Ala Leu Val Leu Ser Asn
           180           185           190
Val His Phe Thr Gly Glu Lys Glu Leu Glu Phe Arg Ser Gly Gly Asp
           195           200           205
Val Asp His Ser Thr Leu Val Thr Leu Phe Lys Leu Leu Gly Tyr Asp
           210           215           220

```

Val His Val Leu Cys Asp Gln Thr Ala Gln Glu Met Gln Glu Lys Leu
 225 230 235 240
 Gln Asn Phe Ala Gln Leu Pro Ala His Arg Val Thr Asp Ser Cys Ile
 245 250 255
 Val Ala Leu Leu Ser His Gly Val Glu Gly Ala Ile Tyr Gly Val Asp
 260 265 270
 Gly Lys Leu Leu Gln Leu Gln Glu Val Phe Gln Leu Phe Asp Asn Ala
 275 280 285
 Asn Cys Pro Ser Leu Gln Asn Lys Pro Lys Met Phe Phe Ile Gln Ala
 290 295 300
 Cys Arg Gly Gly Ala Ile Gly Ser Leu Gly His Leu Leu Leu Phe Thr
 305 310 315 320
 Ala Ala Thr Ala Ser Leu Ala Leu Glu Thr Asp Arg Gly Val Asp Gln
 325 330 335
 Gln Asp Gly Lys Asn His Ala Gly Ser Pro Gly Cys Glu Glu Ser Asp
 340 345 350
 Ala Gly Lys Glu Lys Leu Pro Lys Met Arg Leu Pro Thr Arg Ser Asp
 355 360 365
 Met Ile Cys Gly Tyr Ala Cys Leu Lys Gly Thr Ala Ala Met Arg Asn
 370 375 380
 Thr Lys Arg Gly Ser Trp Tyr Ile Glu Ala Leu Ala Gln Val Phe Ser
 385 390 395 400
 Glu Arg Ala Cys Asp Met His Val Ala Asp Met Leu Val Lys Val Asn
 405 410 415
 Ala Leu Ile Lys Asp Arg Glu Gly Tyr Ala Pro Gly Thr Glu Phe His
 420 425 430
 Arg Cys Lys Glu Met Ser Glu Tyr Cys Ser Thr Leu Cys Arg His Leu
 435 440 445
 Tyr Leu Phe Pro Gly His Pro Pro Thr
 450 455 457

<210> 1282

<211> 195

<212> Amino acid

<213> Homo sapiens

<400> 1282

Val Arg Gly Lys Glu Val Met Ala Ala Leu Cys Arg Thr Arg Ala Val
 1 5 10 15
 Ala Ala Glu Ser His Phe Leu Arg Val Phe Leu Phe Phe Arg Pro Phe
 20 25 30
 Arg Gly Val Gly Thr Glu Ser Gly Ser Glu Ser Gly Ser Ser Asn Ala
 35 40 45
 Lys Glu Pro Lys Thr Arg Ala Gly Gly Phe Ala Ser Ala Leu Glu Arg
 50 55 60
 His Ser Glu Leu Leu Gln Lys Val Glu Pro Leu Gln Lys Gly Ser Pro
 65 70 75 80
 Lys Asn Val Glu Ser Phe Ala Ser Met Leu Arg His Ser Pro Leu Thr
 85 90 95
 Gln Met Gly Pro Ala Lys Asp Lys Leu Val Ile Gly Arg Ile Phe His
 100 105 110
 Ile Val Glu Asn Asp Leu Tyr Ile Asp Phe Gly Gly Lys Phe His Cys
 115 120 125
 Val Cys Arg Arg Pro Glu Val Asp Gly Glu Lys Tyr Gln Lys Gly Thr
 130 135 140
 Arg Val Arg Leu Arg Leu Leu Asp Leu Glu Leu Thr Ser Arg Phe Leu
 145 150 155 160
 Gly Ala Thr Thr Asp Thr Thr Val Leu Glu Ala Asn Ala Val Leu Leu
 165 170 175

```
<210> 1283
<211> 1499
<212> Amino acid
<213> Homo sapiens
```

789

Leu Gln Thr Tyr Lys Leu Trp His Leu Asp Pro Asp Thr Glu Tyr Glu
 385 390 395 400
 Ile Ser Val Leu Leu Thr Arg Pro Gly Asp Gly Gly Thr Gly Arg Pro
 405 410 415
 Gly Pro Pro Leu Ile Ser Arg Thr Lys Cys Ala Glu Pro Met Arg Ala
 420 425 430
 Pro Lys Gly Leu Ala Phe Ala Glu Ile Gln Ala Arg Gln Leu Thr Leu
 435 440 445
 Gln Trp Glu Pro Leu Gly Tyr Asn Val Thr Arg Cys His Thr Tyr Thr
 450 455 460
 Val Ser Leu Cys Tyr His Tyr Thr Leu Gly Ser Ser His Asn Gln Thr
 465 470 475 480
 Ile Arg Glu Cys Val Lys Thr Glu Gln Gly Val Ser Arg Tyr Thr Met
 485 490 495
 Lys Asn Leu Leu Pro Tyr Arg Asn Val His Val Arg Leu Val Leu Thr
 500 505 510
 Asn Pro Glu Gly Arg Lys Glu Gly Lys Glu Val Thr Phe Gln Thr Asp
 515 520 525
 Glu Asp Val Pro Ser Gly Ile Ala Ala Glu Ser Leu Thr Phe Thr Pro
 530 535 540
 Leu Glu Asp Met Ile Phe Leu Lys Trp Glu Glu Pro Gln Glu Pro Asn
 545 550 555 560
 Gly Leu Ile Thr Gln Tyr Glu Ile Ser Tyr Gln Ser Ile Glu Ser Ser
 565 570 575
 Asp Pro Ala Val Asn Val Pro Gly Pro Arg Arg Thr Ile Ser Lys Leu
 580 585 590
 Arg Asn Glu Thr Tyr His Val Phe Ser Asn Leu His Pro Gly Thr Thr
 595 600 605
 Tyr Leu Phe Ser Val Arg Ala Arg Thr Gly Lys Gly Phe Gly Gln Ala
 610 615 620
 Ala Leu Thr Glu Ile Thr Thr Asn Ile Ser Ala Pro Ser Phe Asp Tyr
 625 630 635 640
 Ala Asp Met Pro Ser Pro Leu Gly Glu Ser Glu Asn Thr Ile Thr Val
 645 650 655
 Leu Leu Arg Pro Ala Gln Gly Arg Gly Ala Pro Ile Ser Val Tyr Gln
 660 665 670
 Val Ile Val Glu Glu Glu Gln Gly Ser Arg Arg Leu Arg Arg Glu Pro
 675 680 685
 Gly Gly Gln Asp Cys Phe Pro Val Pro Leu Thr Phe Glu Ala Ala Leu
 690 695 700
 Ala Arg Gly Leu Val Asp Tyr Phe Gly Ala Glu Leu Ala Ala Ser Ser
 705 710 715 720
 Leu Pro Glu Ala Met Pro Phe Thr Val Gly Asp Asn Lys Thr Tyr Arg
 725 730 735
 Gly Phe Trp Asn Pro Pro Leu Glu Pro Arg Lys Ala Tyr Leu Ile Tyr
 740 745 750
 Phe Gln Ala Ala Ser His Leu Lys Gly Glu Thr Arg Leu Asn Cys Ile
 755 760 765
 Arg Ile Ala Arg Lys Ala Ala Cys Lys Glu Ser Lys Arg Pro Leu Glu
 770 775 780
 Val Ser Gln Arg Ser Glu Glu Met Gly Leu Ile Leu Gly Ile Cys Ala
 785 790 795 800
 Gly Gly Leu Ala Val Leu Ile Leu Leu Leu Gly Ala Ile Ile Val Ile
 805 810 815
 Ile Arg Lys Gly Arg Asp His Tyr Ala Tyr Ser Tyr Tyr Pro Lys Pro
 820 825 830
 Val Asn Met Thr Lys Ala Thr Val Asn Tyr Arg Gln Glu Lys Thr His
 835 840 845
 Met Met Ser Ala Val Asp Arg Ser Phe Thr Asp Gln Ser Thr Leu Gln
 850 855 860
 Glu Asp Glu Arg Leu Gly Leu Ser Phe Met Asp Thr His Gly Tyr Ser
 865 870 875 880
 Thr Arg Gly Asp Gln Arg Ser Gly Gly Val Thr Glu Ala Ser Ser Leu
 885 890 895

Leu Gly Gly Ser Pro Arg Arg Pro Cys Gly Arg Lys Gly Ser Pro Tyr
 900 905 910
 His Thr Gly Gln Leu His Pro Ala Val Arg Val Ala Asp Leu Leu Gln
 915 920 925
 His Ile Asn Gln Met Lys Thr Ala Glu Gly Tyr Gly Phe Lys Gln Glu
 930 935 940
 Tyr Glu Ser Phe Phe Glu Gly Trp Asp Ala Thr Lys Lys Lys Asp Lys
 945 950 955 960
 Val Lys Gly Ser Arg Gln Glu Pro Met Pro Ala Tyr Asp Arg His Arg
 965 970 975
 Val Lys Leu His Pro Met Leu Gly Asp Pro Asn Ala Asp Tyr Ile Asn
 980 985 990
 Ala Asn Tyr Ile Asp Ile Arg Ile Asn Arg Glu Gly Tyr His Arg Ser
 995 1000 1005
 Asn His Phe Ile Ala Thr Gln Gly Pro Lys Pro Glu Met Val Tyr Asp
 1010 1015 1020
 Phe Trp Arg Met Val Trp Gln Glu His Cys Ser Ser Ile Val Met Ile
 1025 1030 1035 1040
 Thr Lys Leu Val Glu Val Gly Arg Val Lys Cys Ser Arg Tyr Trp Pro
 1045 1050 1055
 Glu Asp Ser Asp Thr Tyr Gly Asp Ile Lys Ile Met Leu Val Lys Thr
 1060 1065 1070
 Glu Thr Leu Ala Glu Tyr Val Val Arg Thr Phe Ala Leu Glu Arg Arg
 1075 1080 1085
 Gly Tyr Ser Ala Arg His Glu Val Arg Gln Phe His Phe Thr Ala Trp
 1090 1095 1100
 Pro Glu His Gly Val Pro Tyr His Ala Thr Gly Leu Leu Ala Phe Ile
 1105 1110 1115 1120
 Arg Arg Val Lys Ala Ser Thr Pro Pro Asp Ala Gly Pro Ile Val Ile
 1125 1130 1135
 His Cys Ser Ala Gly Thr Gly Arg Thr Gly Cys Tyr Ile Val Leu Asp
 1140 1145 1150
 Val Met Leu Asp Met Ala Glu Cys Glu Gly Val Val Asp Ile Tyr Asn
 1155 1160 1165
 Cys Val Lys Thr Leu Cys Ser Arg Arg Val Asn Met Ile Gln Thr Glu
 1170 1175 1180
 Glu Gln Tyr Ile Phe Ile His Asp Ala Ile Leu Glu Ala Cys Leu Cys
 1185 1190 1195 1200
 Gly Glu Thr Thr Ile Pro Val Ser Glu Phe Lys Ala Thr Tyr Lys Glu
 1205 1210 1215
 Met Ile Arg Ile Asp Pro Gln Ser Asn Ser Ser Gln Leu Arg Glu Glu
 1220 1225 1230
 Phe Gln Thr Leu Asn Ser Val Thr Pro Pro Leu Asp Val Glu Glu Cys
 1235 1240 1245
 Ser Ile Ala Leu Leu Pro Arg Asn Arg Asp Lys Asn Arg Ser Met Asp
 1250 1255 1260
 Val Leu Pro Pro Asp Arg Cys Leu Pro Phe Leu Ile Ser Thr Asp Gly
 1265 1270 1275 1280
 Asp Ser Asn Asn Tyr Ile Asn Ala Ala Leu Thr Asp Ser Tyr Thr Arg
 1285 1290 1295
 Ser Ala Ala Phe Ile Val Thr Leu His Pro Leu Gln Ser Thr Thr Pro
 1300 1305 1310
 Asp Phe Trp Gly Leu Val Tyr Asp Tyr Gly Cys Thr Ser Ile Val Met
 1315 1320 1325
 Leu Asn Gln Leu Asn Gln Ser Asn Ser Ala Trp Pro Cys Leu Gln Tyr
 1330 1335 1340
 Trp Pro Glu Pro Gly Arg Gln Gln Tyr Gly Leu Met Glu Val Glu Phe
 1345 1350 1355 1360
 Met Ser Gly Thr Ala Asp Glu Asp Leu Val Ala Arg Val Phe Arg Val
 1365 1370 1375
 Gln Asn Ile Ser Arg Leu Gln Glu Gly His Leu Leu Val Arg His Phe
 1380 1385 1390
 Gln Phe Leu Arg Trp Ser Ala Tyr Arg Asp Thr Pro Asp Ser Lys Lys
 1395 1400 1405

Ala Phe Leu His Leu Leu Ala Glu Gly Asp Lys Trp Gln Ala Glu Ser
 1410 1415 1420
 Gly Asp Gly Arg Thr Ile Val His Cys Leu Asn Gly Gly Gly Arg Ser
 1425 1430 1435 1440
 Gly Thr Phe Cys Ala Cys Ala Thr Val Leu Glu Met Ile Arg Cys His
 1445 1450 1455
 Asn Leu Val Asp Val Phe Phe Ala Ala Lys Thr Leu Arg Asn Tyr Lys
 1460 1465 1470
 Pro Asn Met Val Glu Thr Met Asp Gln Tyr His Phe Cys Tyr Asp Val
 1475 1480 1485
 Ala Leu Glu Tyr Leu Glu Gly Leu Glu Ser Arg
 1490 1495 1499

<210> 1284
 <211> 430
 <212> Amino acid
 <213> Homo sapiens

<400> 1284
 Thr Lys Pro Arg Lys Arg Arg His Gln Pro Ala Ser Gln Arg Gln Arg
 1 5 10 15
 Pro Trp Ser Ser Asp Ser Thr Gly Asp Leu Leu Ala Arg Gly Lys Gly
 20 25 30
 Arg Lys Glu Glu Asn Lys Gly Ser Asp Arg Val Ser Leu Ala Pro Pro
 35 40 45
 Ser Leu Arg Arg Pro Met Met Cys Gln Ser Glu Ala Arg Gln Gly Pro
 50 55 60
 Glu Leu Arg Ala Ala Lys Trp Leu His Phe Pro Gln Leu Ala Leu Arg
 65 70 75 80
 Arg Arg Leu Gly Gln Leu Ser Cys Met Ser Arg Pro Ala Leu Lys Leu
 85 90 95
 Arg Ser Trp Pro Leu Thr Val Leu Tyr Tyr Leu Leu Pro Phe Gly Ala
 100 105 110
 Leu Arg Pro Leu Ser Arg Val Gly Trp Arg Pro Val Ser Arg Val Ala
 115 120 125
 Leu Tyr Lys Ser Val Pro Thr Arg Leu Leu Ser Arg Ala Trp Gly Arg
 130 135 140
 Leu Asn Gln Val Glu Leu Pro His Trp Leu Arg Arg Pro Val Tyr Ser
 145 150 155 160
 Leu Tyr Ile Trp Thr Phe Gly Val Asn Met Lys Glu Ala Ala Val Glu
 165 170 175
 Asp Leu His His Tyr Arg Asn Leu Ser Glu Phe Phe Arg Arg Lys Leu
 180 185 190
 Lys Pro Gln Ala Arg Pro Val Cys Gly Leu His Ser Val Ile Ser Pro
 195 200 205
 Ser Asp Gly Arg Ile Leu Asn Phe Gly Gln Val Lys Asn Cys Glu Val
 210 215 220
 Glu Gln Val Lys Gly Val Thr Tyr Ser Leu Glu Ser Phe Leu Gly Pro
 225 230 235 240
 Arg Met Cys Thr Glu Asp Leu Pro Phe Pro Pro Ala Ala Ser Cys Asp
 245 250 255
 Ser Phe Lys Asn Gln Leu Val Thr Arg Glu Gly Asn Glu Leu Tyr His
 260 265 270
 Cys Val Ile Tyr Leu Ala Pro Gly Asp Tyr His Cys Phe His Ser Pro
 275 280 285
 Thr Asp Trp Thr Val Ser His Arg Arg His Phe Pro Gly Ser Leu Met
 290 295 300
 Ser Val Asn Pro Gly Met Ala Arg Trp Ile Lys Glu Leu Phe Cys His
 305 310 315 320

```

Asn Glu Arg Val Val Leu Thr Gly Asp Trp Lys His Gly Phe Phe Ser
              325                      330                      335
Leu Thr Ala Val Gly Ala Thr Asn Trp Gly Ser Ile Arg Ile Tyr Phe
              340                      345                      350
Asp Arg Asp Leu His Thr Asn Ser Pro Arg His Ser Lys Gly Ser Tyr
              355                      360                      365
Asn Asp Phe Ser Phe Val Thr His Thr Asn Arg Glu Gly Val Pro Met
              370                      375                      380
Ala Leu Arg Gly Glu His Leu Gly Gln Ser Phe Asn Leu Gly Ser Thr
385                      390                      395                      400
Ile Val Leu Ile Phe Glu Ala Pro Lys Asp Phe Asn Phe Gln Leu Lys
              405                      410                      415
Thr Gly Gln Lys Ile Arg Phe Gly Glu Ala Leu Gly Ser Leu
              420                      425                      430

```

<210> 1285

<211> 957

<212>Amino acid

<213> Homo sapiens

<400> 1285

```

Ala Glu Leu Gly Leu Phe Gly Ser Leu Arg Phe Ser Ser Leu Leu His
1              5              10              15
Phe Pro Pro Arg Pro Arg Ser Pro Ala Ser Ala Cys Gly Pro Gly Glu
20              25              30
Gly Arg Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Val Leu Ala Leu
35              40              45
Val Leu Ala Pro Ala Gly Ala Phe Arg Asn Asp Lys Cys Gly Asp Thr
50              55              60
Ile Lys Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His
65              70              75              80
Ser Tyr His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp
85              90              95
Pro Tyr Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu
100             105             110
Asp Arg Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn
115             120             125
Glu Asn Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro
130             135             140
Pro Val Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp
145             150             155             160
Tyr Glu Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys
165             170             175
Arg Gly Pro Glu Cys Ser Gln Asn Tyr Thr Thr Pro Ser Gly Val Ile
180             185             190
Lys Ser Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr
195             200             205
Tyr Ile Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Asp Phe Glu
210             215             220
Ser Phe Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys
225             230             235             240
Arg Tyr Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro
245             250             255
His Ile Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser
260             265             270
Ser Ser Gly Ile Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala
275             280             285
Lys Glu Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Val Ser
290             295             300

```

Glu Asp Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile
 305 310 315 320
 His Ser Asp Gln Ile Thr Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser
 325 330 335
 Ala Glu Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly
 340 345 350
 Glu Asp Ser Tyr Arg Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg
 355 360 365
 Phe Val Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys
 370 375 380
 Lys Lys Tyr Tyr Val Lys Thr Tyr Lys Ile Asp Val Ser Ser Asn Gly
 385 390 395 400
 Glu Asp Trp Ile Thr Ile Lys Glu Gly Asn Lys Pro Val Leu Phe Gln
 405 410 415
 Gly Asn Thr Asn Pro Thr Asp Val Val Val Ala Val Phe Pro Lys Pro
 420 425 430
 Leu Ile Thr Arg Phe Val Arg Ile Lys Pro Ala Thr Trp Glu Thr Gly
 435 440 445
 Ile Ser Met Arg Phe Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro
 450 455 460
 Cys Ser Gly Met Leu Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln
 465 470 475 480
 Ile Thr Ser Ser Asn Gln Gly Asp Arg Asn Trp Met Pro Glu Asn Ile
 485 490 495
 Arg Leu Val Thr Ser Arg Ser Gly Trp Ala Leu Pro Pro Ala Pro His
 500 505 510
 Ser Tyr Ile Asn Glu Trp Leu Gln Ile Asp Leu Gly Glu Glu Lys Ile
 515 520 525
 Val Arg Gly Ile Ile Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val
 530 535 540
 Phe Met Arg Lys Phe Lys Ile Gly Tyr Ser Asn Asn Gly Ser Asp Trp
 545 550 555 560
 Lys Met Ile Met Asp Asp Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly
 565 570 575
 Asn Asn Asn Tyr Asp Thr Pro Glu Leu Arg Thr Phe Pro Ala Leu Ser
 580 585 590
 Thr Arg Phe Ile Arg Ile Tyr Pro Glu Arg Ala Thr His Gly Gly Leu
 595 600 605
 Gly Leu Arg Met Glu Leu Leu Gly Cys Glu Val Glu Ala Pro Thr Ala
 610 615 620
 Gly Pro Thr Thr Pro Asn Gly Asn Leu Val Asp Glu Cys Asp Asp Asp
 625 630 635 640
 Gln Ala Asn Cys His Ser Gly Thr Gly Asp Asp Phe Gln Leu Thr Gly
 645 650 655
 Gly Thr Thr Val Leu Ala Thr Glu Lys Pro Thr Val Ile Asp Ser Thr
 660 665 670
 Ile Gln Ser Glu Phe Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp
 675 680 685
 Gly Ser His Lys Thr Phe Cys His Trp Glu His Asp Asn His Val Gln
 690 695 700
 Leu Lys Trp Ser Val Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His
 705 710 715 720
 Thr Gly Asp Gly Asn Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys
 725 730 735
 Gly Lys Val Ala Arg Leu Val Ser Pro Val Val Tyr Ser Gln Asn Ser
 740 745 750
 Ala His Cys Met Thr Phe Trp Tyr His Met Ser Gly Ser His Val Gly
 755 760 765
 Thr Leu Arg Val Lys Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln
 770 775 780
 Leu Val Trp Met Ala Ile Gly His Gln Gly Asp His Trp Lys Glu Gly
 785 790 795 800
 Arg Val Leu Leu His Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu
 805 810 815

Gly Glu Ile Gly Lys Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile
 820 825 830
 Ser Ile Asn Asn His Ile Ser Gln Glu Asp Cys Ala Lys Pro Ala Asp
 835 840 845
 Leu Asp Lys Lys Asn Pro Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr
 850 855 860
 Pro Gly Tyr Glu Gly Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys
 865 870 875 880
 Pro Gly Asn Val Leu Lys Thr Leu Glu Pro Ile Leu Ile Thr Ile Ile
 885 890 895
 Ala Met Ser Ala Leu Gly Val Leu Leu Gly Ala Val Cys Gly Val Val
 900 905 910
 Leu Tyr Cys Ala Cys Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser
 915 920 925
 Ala Leu Glu Asn Tyr Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys
 930 935 940
 Lys Asp Lys Leu Asn Thr Gln Ser Thr Tyr Ser Glu Ala
 945 950 955 957

<210> 1286

<211> 173

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(173)

<223> X = any amino acid or stop code

<400> 1286

His Glu Gly Ser Ala Leu Thr Trp Ala Ser His Tyr Gln Glu Arg Leu
 1 5 10 15
 Asn Ser Glu Gln Ser Cys Leu Asn Glu Trp Thr Ala Met Ala Asp Leu
 20 25 30
 Glu Ser Leu Arg Pro Pro Ser Ala Glu Pro Gly Gly Ser Val Cys Gly
 35 40 45
 Gly Glu Gly Leu Gly Gly Gly Glu Gly Arg Ile Met Gln Trp Gly Ala
 50 55 60
 Trp Trp Arg Gly Glu Arg Ala Pro Xaa Leu Arg Gly Ser Ala Pro Arg
 65 70 75 80
 Ser Ser Glu Gln Glu Gln Met Glu Gln Ala Ile Arg Ala Glu Leu Trp
 85 90 95
 Lys Val Leu Asp Val Ser Asp Leu Glu Ser Val Thr Ser Lys Glu Ile
 100 105 110
 Arg Gln Ala Leu Glu Leu Arg Leu Gly Leu Pro Leu Gln Pro Val Pro
 115 120 125
 Xaa Leu His Arg Gln Pro Asp Ala Ala Ala Gly Gly Thr Ala Gly Pro
 130 135 140
 Ser Leu Pro His Leu Pro Pro Pro Leu Pro Gly Leu Arg Val Glu Arg
 145 150 155 160
 Ser Lys Pro Gly Gly Ala Ala Glu Glu Gln Val Gly Leu
 165 170 173

<210> 1287

<211> 181

<212>Amino acid

<213> Homo sapiens

<400> 1287

```

Met Ala Ala Leu Asp Leu Arg Ala Glu Leu Asp Ser Leu Val Leu Gln
 1          5          10          15
Leu Leu Gly Asp Leu Glu Glu Leu Glu Lys Arg Thr Val Leu Asn
          20          25          30
Ala Arg Val Glu Glu Gly Trp Leu Ser Leu Ala Lys Ala Arg Tyr Ala
          35          40          45
Met Gly Ala Lys Ser Val Gly Pro Leu Gln Tyr Ala Ser His Met Glu
          50          55          60
Pro Gln Val Cys Leu His Ala Ser Glu Ala Gln Glu Gly Leu Gln Lys
          65          70          75          80
Phe Lys Val Val Arg Ala Gly Val His Ala Pro Glu Glu Val Gly Pro
          85          90          95
Arg Glu Ala Gly Leu Arg Arg Arg Lys Gly Pro Thr Lys Thr Pro Glu
          100          105          110
Pro Glu Ser Ser Glu Ala Pro Gln Asp Pro Leu Asn Trp Phe Gly Ile
          115          120          125
Leu Val Pro His Ser Leu Arg Gln Ala Gln Ala Ser Phe Arg Asp Gly
          130          135          140
Leu Gln Leu Ala Ala Asp Ile Ala Ser Leu Gln Asn Arg Ile Asp Trp
          145          150          155          160
Gly Arg Ser Gln Leu Arg Gly Leu Gln Glu Lys Leu Lys Gln Leu Glu
          165          170          175
Pro Gly Ala Ala *
          180

```

<210> 1288

<211> 216

<212> Amino acid

<213> Homo sapiens

<400> 1288

```

His Ser Asp Val Gly Ala Ala Thr Ala Val Leu Pro Leu Leu Thr Ala
 1          5          10          15
Val Leu Gly Val Thr Val Val Thr Arg Arg Asp Thr Glu Gly Pro Gly
          20          25          30
Arg Ala Ala Leu Val His Leu Thr Gly Ser Pro Arg Gln Lys Val Gly
          35          40          45
Thr Ser Gly Arg Glu Gly Leu Pro Gly Leu Gly Ala Ser Cys Ala Glu
          50          55          60
Ser Glu Leu Glu Arg Glu Thr Gln Glu Pro Arg Ser Arg Gly Arg Cys
          65          70          75          80
Ile Phe Gly Ala Ala Arg Trp Arg Gln Val Pro Leu Ala Ser Pro Gln
          85          90          95
Arg Pro Phe Leu Leu Ser Pro Gly Pro Arg Leu His Arg Met Gly Leu
          100          105          110
Pro Val Ser Trp Ala Pro Pro Ala Leu Trp Val Leu Gly Cys Cys Ala
          115          120          125
Leu Leu Leu Ser Leu Trp Ala Leu Cys Thr Ala Cys Arg Arg Pro Glu
          130          135          140
Asp Ala Val Ala Pro Arg Lys Arg Ala Arg Arg Gln Arg Ala Arg Leu
          145          150          155          160
Gln Gly Ser Ala Thr Ala Ala Glu Ala Val Ser Ala Lys Leu Ser Arg
          165          170          175
Gly Pro Gly Trp Gly Pro Gln Gly Thr Asp Gln Pro Ser Ser Pro Pro

```

```

      180      185      190
Val Pro Thr Glu Ala Asp Pro Pro Leu Leu Pro Gln Gln Val Gly His
      195      200      205
Gln Thr Ala Arg Ala Ala Pro Gly
      210      215 216

```

```

<210> 1289
<211> 148
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(148)
<223> X = any amino acid or stop code

```

```

<400> 1289
Leu Thr Gly Pro Gly Gln Arg Leu Ala Gly Thr Thr Glu Gly Pro Arg
 1          5          10          15
Arg Cys Arg Gly Ser Ser Gln Ala Pro Thr Pro Thr Trp Lys Leu Val
      20          25          30
Asp Thr Arg Leu Cys Ala Ala Ala Pro Trp Leu Ala Ser Arg Ala Pro
      35          40          45
Gly His Tyr Ser Gln Met Leu Leu Val Asn Xaa Pro Cys Arg Lys Asp
      50          55          60
Trp Leu Val Ser Lys Trp Met Arg Thr Pro Val Cys Gly Gln Ser Pro
      65          70          75          80
Ala Met Thr Asp Arg Pro Arg Ser Glu Ala Gly Arg Asp His Arg Arg
      85          90          95
Ala Lys Ala Leu Pro Gly Leu Ile Pro Gly Ser Asn Pro Asn Leu Glu
      100          105          110
Ala Cys Gly His Gln Ala Leu Cys Ser Ser Ser Val Ala Ser Val Gln
      115          120          125
Gly Pro Trp Pro Leu Leu Pro Asn Ala Ser Ser Pro Pro Thr Pro Gly
      130          135          140
Gln Pro Gln Pro
145          148

```

```

<210> 1290
<211> 170
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(170)
<223> X = any amino acid or stop code

```

```

<400> 1290
Lys His Arg Leu Cys Ser Leu Glu Gln Leu Met Thr Leu Ile Ser Ala
 1          5          10          15
Ala Arg Glu Tyr Glu Ile Glu Phe Ile Tyr Ala Ile Ser Pro Gly Leu
      20          25          30
Asp Ile Thr Phe Ser Asn Pro Lys Glu Val Ser Thr Leu Lys Arg Lys

```

```

      35              40              45
Leu Asp Gln Val Ser Gln Phe Gly Cys Arg Ser Phe Ala Leu Leu Phe
  50              55              60
Asp Asp Ile Asp His Asn Met Cys Ala Ala Asp Lys Glu Val Phe Ser
  65              70              75              80
Ser Phe Ala His Ala Gln Val Ser Ile Thr Asn Glu Ile Tyr Gln Tyr
      85              90              95
Leu Gly Glu Pro Glu Thr Phe Leu Phe Cys Pro Thr Glu Tyr Cys Ile
      100              105              110
Xaa Trp Leu Tyr Ile Xaa Leu Val Phe Leu Glu Tyr Ile Thr Tyr Lys
      115              120              125
Gly Pro Trp Ala Pro Phe Ser Leu His Phe Pro Pro Pro Leu Val Cys
      130              135              140
Lys Ser Arg Asn Leu Phe Leu Glu Asp Ile Phe Gln Asp Pro Lys Leu
      145              150              155              160
Glu Lys Phe Xaa Glu Leu Ile Asn Asp Asn
      165              170

```

<210> 1291
 <211> 98
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 1291
Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu Gly
  1              5              10              15
Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp Leu
      20              25              30
Glu Asn Asp Glu Gln Ala Ala Ser Ala Ile Ser Glu Leu Val Ser Thr
      35              40              45
Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Phe Lys Arg
      50              55              60
Leu Ser Val Val Phe Gly Glu His Thr Leu Leu Val Thr Val Ser Gly
      65              70              75              80
Gln Arg Val Phe Val Val Lys Arg Gln Asn Arg Gly Arg Glu Pro Ile
      85              90              95
Asp Val
  98

```

<210> 1292
 <211> 142
 <212> Amino acid
 <213> Homo sapiens

```

      <400> 1292
Ala Lys Arg Ala Glu Arg Thr Ser Arg Leu Gln Gly Leu Gln His Pro
  1              5              10              15
Ser Pro Pro Tyr Pro Pro Ala Thr Leu Gly Val Thr Pro Gly Gln Asp
      20              25              30
Arg Thr Leu Gln Leu Gln His Gln Cys Pro Ala Gly Arg Lys Ser Arg
      35              40              45
Lys Lys Lys Ser Lys Ala Thr Gln Leu Ser Pro Glu Asp Arg Val Glu
      50              55              60
Asp Ala Leu Pro Pro Ser Lys Ala Pro Ser Arg Thr Arg Arg Ala Lys

```



```

65              70              75              80
Arg Asp Leu Pro Lys Arg Thr Ala Thr Gln Arg Pro Glu Gly Thr Ser
              85              90              95
Leu Gln Gln Asp Pro Glu Ala Pro Thr Val Pro Lys Lys Gly Arg Arg
              100              105              110
Lys Gly Arg Gln Ala Ala Ser Gly His Cys Arg Pro Arg Lys Val Lys
              115              120              125
Ala Asp Ile Pro Ser Leu Glu Pro Glu Gly Thr Ser Ala Ser
              130              135              140              142

```

<210> 1293

<211> 89

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(89)

<223> X = any amino acid or stop code

<400> 1293

```

Arg Lys Ser Ser Trp Leu Gly Ala Val Ala His Ala Cys Asn Pro Ser
1          5          10          15
Ser Leu Gly Gly Pro Gly Arg Gln Ile Thr Arg Ser Gly Val Arg Asp
          20          25          30
Gln Pro Gly Gln Tyr Gly Glu Thr Pro Ser Leu Leu Lys Ile Gln Thr
          35          40          45
Leu Ala Gly Arg Gly Gly Ala Cys Leu Xaa Ser His Ile Leu Arg Arg
          50          55          60
Leu Arg Gln Lys Asn Arg Leu Asn Leu Gly Gly Arg Gly Cys Ser Glu
65          70          75          80
Leu Arg Ser Arg His Cys Ala Pro Ala
          85          89

```

<210> 1294

<211> 80

<212>Amino acid

<213> Homo sapiens

<400> 1294

```

Ala Trp Asn Ser Ala Arg Gly Ala Val Ser Pro Leu Trp Val Pro Gly
1          5          10          15
Cys Phe Leu Thr Leu Ser Val Thr Trp Ile Gly Ala Ala Pro Leu Ile
          20          25          30
Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln Pro
          35          40          45
Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly Val
          50          55          60
Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg Lys
65          70          75          80

```

<210> 1295
 <211> 281
 <212> Amino acid
 <213> Homo sapiens

<400> 1295
 Ala Glu Met Ala Asp Asp Leu Gly Asp Glu Trp Trp Glu Asn Gln Pro
 1 5 10 15
 Thr Gly Ala Gly Ser Ser Pro Glu Ala Ser Asp Gly Glu Gly Glu Gly
 20 25 30
 Asp Thr Glu Val Met Gln Gln Glu Thr Val Pro Val Pro Val Pro Ser
 35 40 45
 Glu Lys Thr Lys Gln Pro Lys Glu Cys Phe Leu Ile Gln Pro Lys Glu
 50 55 60
 Arg Lys Glu Asn Thr Thr Lys Thr Arg Lys Arg Arg Lys Lys Lys Ile
 65 70 75 80
 Thr Asp Val Leu Ala Lys Ser Glu Pro Lys Pro Gly Leu Pro Glu Asp
 85 90 95
 Leu Gln Lys Leu Met Lys Asp Tyr Tyr Ser Ser Arg Arg Leu Val Ile
 100 105 110
 Glu Leu Glu Glu Leu Asn Leu Pro Asp Ser Cys Phe Leu Lys Ala Asn
 115 120 125
 Asp Leu Thr His Ser Leu Ser Ser Tyr Leu Lys Glu Ile Cys Pro Lys
 130 135 140
 Trp Val Lys Leu Arg Lys Asn His Ser Glu Lys Lys Ser Val Leu Met
 145 150 155 160
 Leu Ile Ile Cys Ser Ser Ala Val Arg Ala Leu Glu Leu Ile Arg Ser
 165 170 175
 Met Thr Ala Phe Arg Gly Asp Gly Lys Val Ile Lys Leu Phe Ala Lys
 180 185 190
 His Ile Lys Val Gln Ala Gln Val Lys Leu Leu Glu Lys Arg Val Val
 195 200 205
 His Leu Gly Val Gly Thr Pro Gly Arg Ile Lys Glu Leu Val Lys Gln
 210 215 220
 Gly Gly Leu Asn Leu Ser Pro Leu Lys Phe Leu Val Phe Asp Trp Asn
 225 230 235 240
 Trp Arg Asp Gln Lys Leu Arg Arg Met Met Asp Ile Pro Glu Ile Arg
 245 250 255
 Lys Glu Val Phe Glu Leu Leu Glu Met Gly Val Leu Ser Leu Cys Lys
 260 265 270
 Ser Glu Ser Leu Lys Leu Gly Leu Phe
 275 280 281

<210> 1296
 <211> 213
 <212> Amino acid
 <213> Homo sapiens

<400> 1296
 Arg Pro Gly Thr Ala Ile Trp Val Val Glu Cys Glu His Gly Arg Pro
 1 5 10 15
 Ile Ala Glu Ser Glu Gly Gln Glu Gly Arg Gly His Ser Pro Pro Gly
 20 25 30
 Pro Cys Ser Val Ala Gly Phe Leu Arg Gly Arg Leu Gly Arg Asn Leu
 35 40 45

Glu Ile Met Gly Ser Thr Trp Gly Ser Pro Gly Trp Val Arg Leu Ala
 50 55 60
 Leu Cys Leu Thr Gly Leu Val Leu Ser Leu Tyr Ala Leu His Val Lys
 65 70 75 80
 Ala Ala Arg Ala Arg Asp Arg Asp Tyr Arg Ala Leu Cys Asp Val Gly
 85 90 95
 Thr Ala Ile Ser Cys Ser Arg Val Phe Ser Ser Arg Trp Gly Arg Gly
 100 105 110
 Phe Gly Leu Val Glu His Val Leu Gly Gln Asp Ser Ile Leu Asn Gln
 115 120 125
 Ser Asn Ser Ile Phe Gly Cys Ile Phe Tyr Thr Leu Gln Leu Leu Leu
 130 135 140
 Gly Cys Leu Arg Thr Arg Trp Ala Ser Val Leu Met Leu Leu Ser Ser
 145 150 155 160
 Leu Val Ser Leu Ala Gly Ser Val Tyr Leu Ala Trp Ile Leu Phe Phe
 165 170 175
 Val Leu Tyr Asp Phe Cys Ile Val Cys Ile Thr Thr Tyr Ala Ile Asn
 180 185 190
 Val Ser Leu Met Trp Leu Ser Phe Arg Lys Val Gln Glu Pro Gln Gly
 195 200 205
 Lys Ala Lys Arg His
 210 213

<210> 1297

<211> 353

<212> Amino acid

<213> Homo sapiens

<400> 1297

Glu Ser Pro Ala Pro Pro Ala Phe Arg Pro Ala Met Ala Ala Val Ala
 1 5 10 15
 Leu Met Pro Pro Pro Leu Leu Leu Leu Leu Leu Leu Ala Ser Pro Pro
 20 25 30
 Ala Ala Ser Ala Pro Ser Ala Arg Asp Pro Phe Ala Pro Gln Leu Gly
 35 40 45
 Asp Thr Gln Asn Cys Gln Leu Arg Cys Arg Asp Arg Asp Leu Gly Pro
 50 55 60
 Gln Pro Ser Gln Ala Gly Leu Glu Gly Ala Ser Glu Ser Pro Tyr Asp
 65 70 75 80
 Arg Ala Val Leu Ile Ser Ala Cys Glu Arg Gly Cys Arg Leu Phe Ser
 85 90 95
 Ile Cys Arg Phe Val Ala Arg Ser Ser Lys Pro Asn Ala Thr Gln Thr
 100 105 110
 Glu Cys Glu Ala Ala Cys Val Glu Ala Tyr Val Lys Glu Ala Glu Gln
 115 120 125
 Gln Ala Cys Ser His Gly Cys Trp Ser Gln Pro Ala Glu Pro Glu Pro
 130 135 140
 Glu Gln Lys Arg Lys Val Leu Glu Ala Pro Ser Gly Ala Leu Ser Leu
 145 150 155 160
 Leu Asp Leu Phe Ser Thr Leu Cys Asn Asp Leu Val Asn Ser Ala Gln
 165 170 175
 Gly Phe Val Ser Ser Thr Trp Thr Tyr Tyr Leu Gln Thr Asp Asn Gly
 180 185 190
 Lys Val Val Val Phe Gln Thr Gln Pro Ile Val Glu Ser Leu Gly Phe
 195 200 205
 Gln Gly Gly Arg Leu Gln Arg Val Glu Val Thr Trp Arg Gly Ser His
 210 215 220
 Pro Glu Ala Leu Glu Val His Val Asp Pro Val Gly Pro Leu Asp Lys
 225 230 235 240

Val Arg Lys Ala Lys Ile Arg Val Lys Thr Ser Ser Lys Ala Lys Val
 245 250 255
 Glu Ser Glu Glu Pro Gln Asp Asn Asp Phe Leu Ser Cys Met Ser Arg
 260 265 270
 Arg Ser Gly Leu Pro Arg Trp Ile Leu Ala Cys Cys Leu Phe Leu Ser
 275 280 285
 Val Leu Val Met Leu Trp Leu Ser Cys Ser Thr Leu Val Thr Ala Pro
 290 295 300
 Gly Gln His Leu Lys Phe Gln Pro Leu Thr Leu Glu Gln His Lys Gly
 305 310 315 320
 Phe Met Met Glu Pro Asp Trp Pro Leu Tyr Pro Pro Pro Ser His Ala
 325 330 335
 Cys Glu Asp Ser Leu Pro Pro Tyr Lys Leu Lys Leu Asp Leu Thr Lys
 340 345 350
 Leu
 353

<210> 1298
 <211> 161
 <212> Amino acid
 <213> Homo sapiens

<400> 1298
 Phe Pro Glu Leu Gly Thr Ser Leu Ser Ala Met Arg Phe Leu Ala Ala
 1 5 10 15
 Thr Phe Leu Leu Leu Ala Leu Ser Thr Ala Ala Gln Ala Glu Pro Val
 20 25 30
 Gln Phe Lys Asp Cys Gly Ser Val Asp Gly Val Ile Lys Glu Val Asn
 35 40 45
 Val Ser Pro Cys Pro Thr Gln Pro Cys Gln Leu Ser Lys Gly Gln Ser
 50 55 60
 Tyr Ser Val Asn Val Thr Phe Thr Ser Asn Ile Gln Ser Lys Ser Ser
 65 70 75 80
 Lys Ala Val Val His Gly Ile Leu Met Gly Val Pro Val Pro Phe Pro
 85 90 95
 Ile Pro Glu Pro Asp Gly Cys Lys Ser Gly Ile Asn Cys Pro Ile Gln
 100 105 110
 Lys Asp Lys Thr Tyr Ser Tyr Leu Asn Lys Leu Pro Val Lys Ser Glu
 115 120 125
 Tyr Pro Ser Ile Lys Leu Val Val Glu Trp Gln Leu Gln Asp Asp Lys
 130 135 140
 Asn Gln Ser Leu Phe Cys Trp Glu Ile Pro Val Gln Ile Val Ser His
 145 150 155 160
 Leu
 161

<210> 1299
 <211> 128
 <212> Amino acid
 <213> Homo sapiens

<400> 1299
 Ala Pro Glu Thr Phe Arg Cys Val Trp Arg Leu Gln Gly Leu Thr Phe
 1 5 10 15

```

Ile Ala Phe Thr Glu Leu Gln Ala Lys Val Ile Asp Thr Gln Gln Lys
      20      25      30
Val Lys Leu Ala Asp Ile Gln Ile Glu Gln Leu Asn Arg Thr Lys Lys
      35      40      45
His Ala His Leu Thr Asp Thr Glu Ile Met Thr Leu Val Asp Glu Thr
      50      55      60
Asn Met Tyr Glu Gly Val Gly Arg Met Phe Ile Leu Gln Ser Lys Glu
      65      70      75      80
Ala Ile His Ser Gln Leu Leu Glu Lys Gln Lys Ile Ala Glu Glu Lys
      85      90      95
Ile Lys Glu Leu Glu Gln Lys Lys Ser Tyr Leu Glu Arg Ser Val Lys
      100      105      110
Glu Ala Glu Asp Asn Ile Arg Glu Met Leu Met Ala Arg Arg Ala Gln
      115      120      125      128

```

<210> 1300

<211> 265

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(265)

<223> X = any amino acid or stop code

<400> 1300

```

His Ser Leu Leu Leu Gly Thr Arg Val Arg Asp Ala Ser Ser Lys Ile
  1      5      10      15
Gln Gly Glu Tyr Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu
      20      25      30
Ser Arg Val Phe His Arg Asp Gly His Tyr Gly Phe Ser Glu Pro Leu
      35      40      45
Thr Phe Cys Ser Val Val Asp Leu Ile Asn His Tyr Arg His Glu Ser
      50      55      60
Leu Ala Gln Tyr Asn Ala Lys Leu Asp Thr Arg Leu Leu Tyr Pro Val
      65      70      75      80
Ser Lys Tyr Gln Gln Val Arg Ala Gly Leu Gly Ala Arg Glu Gly Ser
      85      90      95
Thr Trp Leu Ala Pro Gly Leu Ser Phe Leu Gly Arg Pro Asp Gln Ala
      100      105      110
Met His Leu Pro Ser Phe Arg His Val Ser Pro Asp Gln Ile Val Lys
      115      120      125
Glu Asp Ser Val Glu Ala Val Gly Ala Gln Leu Lys Val Tyr His Gln
      130      135      140
Gln Tyr Gln Asp Lys Ser Arg Glu Tyr Asp Gln Leu Tyr Glu Glu Tyr
      145      150      155      160
Thr Arg Thr Ser Gln Glu Leu Gln Met Lys Arg Thr Ala Ile Glu Ala
      165      170      175
Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu Gln Gly Gln Thr Gln Glu
      180      185      190
Lys Cys Ser Lys Glu Tyr Leu Glu Arg Phe Arg Arg Glu Gly Asn Gln
      195      200      205
Thr Lys Glu Met Gln Arg Ile Leu Leu Asn Ser Glu Arg Leu Lys Ser
      210      215      220
Arg Ile Ala Glu Ile His Glu Ser Pro His Arg Ser Trp Glu Gln Gln
      225      230      235      240
Leu Leu Val Pro Arg Ala Ser Asp Asn Lys Arg Asp Ile Asp Lys Pro

```

```
<210> 1301
<211> 490
<212> Amino acid
<213> Homo sapiens
```

804

```

385          390          395          400
Trp Val Ser Ser Gln Leu Ala Ala Thr Cys Asn Val Glu Pro Ser Leu
          405          410          415
Phe Thr Asn Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His His
          420          425          430
Leu Phe Pro Arg Met Pro Arg His Asn Tyr Ser Arg Val Ala Pro Leu
          435          440          445
Val Lys Ser Leu Cys Ala Lys His Gly Leu Ser Tyr Glu Val Lys Pro
          450          455          460
Phe Leu Thr Ala Leu Val Asp Ile Val Arg Ser Leu Lys Lys Ser Gly
465          470          475          480
Asp Ile Trp Leu Asp Ala Tyr Leu His Gln
          485          490

```

<210> 1302

<211> 110

<212>Amino acid

<213> Homo sapiens

```

<400> 1302
Lys Ser Arg Ala Thr Arg Leu Arg Glu Ser Ala Glu Met Thr Gly Phe
 1          5          10          15
Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser Cys Ser Arg Ser
          20          25          30
Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn Pro Ser Ser Phe Val Ala
          35          40          45
Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro Gly Ala Ser Pro
          50          55          60
Thr Thr Leu Ala Phe Pro Pro Val Val Leu Thr Gly Pro Ser Thr Asp
          65          70          75          80
Gly Ile Pro Phe Ala Leu Ser Leu Gln Arg Val Pro Phe Val Leu Pro
          85          90          95
Ser Pro Gln Val Ala Ser Leu Pro Leu Gly His Ser Arg Gly
          100          105          110

```

<210> 1303

<211> 138

<212>Amino acid

<213> Homo sapiens

```

<400> 1303
Ile Gln Tyr Arg Ser Asp Leu Glu Leu His Ser Ile Thr Met Lys Lys
 1          5          10          15
Ser Gly Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val Leu Ile Gly
          20          25          30
Val Gln Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser Cys Ile Ser
          35          40          45
Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp Leu Lys Gln
          50          55          60
Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile Ala Thr Leu
          65          70          75          80
Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala Asp Val Lys
          85          90          95
Glu Leu Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys Lys Lys Gln

```

100 105 110
 Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys Val Arg Lys
 115 120 125
 Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr
 130 135 138

<210> 1304
 <211> 1000
 <212> Amino acid
 <213> Homo sapiens

<400> 1304
 Ile Pro Gly Ser Thr Ile Ser Cys Arg Gly Cys Cys Gly Lys Trp Pro
 1 5 10 15
 Val Gln Glu Ala Asp Pro Pro Arg Ala Leu Arg Gly Arg Phe Pro
 20 25 30
 Ala Leu Leu Thr Arg His Cys Pro Ser Pro Arg Ala Glu Lys Glu Lys
 35 40 45
 Arg Ser Leu Arg Arg Cys Gly Cys Arg Pro Leu Leu Val Glu Leu Ala
 50 55 60
 Gly Pro Ala Gly Gln Ala Val Glu Val Leu Pro His Phe Glu Ser Leu
 65 70 75 80
 Gly Lys Gln Glu Lys Ile Pro Asn Lys Met Ser Ala Phe Arg Asn His
 85 90 95
 Cys Pro His Leu Asp Ser Val Gly Glu Ile Thr Lys Glu Asp Leu Ile
 100 105 110
 Gln Lys Ser Leu Gly Thr Cys Gln Asp Cys Lys Val Gln Gly Pro Asn
 115 120 125
 Leu Trp Ala Cys Leu Glu Asn Arg Cys Ser Tyr Val Gly Cys Gly Glu
 130 135 140
 Ser Gln Val Asp His Ser Thr Ile His Ser Gln Glu Thr Lys His Tyr
 145 150 155 160
 Leu Thr Val Asn Leu Thr Thr Leu Arg Val Trp Cys Tyr Ala Cys Ser
 165 170 175
 Lys Glu Val Phe Leu Asp Arg Lys Leu Gly Thr Gln Pro Ser Leu Pro
 180 185 190
 His Val Arg Gln Pro His Gln Ile Gln Glu Asn Ser Val Gln Asp Phe
 195 200 205
 Lys Ile Pro Ser Asn Thr Thr Leu Lys Thr Pro Leu Val Ala Val Phe
 210 215 220
 Asp Asp Leu Asp Ile Glu Ala Asp Glu Glu Asp Glu Leu Arg Ala Arg
 225 230 235 240
 Gly Leu Thr Gly Leu Lys Asn Ile Gly Asn Thr Cys Tyr Met Asn Ala
 245 250 255
 Ala Leu Gln Ala Leu Ser Asn Cys Pro Leu Thr Gln Phe Phe Leu
 260 265 270
 Asp Cys Gly Gly Leu Ala Arg Thr Asp Lys Lys Pro Ala Ile Cys Lys
 275 280 285
 Ser Tyr Leu Lys Leu Met Thr Glu Leu Trp Tyr Lys Ser Arg Pro Gly
 290 295 300
 Ser Val Val Pro Thr Thr Leu Phe Gln Gly Ile Lys Thr Val Asn Pro
 305 310 315 320
 Thr Phe Arg Gly Tyr Ser Gln Gln Asp Ala Gln Glu Phe Leu Arg Cys
 325 330 335
 Leu Met Asp Leu Leu His Glu Glu Leu Lys Glu Gln Val Met Glu Val
 340 345 350
 Glu Glu Asp Pro Gln Thr Ile Thr Thr Glu Glu Thr Met Glu Glu Asp
 355 360 365
 Lys Ser Gln Ser Asp Val Asp Phe Gln Ser Cys Glu Ser Cys Ser Asn

370	375	380
Ser Asp Arg Ala Glu Asn Glu Asn Gly Ser Arg Cys Phe Ser Glu Asp		
385	390	400
Asn Asn Glu Thr Thr Met Leu Ile Gln Asp Asp Glu Asn Asn Ser Glu		
	405	415
Met Ser Lys Asp Trp Gln Lys Glu Lys Met Cys Asn Lys Ile Asn Lys		
	420	430
Val Asn Ser Glu Gly Glu Phe Asp Lys Asp Arg Asp Ser Ile Ser Glu		
	435	445
Thr Val Asp Leu Asn Asn Gln Glu Thr Val Lys Val Gln Ile His Ser		
	450	460
Arg Ala Ser Glu Tyr Ile Thr Asp Val His Ser Asn Asp Leu Ser Thr		
465	470	480
Pro Gln Ile Leu Pro Ser Asn Glu Gly Val Asn Pro Arg Leu Ser Ala		
	485	495
Ser Pro Pro Lys Ser Gly Asn Leu Trp Pro Gly Leu Ala Pro Pro His		
	500	510
Lys Lys Ala Gln Ser Ala Ser Pro Lys Arg Lys Lys Gln His Lys Lys		
	515	525
Tyr Arg Ser Val Ile Ser Asp Ile Phe Asp Gly Thr Ile Ile Ser Ser		
	530	540
Val Gln Cys Leu Thr Cys Asp Arg Val Ser Val Thr Leu Glu Thr Phe		
545	550	560
Gln Asp Leu Ser Leu Pro Ile Pro Gly Lys Glu Asp Leu Ala Lys Leu		
	565	575
His Ser Ser Ser His Pro Thr Ser Ile Val Lys Ala Gly Ser Cys Gly		
	580	590
Glu Ala Tyr Ala Pro Gln Gly Trp Ile Ala Phe Phe Met Glu Tyr Val		
	595	605
Lys Arg Phe Val Val Ser Cys Val Pro Ser Trp Phe Trp Gly Pro Val		
	610	620
Val Thr Leu Gln Asp Cys Leu Ala Ala Phe Phe Ala Arg Asp Glu Leu		
625	630	640
Lys Gly Asp Asn Met Tyr Ser Cys Glu Lys Cys Lys Lys Leu Arg Asn		
	645	655
Gly Val Lys Phe Cys Lys Val Gln Asn Phe Pro Glu Ile Leu Cys Ile		
	660	670
His Leu Lys Arg Phe Arg His Glu Leu Met Phe Ser Thr Lys Ile Ser		
	675	685
Thr His Val Ser Phe Pro Leu Glu Gly Leu Asp Leu Gln Pro Phe Leu		
	690	700
Ala Lys Asp Ser Pro Ala Gln Ile Val Thr Tyr Asp Leu Leu Ser Val		
705	710	720
Ile Cys His His Gly Thr Ala Ser Ser Gly His Tyr Ile Ala Tyr Cys		
	725	735
Arg Asn Asn Leu Asn Asn Leu Trp Tyr Glu Phe Asp Asp Gln Ser Val		
	740	750
Thr Glu Val Ser Glu Ser Thr Val Gln Asn Ala Glu Ala Tyr Val Leu		
	755	765
Phe Tyr Arg Lys Ser Ser Glu Ala Gln Lys Glu Arg Arg Arg Ile		
	770	780
Ser Asn Leu Leu Asn Ile Met Glu Pro Ser Leu Leu Gln Phe Tyr Ile		
785	790	800
Ser Arg Gln Trp Leu Asn Lys Phe Lys Thr Phe Ala Glu Pro Gly Pro		
	805	815
Ile Ser Asn Asn Asp Phe Leu Cys Ile His Gly Gly Val Pro Pro Arg		
	820	830
Lys Ala Gly Tyr Ile Glu Asp Leu Val Leu Met Leu Pro Gln Asn Ile		
	835	845
Trp Asp Asn Leu Tyr Ser Arg Tyr Gly Gly Gly Pro Ala Val Asn His		
	850	860
Leu Tyr Ile Cys His Thr Cys Gln Ile Glu Ala Glu Lys Ile Glu Lys		
865	870	880
Arg Arg Lys Thr Glu Leu Glu Ile Phe Ile Arg Leu Asn Arg Ala Phe		

885 890 895
 Gln Lys Glu Asp Ser Pro Ala Thr Phe Tyr Cys Ile Ser Met Gln Trp
 900 905 910
 Phe Arg Glu Trp Glu Ser Phe Val Lys Gly Lys Asp Gly Asp Pro Pro
 915 920 925
 Gly Pro Ile Asp Asn Thr Lys Ile Ala Val Thr Lys Cys Gly Asn Val
 930 935 940
 Met Leu Arg Gln Gly Ala Asp Ser Gly Gln Ile Ser Glu Glu Thr Trp
 945 950 955 960
 Asn Phe Leu Gln Ser Ile Tyr Gly Gly Gly Pro Glu Val Ile Leu Arg
 965 970 975
 Pro Pro Val Val His Val Asp Pro Asp Ile Leu Gln Ala Glu Glu Lys
 980 985 990
 Ile Glu Val Glu Thr Arg Ser Leu
 995 1000

<210> 1305
 <211> 141
 <212> Amino acid
 <213> Homo sapiens

<400> 1305
 Ser Pro Ser Ala Ala Gly Gly Leu Ala Trp Val Ser Leu Ala Leu Gly
 1 5 10 15
 Ser Gly Ser Arg Gly Arg Asp His Ser Gly Ser Gly Val Gly Thr Ala
 20 25 30
 Met Ala Gly Ala Leu Val Arg Lys Ala Ala Asp Tyr Val Arg Ser Lys
 35 40 45
 Asp Phe Arg Asp Tyr Leu Met Ser Thr His Phe Trp Gly Pro Val Ala
 50 55 60
 Asn Trp Gly Leu Pro Ile Ala Ala Ile Asn Asp Met Lys Lys Ser Pro
 65 70 75 80
 Glu Ile Ile Ser Gly Arg Met Thr Phe Ala Leu Cys Cys Tyr Ser Leu
 85 90 95
 Thr Phe Met Arg Phe Ala Tyr Lys Val Gln Pro Arg Asn Trp Leu Leu
 100 105 110
 Phe Ala Cys His Ala Thr Asn Glu Val Ala Gln Leu Ile Gln Gly Gly
 115 120 125
 Arg Leu Ile Lys His Glu Met Thr Lys Thr Ala Ser Ala
 130 135 140 141

<210> 1306
 <211> 386
 <212> Amino acid
 <213> Homo sapiens

<400> 1306
 Leu Gly Ser Arg Gln Ala Ala Gly Thr Met Arg Gly Gln Arg Ser Leu
 1 5 10 15
 Leu Leu Gly Pro Ala Arg Leu Cys Leu Arg Leu Leu Leu Leu Gly
 20 25 30
 Tyr Arg Arg Arg Cys Pro Pro Leu Arg Gly Leu Val Gln Arg Trp
 35 40 45
 Arg Tyr Gly Lys Val Cys Leu Arg Ser Leu Leu Tyr Asn Ser Phe Gly

50	55	60
Gly Ser Asp Thr Ala Val	Asp Ala Ala Phe Glu Pro Val Tyr Trp Leu	
65	70	75
Val Asp Asn Val Ile Arg Trp Phe Gly Val Val Phe Val Val Leu Val		80
	85	90
Ile Val Leu Thr Gly Ser Ile Val Ala Ile Ala Tyr Leu Cys Val Leu		95
	100	105
Pro Leu Ile Leu Arg Thr Tyr Ser Val Pro Arg Leu Cys Trp His Phe		110
	115	120
Phe Tyr Ser His Trp Asn Leu Ile Leu Ile Val Phe His Tyr Tyr Gln		125
	130	135
Ala Ile Thr Thr Pro Pro Gly Tyr Pro Pro Gln Gly Arg Asn Asp Ile		140
145	150	155
Ala Thr Val Ser Ile Cys Lys Lys Cys Ile Tyr Pro Lys Pro Ala Arg		160
	165	170
Thr His His Cys Ser Ile Cys Asn Arg Cys Val Leu Lys Met Asp His		175
	180	185
His Cys Pro Trp Leu Asn Asn Cys Val Gly His Tyr Asn His Arg Tyr		190
	195	200
Phe Phe Ser Phe Cys Phe Phe Met Thr Leu Gly Cys Val Tyr Cys Ser		205
	210	215
Tyr Gly Ser Trp Asp Leu Phe Arg Glu Ala Tyr Ala Ala Ile Glu Lys		220
225	230	235
Met Lys Gln Leu Asp Lys Asn Lys Leu Gln Ala Val Ala Asn Gln Thr		240
	245	250
Tyr His Gln Thr Pro Pro Pro Thr Phe Ser Phe Arg Glu Arg Met Thr		255
	260	265
His Lys Ser Leu Val Tyr Leu Trp Phe Leu Cys Ser Ser Val Ala Leu		270
	275	280
Ala Leu Gly Ala Leu Thr Val Trp His Ala Val Leu Ile Ser Arg Gly		285
	290	295
Glu Thr Ser Ile Glu Arg His Ile Asn Lys Lys Glu Arg Arg Arg Leu		300
305	310	315
Gln Ala Lys Gly Arg Val Phe Arg Asn Pro Tyr Asn Tyr Gly Cys Leu		320
	325	330
Asp Asn Trp Lys Val Phe Leu Gly Val Asp Thr Gly Arg His Trp Leu		335
	340	345
Thr Arg Val Leu Leu Pro Ser Ser His Leu Pro His Gly Asn Gly Met		350
	355	360
Ser Trp Glu Pro Pro Pro Trp Val Thr Ala His Ser Ala Ser Val Met		365
	370	375
Ala Val		380
385	386	

<210> 1307
 <211> 298
 <212> Amino acid
 <213> Homo sapiens

<400> 1307
 Ala Thr Arg Arg Arg Ala Ala Glu Ala Gly Met Ala Ala Val Leu Gln
 1 5 10 15
 Arg Val Glu Arg Leu Ser Asn Arg Val Val Arg Val Leu Gly Cys Asn
 20 25 30
 Pro Gly Pro Met Thr Leu Gln Gly Thr Asn Thr Tyr Leu Val Gly Thr
 35 40 45
 Gly Pro Arg Arg Ile Leu Ile Asp Thr Gly Glu Pro Ala Ile Pro Glu
 50 55 60
 Tyr Ile Ser Cys Leu Lys Gln Ala Leu Thr Glu Phe Asn Thr Ala Ile

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65          70          75          80
Gln Glu Ile Val Val Thr His Trp His Arg Asp His Ser Gly Gly Ile
      85          90          95
Gly Asp Ile Cys Lys Ser Ile Asn Asn Asp Thr Thr Tyr Cys Ile Lys
      100          105          110
Lys Leu Pro Arg Asn Pro Gln Arg Glu Glu Ile Ile Gly Asn Gly Glu
      115          120          125
Gln Gln Tyr Val Tyr Leu Lys Asp Gly Asp Val Ile Lys Thr Glu Gly
      130          135          140
Ala Thr Leu Arg Val Leu Tyr Thr Pro Gly His Thr Asp Asp His Met
      145          150          155          160
Ala Leu Leu Leu Glu Glu Glu Asn Ala Ile Phe Ser Gly Asp Cys Ile
      165          170          175
Leu Gly Glu Gly Thr Thr Val Phe Glu Asp Leu Tyr Asp Tyr Met Asn
      180          185          190
Ser Leu Lys Glu Leu Leu Lys Ile Lys Ala Asp Ile Ile Tyr Pro Gly
      195          200          205
His Gly Pro Val Ile His Asn Ala Glu Ala Lys Ile Gln Gln Tyr Ile
      210          215          220
Ser His Arg Asn Ile Arg Glu Gln Gln Ile Leu Thr Leu Phe Arg Glu
      225          230          235          240
Asn Phe Glu Lys Ser Phe Thr Val Met Glu Leu Val Lys Ile Ile Tyr
      245          250          255
Lys Asn Thr Pro Glu Asn Leu His Glu Met Ala Lys His Asn Leu Leu
      260          265          270
Leu His Leu Lys Lys Leu Glu Lys Glu Gly Lys Ile Phe Ser Asn Thr
      275          280          285
Asp Pro Asp Lys Lys Trp Lys Ala His Leu
      290          295          298

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<210> 1308

<211> 306

<212>Amino acid

<213> Homo sapiens

<400> 1308

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Glu Leu His Arg Ala Gly Gln Val Ala Gly Gly Ala Arg Arg Ser Arg
1          5          10          15
Arg Glu Ser Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu Ala
      20          25          30
Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp Glu
      35          40          45
Val Ile Phe Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro Ser
      50          55          60
Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met Met
      65          70          75          80
Glu Ala Tyr Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile Gly
      85          90          95
Asp Met Met Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn Lys
      100          105          110
Glu Asn Leu Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro Ile
      115          120          125
Ser Pro Glu Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr Arg
      130          135          140
Ser Ser Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly Ala
      145          150          155          160
Glu Glu Glu Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe Pro
      165          170          175
Thr Cys Ser Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg Gly

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      180      185      190
Asp Leu Glu Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu Gly
      195      200      205
Pro Ala Ala Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu Arg
      210      215      220
Gly Pro Gln Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr Met
225      230      235      240
Met Val Asp Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala Pro
      245      250      255
Lys Glu Ala Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val Val
      260      265      270
Ser Thr Lys Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala Glu
      275      280      285
Glu Met Lys Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr Arg
290      295      300
Phe His
305 306

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<210> 1309
<211> 174
<212>Amino acid
<213> Homo sapiens

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      <400> 1309
Phe Ile Thr Gly Lys Gly Ile Val Ala Ile Leu Arg Cys Leu Gln Phe
  1      5      10      15
Asn Glu Thr Leu Thr Glu Leu Arg Phe His Asn Gln Arg His Met Leu
      20      25      30
Gly His His Ala Glu Met Glu Ile Ala Arg Leu Leu Lys Ala Asn Asn
      35      40      45
Thr Leu Leu Lys Met Gly Tyr His Phe Glu Leu Pro Gly Pro Arg Met
  50      55      60
Val Val Thr Asn Leu Leu Thr Arg Asn Gln Asp Lys Gln Arg Gln Lys
  65      70      75      80
Arg Gln Glu Glu Gln Lys Gln Gln Gln Leu Lys Glu Gln Lys Lys Leu
      85      90      95
Ile Ala Met Leu Glu Asn Gly Leu Gly Leu Pro Pro Gly Met Trp Glu
      100      105      110
Leu Leu Gly Gly Pro Lys Pro Asp Ser Arg Met Gln Glu Phe Phe Gln
      115      120      125
Pro Pro Pro Pro Arg Pro Pro Asn Pro Gln Asn Val Pro Phe Ser Gln
      130      135      140
Arg Ser Glu Met Met Lys Lys Pro Ser Gln Ala Pro Lys Tyr Arg Thr
145      150      155      160
Asp Pro Asp Ser Phe Arg Val Val Lys Leu Lys Arg Ile Gln
      165      170      174

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<210> 1310
<211> 616
<212>Amino acid
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(616)
<223> X = any amino acid or stop code

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<400> 1310

Gly	Gly	Arg	Ala	Gly	Thr	Gln	Cys	Cys	Trp	Arg	Ala	Gly	Ala	Arg	Leu	1	5	10	15
Arg	Gly	Ile	Ser	Pro	Ser	Pro	Ala	Leu	Pro	Glu	Ala	Pro	Gly	Leu	Cys	20	25	30	
Arg	Val	Arg	Ala	Gly	Leu	Gly	Ala	Gly	Ala	Leu	Gly	Arg	Ser	Pro	Ala	35	40	45	
Gly	Arg	Arg	Arg	Arg	Gly	Pro	Arg	Val	Ser	Ser	Ser	Pro	Ala	Pro	His	50	55	60	
Pro	Arg	Arg	Val	Leu	Cys	Arg	Cys	Leu	Leu	Phe	Leu	Phe	Phe	Ser	Cys	65	70	75	80
His	Asp	Arg	Arg	Gly	Asp	Ser	Gln	Pro	Tyr	Gln	Ala	Leu	Lys	Tyr	Ser	85	90	95	
Ser	Lys	Ser	His	Pro	Ser	Ser	Gly	Asp	His	Arg	His	Glu	Lys	Met	Arg	100	105	110	
Asp	Ala	Gly	Asp	Pro	Ser	Pro	Pro	Asn	Lys	Met	Leu	Arg	Arg	Ser	Asp	115	120	125	
Ser	Pro	Glu	Asn	Lys	Tyr	Ser	Asp	Ser	Thr	Gly	His	Ser	Lys	Ala	Lys	130	135	140	
Asn	Val	His	Thr	His	Arg	Val	Arg	Glu	Arg	Asp	Gly	Gly	Thr	Ser	Tyr	145	150	155	160
Ser	Pro	Gln	Glu	Asn	Ser	His	Asn	His	Ser	Ala	Leu	His	Ser	Ser	Asn	165	170	175	
Phe	Thr	Phe	Phe	Leu	Ile	Pro	Ser	Asn	Xaa	Pro	Gln	Gly	Lys	Thr	Phe	180	185	190	
Arg	Ile	Ala	Pro	Tyr	Asp	Ser	Ala	Asp	Asp	Trp	Ser	Leu	Glu	His	Ile	195	200	205	
Ser	Ser	Ser	Gly	Glu	Lys	Tyr	Tyr	Tyr	Asn	Cys	Arg	Thr	Glu	Val	Ser	210	215	220	
Gln	Trp	Gly	Lys	Thr	Pro	Lys	Ser	Gly	Leu	Glu	Arg	Gly	Gln	Arg	Gln	225	230	235	240
Lys	Glu	Ala	Asn	Lys	Met	Ala	Val	Asn	Ser	Phe	Pro	Lys	Asp	Arg	Asp	245	250	255	
Tyr	Arg	Arg	Glu	Val	Met	Gln	Ala	Thr	Ala	Thr	Ser	Gly	Phe	Ala	Ser	260	265	270	
Gly	Lys	Ser	Thr	Ser	Gly	Asp	Lys	Pro	Val	Ser	His	Ser	Cys	Thr	Thr	275	280	285	
Pro	Ser	Thr	Ser	Ser	Ala	Ser	Gly	Leu	Asn	Pro	Thr	Ser	Ala	Pro	Pro	290	295	300	
Thr	Ser	Ala	Ser	Ala	Val	Pro	Val	Ser	Pro	Val	Pro	Gln	Ser	Pro	Ile	305	310	315	320
Pro	Pro	Leu	Leu	Gln	Asp	Pro	Asn	Leu	Leu	Arg	Gln	Leu	Leu	Pro	Ala	325	330	335	
Leu	Glu	Ala	Thr	Leu	Gln	Leu	Asn	Asn	Ser	Asn	Val	Asp	Ile	Ser	Ile	340	345	350	
Ile	Asn	Glu	Val	Leu	Thr	Gly	Asp	Val	Thr	Gln	Ala	Ser	Leu	Gln	Thr	355	360	365	
Ile	Ile	His	Lys	Cys	Leu	Thr	Ala	Gly	Pro	Ser	Val	Phe	Lys	Ile	Thr	370	375	380	
Ser	Leu	Ile	Ser	Gln	Ala	Ala	Gln	Leu	Ser	Thr	Gln	Ala	Gln	Ala	Ser	385	390	395	400
Asn	Gln	Ser	Pro	Met	Ser	Leu	Thr	Ser	Asp	Ala	Ser	Ser	Pro	Arg	Ser	405	410	415	
Tyr	Val	Ser	Pro	Arg	Asn	Lys	Ala	His	Leu	Lys	Leu	Asn	Thr	Val	Pro	420	425	430	
Ile	Gln	Thr	Phe	Gly	Phe	Ser	Thr	Pro	Pro	Val	Ser	Ser	Gln	Pro	Lys	435	440	445	
Val	Ser	Thr	Pro	Val	Val	Lys	Gln	Gly	Pro	Val	Ser	Gln	Ser	Ala	Thr	450	455	460	
Gln	Gln	Pro	Val	Thr	Ala	Asp	Lys	Gln	Gln	Gly	His	Glu	Pro	Val	Ser	465	470	475	480

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<210> 1311
<211> 387
<212> Amino acid
<213> Homo sapiens
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813

Asp Pro Ser Thr Lys Lys Gln His Thr Ile Trp Pro Ser Pro His Gln
 275 280 285
 Gly Asn Ser Pro Asp Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser
 290 295 300
 Glu Ala Asp Leu Ala Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe
 305 310 315 320
 Arg Val Cys Ser Gly Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr
 325 330 335
 Asp Asn Met Ala Val Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val
 340 345 350
 Ser Val Glu Ser Gly Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro
 355 360 365
 Asp Gln Met Gly Arg Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile
 370 375 380
 Tyr Gly Tyr
 385 387

<210> 1312
 <211> 470
 <212> Amino acid
 <213> Homo sapiens

<400> 1312
 Thr Glu Trp Gly Leu Ser Gly Ser Cys Pro Gly Cys Ser Pro Leu Glu
 1 5 10 15
 Pro Gly Ser Arg Gly Arg Gly Ala Ala Ala Trp Arg Ile Leu Arg Cys
 20 25 30
 Arg Arg Leu Pro Glu Pro Ser Pro Phe Leu Thr Gln Pro Asn Leu Ala
 35 40 45
 Gln Ser Gln Pro Pro Ala Pro Val Pro Val Thr Asp Pro Ser Val Thr
 50 55 60
 Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser Leu
 65 70 75 80
 Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu Ile Thr
 85 90 95
 Ser Leu Asp Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn Ala Asp Val
 100 105 110
 Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe Ser Gln Met Leu
 115 120 125
 His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile Lys Glu Glu Phe Pro
 130 135 140
 Asn Glu Asn Gln Val Val Phe Ala Arg Val Asp Cys Asp Gln His Ser
 145 150 155 160
 Asp Ile Ala Gln Arg Tyr Arg Ile Ser Lys Tyr Pro Thr Leu Lys Leu
 165 170 175
 Phe Arg Asn Gly Met Met Met Lys Arg Glu Tyr Arg Gly Gln Arg Ser
 180 185 190
 Val Lys Ala Leu Ala Asp Tyr Ile Arg Gln Gln Lys Ser Asp Pro Ile
 195 200 205
 Gln Glu Ile Arg Asp Leu Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys
 210 215 220
 Arg Asn Ile Ile Gly Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg
 225 230 235 240
 Val Phe Glu Arg Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu
 245 250 255
 Ser Ala Phe Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn
 260 265 270
 Ile Ile Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu
 275 280 285

Gly Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys
 290 295 300
 Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu Leu
 305 310 315 320
 Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys Glu Asp
 325 330 335
 Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg Gln Leu Ile
 340 345 350
 Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp Cys Asp Lys Phe
 355 360 365
 Arg His Pro Leu Leu His Ile Gln Lys Thr Pro Ala Asp Cys Pro Val
 370 375 380
 Ile Ala Ile Asp Ser Phe Arg His Met Tyr Val Phe Gly Asp Phe Lys
 385 390 395 400
 Asp Val Leu Ile Pro Gly Lys Leu Lys Gln Phe Val Phe Asp Leu His
 405 410 415
 Ser Gly Lys Leu His Arg Glu Phe His His Gly Pro Asp Pro Thr Asp
 420 425 430
 Thr Ala Pro Gly Glu Gln Ala Gln Asp Val Ala Ser Ser Pro Pro Glu
 435 440 445
 Ser Ser Phe Gln Lys Leu Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu
 450 455 460
 Arg Asp Arg Asp Glu Leu
 465 470

<210> 1313

<211> 262

<212> Amino acid

<213> Homo sapiens

<400> 1313

Leu Thr Pro Ser Val Gly Pro Val Phe Pro Gly Arg Pro Thr Arg Pro
 1 5 10 15
 Leu Ala Ser Pro Phe Pro Val Pro Leu His Arg Cys Ser Ala Gly Ser
 20 25 30
 Gln Pro Pro Gly Pro Val Pro Glu Gly Leu Ile Arg Ile Tyr Ser Met
 35 40 45
 Arg Phe Cys Pro Tyr Ser His Arg Thr Arg Leu Val Leu Lys Ala Lys
 50 55 60
 Asp Ile Arg His Glu Val Val Asn Ile Asn Leu Arg Asn Lys Pro Glu
 65 70 75 80
 Trp Tyr Tyr Thr Lys His Pro Phe Gly His Ile Pro Val Leu Glu Thr
 85 90 95
 Ser Gln Cys Gln Leu Ile Tyr Glu Ser Val Ile Ala Cys Glu Tyr Leu
 100 105 110
 Asp Asp Ala Tyr Pro Gly Arg Lys Leu Phe Pro Tyr Asp Pro Tyr Glu
 115 120 125
 Arg Ala Arg Gln Lys Met Leu Leu Glu Leu Phe Cys Lys Val Pro His
 130 135 140
 Leu Thr Lys Glu Cys Leu Val Ala Leu Arg Cys Gly Arg Glu Cys Thr
 145 150 155 160
 Asn Leu Lys Ala Ala Leu Arg Gln Glu Phe Ser Asn Leu Glu Glu Ile
 165 170 175
 Leu Glu Tyr Gln Asn Thr Thr Phe Phe Gly Gly Thr Cys Ile Ser Met
 180 185 190
 Ile Asp Tyr Leu Leu Trp Pro Trp Phe Glu Arg Leu Asp Val Tyr Gly
 195 200 205
 Ile Leu Asp Cys Val Ser His Thr Pro Ala Leu Arg Leu Trp Ile Ser
 210 215 220

Ala Met Lys Trp Asp Pro Thr Val Cys Ala Leu Leu Met Asp Lys Ser
 225 230 235 240
 Ile Phe Gln Gly Phe Leu Asn Leu Tyr Phe Gln Asn Asn Pro Asn Ala
 245 250 255
 Phe Asp Phe Gly Leu Cys
 260 262

<210> 1314
 <211> 173
 <212> Amino acid
 <213> Homo sapiens

<400> 1314
 Asn Thr Ala Thr Asn Met Thr Gln Pro Asn Ala Gly Thr Arg Lys Tyr
 1 5 10 15
 Ser Val Pro Ala Ile Ser Val His Thr Ser Ser Ser Ser Phe Ala Tyr
 20 25 30
 Asp Arg Glu Phe Leu Arg Thr Leu Pro Gly Phe Leu Ile Val Ala Glu
 35 40 45
 Ile Val Leu Gly Leu Leu Val Trp Thr Leu Ile Ala Gly Thr Glu Tyr
 50 55 60
 Phe Arg Val Pro Ala Phe Gly Trp Val Met Phe Val Ala Val Phe Tyr
 65 70 75 80
 Trp Val Leu Thr Val Phe Phe Leu Ile Ile Tyr Ile Thr Met Thr Tyr
 85 90 95
 Thr Arg Ile Pro Gln Val Pro Trp Thr Thr Val Gly Leu Cys Phe Asn
 100 105 110
 Gly Ser Ala Phe Val Leu Tyr Leu Ser Ala Ala Val Val Asp Ala Ser
 115 120 125
 Ser Val Ser Pro Glu Arg Asp Ser His Asn Phe Asn Ser Trp Ala Ala
 130 135 140
 Ser Ser Phe Phe Ala Phe Leu Val Thr Ile Cys Tyr Ala Gly Asn Thr
 145 150 155 160
 Tyr Phe Ser Phe Ile Ala Trp Arg Ser Arg Thr Ile Gln
 165 170 173

<210> 1315
 <211> 259
 <212> Amino acid
 <213> Homo sapiens

<400> 1315
 Gly Leu Arg Asp Pro Phe Arg Arg Lys Arg Arg Leu Lys Pro Gln Val
 1 5 10 15
 Lys Met Ser Asn Tyr Val Asn Asp Met Trp Pro Gly Ser Pro Gln Glu
 20 25 30
 Lys Asp Ser Pro Ser Thr Ser Arg Ser Gly Gly Ser Ser Arg Leu Ser
 35 40 45
 Ser Arg Ser Arg Ser Arg Ser Phe Ser Arg Ser Ser Arg Ser His Ser
 50 55 60
 Arg Val Ser Ser Arg Phe Ser Ser Arg Ser Arg Ser Lys Ser Arg
 65 70 75 80
 Ser Arg Ser Arg Arg Arg His Gln Arg Lys Tyr Arg Arg Tyr Ser Arg
 85 90 95

Ser Tyr Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Arg Tyr Arg Glu
 100 105 110
 Arg Arg Tyr Gly Phe Thr Arg Arg Tyr Tyr Arg Ser Pro Ser Arg Tyr
 115 120 125
 Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Gly Arg Ser Tyr Cys
 130 135 140
 Gly Arg Ala Tyr Ala Ile Ala Arg Gly Gln Arg Tyr Tyr Gly Phe Gly
 145 150 155 160
 Arg Thr Val Tyr Pro Glu Glu His Ser Arg Trp Arg Asp Arg Ser Arg
 165 170 175
 Thr Arg Ser Arg Ser Arg Thr Pro Phe Arg Leu Ser Glu Lys Asp Arg
 180 185 190
 Met Glu Leu Leu Glu Ile Ala Lys Thr Asn Ala Ala Lys Ala Leu Gly
 195 200 205
 Thr Thr Asn Ile Asp Leu Pro Ala Ser Leu Arg Thr Val Pro Ser Ala
 210 215 220
 Lys Glu Thr Ser Arg Gly Ile Gly Val Ser Ser Asn Gly Ala Lys Pro
 225 230 235 240
 Glu Val Ser Ile Leu Gly Leu Ser Glu Gln Asn Phe Gln Lys Ala Asn
 245 250 255
 Cys Gln Ile
 259

<210> 1316
 <211> 678
 <212> Amino acid
 <213> Homo sapiens

<400> 1316
 Ala Glu Gly Ser Thr Met Asp Leu Thr Lys Met Gly Met Ile Gln Leu
 1 5 10 15
 Gln Asn Pro Asn His Pro Thr Gly Leu Leu Cys Lys Ala Asn Gln Met
 20 25 30
 Arg Leu Ala Gly Thr Leu Cys Asp Val Val Ile Met Val Asp Ser Gln
 35 40 45
 Glu Phe His Ala His Arg Thr Val Leu Ala Cys Thr Ser Lys Met Phe
 50 55 60
 Glu Ile Leu Phe His Arg Asn Ser Gln His Tyr Thr Leu Asp Phe Leu
 65 70 75 80
 Ser Pro Lys Thr Phe Gln Gln Ile Leu Glu Tyr Ala Tyr Thr Ala Thr
 85 90 95
 Leu Gln Ala Lys Ala Glu Asp Leu Asp Asp Leu Leu Tyr Ala Ala Glu
 100 105 110
 Ile Leu Glu Ile Glu Tyr Leu Glu Glu Gln Cys Leu Lys Met Leu Glu
 115 120 125
 Thr Ile Gln Ala Ser Asp Asp Asn Asp Thr Glu Ala Thr Met Ala Asp
 130 135 140
 Gly Gly Ala Glu Glu Lys Lys Asp Arg Lys Ala Arg Tyr Leu Lys Asn
 145 150 155 160
 Ile Phe Ile Ser Lys His Ser Ser Glu Glu Ser Gly Tyr Ala Ser Val
 165 170 175
 Ala Gly Gln Ser Leu Pro Gly Pro Met Val Asp Gln Ser Pro Ser Val
 180 185 190
 Ser Thr Ser Phe Gly Leu Ser Ala Met Ser Pro Thr Lys Ala Ala Val
 195 200 205
 Asp Ser Leu Met Thr Ile Gly Gln Ser Leu Leu Gln Gly Thr Leu Gln
 210 215 220
 Pro Pro Ala Gly Pro Glu Glu Pro Thr Leu Ala Gly Gly Gly Arg His
 225 230 235 240

Pro Gly Val Ala Glu Val Lys Thr Glu Met Met Gln Val Asp Glu Val
 245 250 255
 Pro Ser Gln Asp Ser Pro Gly Ala Ala Glu Ser Ser Ile Ser Gly Gly
 260 265 270
 Met Gly Asp Lys Val Glu Glu Arg Gly Lys Glu Gly Pro Gly Thr Pro
 275 280 285
 Thr Arg Ser Ser Val Ile Thr Ser Ala Arg Glu Leu His Tyr Gly Arg
 290 295 300
 Glu Glu Ser Ala Glu Gln Val Pro Pro Pro Ala Glu Ala Gly Gln Ala
 305 310 315 320
 Pro Thr Gly Arg Pro Glu His Pro Ala Pro Pro Pro Glu Lys His Leu
 325 330 335
 Gly Ile Tyr Ser Val Leu Pro Asn His Lys Ala Asp Ala Val Leu Ser
 340 345 350
 Met Pro Ser Ser Val Thr Ser Gly Leu His Val Gln Pro Ala Leu Ala
 355 360 365
 Val Ser Met Asp Phe Ser Thr Tyr Gly Gly Leu Leu Pro Gln Gly Phe
 370 375 380
 Ile Gln Arg Glu Leu Phe Ser Lys Leu Gly Glu Leu Ala Val Gly Met
 385 390 395 400
 Lys Ser Glu Ser Arg Thr Ile Gly Glu Gln Cys Ser Val Cys Gly Val
 405 410 415
 Glu Leu Pro Asp Asn Glu Ala Val Glu Gln His Arg Lys Leu His Ser
 420 425 430
 Gly Met Lys Thr Tyr Gly Cys Glu Leu Cys Gly Lys Arg Phe Leu Asp
 435 440 445
 Ser Leu Arg Leu Arg Met His Leu Leu Ala His Ser Ala Gly Ala Lys
 450 455 460
 Ala Phe Val Cys Asp Gln Cys Gly Ala Gln Phe Ser Lys Glu Asp Ala
 465 470 475 480
 Leu Glu Thr His Arg Gln Thr His Thr Gly Thr Asp Met Ala Val Phe
 485 490 495
 Cys Leu Leu Cys Gly Lys Arg Phe Gln Ala Gln Ser Ala Leu Gln Gln
 500 505 510
 His Met Glu Val His Ala Gly Val Arg Ser Tyr Ile Cys Ser Glu Cys
 515 520 525
 Asn Arg Thr Phe Pro Ser His Thr Ala Leu Lys Arg His Leu Arg Ser
 530 535 540
 His Thr Gly Asp His Pro Tyr Glu Cys Glu Phe Cys Gly Ser Cys Phe
 545 550 555 560
 Arg Asp Glu Ser Thr Leu Lys Ser His Lys Arg Ile His Thr Gly Glu
 565 570 575
 Lys Pro Tyr Glu Cys Asn Gly Cys Gly Lys Lys Phe Ser Leu Lys His
 580 585 590
 Gln Leu Glu Thr His Tyr Arg Val His Thr Gly Glu Lys Pro Phe Glu
 595 600 605
 Cys Lys Leu Cys His Gln Arg Ser Arg Asp Tyr Ser Ala Met Ile Lys
 610 615 620
 His Leu Arg Thr His Asn Gly Ala Ser Pro Tyr Gln Cys Thr Ile Cys
 625 630 635 640
 Thr Glu Tyr Cys Pro Ser Leu Ser Ser Met Gln Lys His Met Lys Gly
 645 650 655
 His Lys Pro Glu Glu Ile Pro Pro Asp Trp Arg Ile Glu Lys Thr Tyr
 660 665 670
 Leu Tyr Leu Cys Tyr Val
 675 678

<210> 1317

<211> 74

<212> Amino acid

<213> Homo sapiens

<400> 1317

```

Ile Trp Glu Ala Pro Thr Leu Ile Phe Thr Leu Ala Gly Gly Arg Ala
 1          5          10          15
Leu Gly His Pro Pro Met Gln Lys Gly Ser Gln Gly Cys Ala Leu Pro
          20          25          30
His Pro Leu Pro Gly Ala Ser Leu Pro Ala Gln Pro Gly Pro Ala Asp
          35          40          45
His Arg Gly Trp Glu Cys Arg Ile Gly Gly Glu Ala Ser Val Phe Thr
          50          55          60
His Leu Phe Cys Leu Pro His Ser Pro Thr
 65          70          74

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<210> 1318

<211> 351

<212> Amino acid

<213> Homo sapiens

<400> 1318

```

Ala Ser Gly Ser Pro Ala Pro Ser Ser Ser Ser Ala Met Ala Ala Ala
 1          5          10          15
Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly Leu His Leu
          20          25          30
Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp Pro Asp Arg
          35          40          45
Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr Asp Arg Tyr
          50          55          60
Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys Cys Val Gly
 65          70          75          80
Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile Gln Cys Gln
          85          90          95
Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys Lys Thr Asp
          100          105          110
Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser Cys Glu Gly
          115          120          125
Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser Cys Gly Leu
          130          135          140
Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys Leu Lys Glu
          145          150          155          160
Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr Tyr Tyr Lys
          165          170          175
Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile Thr Ile Val
          180          185          190
Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp
          195          200          205
Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His
          210          215          220
Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro Pro Gly Phe
          225          230          235          240
Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser
          245          250          255
Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly
          260          265          270
Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu
          275          280          285
Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr
          290          295          300

```

Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser
 305 310 315 320
 Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp
 325 330 335
 Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
 340 345 350 351

<210> 1319
 <211> 310
 <212> Amino acid
 <213> Homo sapiens

<400> 1319
 Gly Arg Cys Gly Ala Met Ala Ala Gly Leu Ala Arg Leu Leu Leu Leu
 1 5 10 15
 Leu Gly Leu Ser Ala Gly Gly Pro Ala Pro Ala Gly Ala Ala Lys Met
 20 25 30
 Lys Val Val Glu Glu Pro Asn Ala Phe Gly Val Asn Asn Pro Phe Leu
 35 40 45
 Pro Gln Ala Ser Arg Leu Gln Ala Lys Arg Asp Pro Ser Pro Val Ser
 50 55 60
 Gly Pro Val His Leu Phe Arg Leu Ser Gly Lys Cys Phe Ser Leu Val
 65 70 75 80
 Glu Ser Thr Tyr Lys Tyr Glu Phe Cys Pro Phe His Asn Val Thr Gln
 85 90 95
 His Glu Gln Thr Phe Arg Trp Asn Ala Tyr Ser Gly Ile Leu Gly Ile
 100 105 110
 Trp His Glu Trp Glu Ile Ala Asn Asn Thr Phe Thr Gly Met Trp Met
 115 120 125
 Arg Asp Gly Asp Ala Cys Arg Ser Arg Ser Arg Gln Ser Lys Val Glu
 130 135 140
 Leu Ala Cys Gly Lys Ser Asn Arg Leu Ala His Val Ser Glu Pro Ser
 145 150 155 160
 Thr Cys Val Tyr Ala Leu Thr Phe Glu Thr Pro Leu Val Cys His Pro
 165 170 175
 His Ala Leu Leu Val Tyr Pro Thr Leu Pro Glu Ala Leu Gln Arg Gln
 180 185 190
 Trp Asp Gln Val Glu Gln Asp Leu Ala Asp Glu Leu Ile Thr Pro Gln
 195 200 205
 Gly His Glu Lys Leu Leu Arg Thr Leu Phe Glu Asp Ala Gly Tyr Leu
 210 215 220
 Lys Thr Pro Glu Glu Asn Glu Pro Thr Gln Leu Glu Gly Gly Pro Asp
 225 230 235 240
 Ser Leu Gly Phe Glu Thr Leu Glu Asn Cys Arg Lys Ala His Lys Glu
 245 250 255
 Leu Ser Lys Glu Ile Lys Arg Leu Lys Gly Leu Leu Thr Gln His Gly
 260 265 270
 Ile Pro Tyr Thr Arg Pro Thr Glu Thr Ser Asn Leu Glu His Leu Gly
 275 280 285
 His Glu Thr Pro Arg Ala Lys Ser Pro Glu Gln Leu Arg Gly Asp Pro
 290 295 300
 Gly Leu Arg Gly Ser Leu
 305 310

<210> 1320
 <211> 313
 <212> Amino acid
 <213> Homo sapiens

<400> 1320

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Asn Ser Phe Trp Ser Val Leu Phe Leu Val Gln Glu Glu Thr Glu Val
 1           5           10           15
Ala Arg Cys Asn Ala Gln His Arg Leu Arg Gln Ser Arg Asp Ser Lys
          20           25           30
Pro Asp Pro Ser Phe Arg Ser Gln Pro Ile Asp Ser Ser Ile Ser Phe
          35           40           45
Ala Gly Ser Asp Ile Gln Pro Leu Phe Ser Phe Ala Ser Val Asp Gly
          50           55           60
Thr Gln Val Gly Glu Ala Glu Glu Trp Ala Gly Pro Trp Ala Glu Ala
          65           70           75           80
Thr Leu Leu Pro Gly Pro Gly Asn Arg Trp Pro Pro Arg Ala Gly Leu
          85           90           95
Ser Gly Asn Trp Leu Glu Glu Asp Gly Asp Trp Pro Ser Leu Pro Glu
          100          105          110
Val Val Gly Phe Val Ser Glu Arg Glu Leu Phe Arg Asp Ala Leu Gly
          115          120          125
Ala Gly Cys Arg Ile Leu Leu Ile Cys Glu Met Gln Leu Thr His Gln
          130          135          140
Leu Asp Leu Phe Pro Glu Cys Arg Val Thr Leu Leu Leu Phe Lys Asp
          145          150          155          160
Val Lys Asn Ala Gly Asp Leu Arg Arg Lys Ala Met Glu Gly Thr Ile
          165          170          175
Asp Gly Ser Leu Ile Asn Pro Thr Val Ile Val Asp Pro Phe Gln Ile
          180          185          190
Leu Val Ala Ala Asn Lys Ala Val His Leu Tyr Lys Leu Gly Lys Met
          195          200          205
Lys Thr Arg Thr Leu Ser Thr Glu Ile Ile Phe Asn Leu Ser Pro Asn
          210          215          220
Asn Asn Ile Ser Glu Ala Leu Lys Lys Phe Gly Ile Ser Ala Asn Asp
          225          230          235          240
Thr Ser Ile Leu Ile Val Tyr Ile Glu Glu Gly Glu Lys Gln Ile Asn
          245          250          255
Gln Glu Tyr Leu Ile Ser Gln Val Glu Gly His Gln Val Ser Leu Lys
          260          265          270
Asn Leu Pro Glu Ile Met Asn Ile Thr Glu Val Lys Lys Ile Tyr Lys
          275          280          285
Leu Ser Ser Gln Glu Glu Ser Ile Gly Thr Leu Leu Asp Ala Ile Ile
          290          295          300
Cys Arg Met Ser Thr Lys Asp Val Leu
          305          310          313

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<210> 1321

<211> 891

<212> Amino acid

<213> Homo sapiens

<400> 1321

```

Gln Arg Ser Trp Ala Gly Pro Gly Ala Gly Pro Glu Ala Gly Thr Arg
 1           5           10           15
Pro Pro Ala Arg Gly Arg Arg Arg Gln Pro Gly Asn Val Asp Pro Arg
          20           25           30
Arg Arg Ala Pro Gln Leu Arg Ser Gln Met Gln Val Ala Met Ala Arg
          35           40           45

```

Ala Thr Thr Ala Thr Gly Asn Arg Leu Trp Pro Gly Leu Leu Ile Met
 50 55 60
 Leu Gly Ser Leu Cys His Arg Gly Ser Pro Cys Gly Leu Ser Thr His
 65 70 75 80
 Ile Glu Ile Gly His Arg Ala Leu Glu Phe Leu Gln Leu His Asn Gly
 85 90 95
 Arg Val Asn Tyr Arg Glu Leu Leu Leu Glu His Gln Asp Ala Tyr Gln
 100 105 110
 Ala Gly Ile Val Phe Pro Asp Cys Phe Tyr Pro Ser Ile Cys Lys Gly
 115 120 125
 Gly Lys Phe His Asp Val Ser Glu Ser Thr His Trp Thr Pro Phe Leu
 130 135 140
 Asn Ala Ser Val His Tyr Ile Arg Glu Asn Tyr Pro Leu Pro Trp Glu
 145 150 155 160
 Lys Asp Thr Glu Lys Leu Val Ala Phe Leu Phe Gly Ile Thr Ser His
 165 170 175
 Met Ala Ala Asp Val Ser Trp His Ser Leu Gly Leu Glu Gln Gly Phe
 180 185 190
 Leu Arg Thr Met Gly Ala Ile Asp Phe His Gly Ser Tyr Ser Glu Ala
 195 200 205
 His Ser Ala Gly Asp Phe Gly Gly Asp Val Leu Ser Gln Phe Glu Phe
 210 215 220
 Asn Phe Asn Tyr Leu Ala Arg Arg Trp Tyr Val Pro Val Lys Asp Leu
 225 230 235 240
 Leu Gly Ile Tyr Glu Lys Leu Tyr Gly Arg Lys Val Ile Thr Glu Asn
 245 250 255
 Val Ile Val Asp Cys Ser His Ile Gln Phe Leu Glu Met Tyr Gly Glu
 260 265 270
 Met Leu Ala Val Ser Lys Leu Tyr Pro Thr Tyr Ser Thr Lys Ser Pro
 275 280 285
 Phe Leu Val Glu Gln Phe Gln Glu Tyr Phe Leu Gly Gly Leu Asp Asp
 290 295 300
 Met Ala Phe Trp Ser Thr Asn Ile Tyr His Leu Thr Ile Phe Met Leu
 305 310 315 320
 Glu Asn Gly Thr Ser Asp Cys Asn Leu Pro Glu Asn Pro Leu Phe Ile
 325 330 335
 Ala Cys Gly Gly Gln Gln Asn His Thr Gln Gly Ser Lys Met Gln Lys
 340 345 350
 Asn Asp Phe His Arg Asn Leu Thr Thr Ser Leu Thr Glu Ser Val Asp
 355 360 365
 Arg Asn Ile Asn Tyr Thr Glu Arg Gly Val Phe Phe Ser Val Asn Ser
 370 375 380
 Trp Thr Pro Asp Ser Met Ser Phe Ile Tyr Lys Ala Leu Glu Arg Asn
 385 390 395 400
 Ile Arg Thr Met Phe Ile Gly Gly Ser Gln Leu Ser Gln Lys His Val
 405 410 415
 Ser Ser Pro Leu Ala Ser Tyr Phe Leu Ser Phe Pro Tyr Ala Arg Leu
 420 425 430
 Gly Trp Ala Met Thr Ser Ala Asp Leu Asn Gln Asp Gly His Gly Asp
 435 440 445
 Leu Val Val Gly Ala Pro Gly Tyr Ser Arg Pro Gly His Ile His Ile
 450 455 460
 Gly Arg Val Tyr Leu Ile Tyr Gly Asn Asp Leu Gly Leu Pro Pro Val
 465 470 475 480
 Asp Leu Asp Leu Asp Lys Glu Ala His Arg Ile Leu Glu Gly Phe Gln
 485 490 495
 Pro Ser Gly Arg Phe Gly Ser Ala Leu Ala Val Leu Asp Phe Asn Val
 500 505 510
 Asp Gly Val Pro Asp Leu Ala Val Gly Ala Pro Ser Val Gly Ser Glu
 515 520 525
 Gln Leu Thr Tyr Lys Gly Ala Val Tyr Val Tyr Phe Gly Ser Lys Gln
 530 535 540
 Gly Gly Met Ser Ser Ser Pro Asn Ile Thr Ile Ser Cys Gln Asp Ile
 545 550 555 560

Tyr Cys Asn Leu Gly Trp Thr Leu Leu Ala Ala Asp Val Asn Gly Asp
 565 570 575
 Ser Glu Pro Asp Leu Val Ile Gly Ser Pro Phe Ala Pro Gly Gly Gly
 580 585 590
 Lys Gln Lys Gly Ile Val Ala Ala Phe Tyr Ser Gly Pro Ser Leu Ser
 595 600 605
 Asp Lys Glu Lys Leu Asn Val Glu Ala Ala Asn Trp Thr Val Arg Gly
 610 615 620
 Glu Glu Asp Phe Ser Trp Phe Gly Tyr Ser Leu His Gly Val Thr Val
 625 630 635 640
 Asp Asn Arg Thr Leu Leu Leu Val Gly Ser Pro Thr Trp Lys Asn Ala
 645 650 655
 Ser Arg Leu Gly His Leu Leu His Ile Arg Asp Glu Lys Lys Ser Leu
 660 665 670
 Gly Arg Val Tyr Gly Tyr Phe Pro Pro Asn Gly Gln Ser Trp Phe Thr
 675 680 685
 Ile Ser Gly Asp Lys Ala Met Gly Lys Leu Gly Thr Ser Leu Ser Ser
 690 695 700
 Gly His Val Leu Met Asn Gly Thr Leu Lys Gln Val Leu Leu Val Gly
 705 710 715 720
 Ala Pro Thr Tyr Asp Asp Val Ser Lys Val Ala Phe Leu Thr Val Thr
 725 730 735
 Leu His Gln Gly Gly Ala Thr Arg Met Tyr Ala Leu Thr Ser Asp Ala
 740 745 750
 Gln Pro Leu Leu Leu Ser Thr Phe Ser Gly Asp Arg Arg Phe Ser Arg
 755 760 765
 Phe Gly Gly Val Leu His Leu Ser Asp Leu Asp Asp Asp Gly Leu Asp
 770 775 780
 Glu Ile Ile Met Ala Ala Pro Leu Arg Ile Ala Asp Val Thr Ser Gly
 785 790 795 800
 Leu Ile Gly Gly Glu Asp Gly Arg Val Tyr Val Tyr Asn Gly Lys Glu
 805 810 815
 Thr Thr Leu Gly Asp Met Thr Gly Lys Cys Lys Ser Trp Ile Thr Pro
 820 825 830
 Cys Pro Glu Glu Lys Ala Gln Tyr Val Leu Ile Ser Pro Glu Ala Ser
 835 840 845
 Ser Arg Phe Gly Ser Ser Leu Ile Thr Val Arg Ser Lys Ala Lys Asn
 850 855 860
 Gln Val Val Ile Ala Ala Gly Arg Ser Ser Leu Gly Ala Arg Leu Ser
 865 870 875 880
 Gly Ala Leu His Val Tyr Ser Leu Gly Ser Asp
 885 890 891

<210> 1322

<211> 119

<212> Amino acid

<213> Homo sapiens

<400> 1322

Ser Leu Arg Asn Ser Ala Arg Gly Leu Lys Met Ala Ala Ser Ala Ala
 1 5 10 15
 Arg Gly Ala Ala Ala Leu Arg Arg Ser Ile Asn Gln Pro Val Ala Phe
 20 25 30
 Val Arg Arg Ile Pro Trp Thr Ala Ala Ser Ser Gln Leu Lys Glu His
 35 40 45
 Phe Ala Gln Phe Gly His Val Arg Arg Cys Ile Leu Pro Phe Asp Lys
 50 55 60
 Glu Thr Gly Phe His Arg Gly Leu Gly Trp Val Gln Phe Ser Ser Glu
 65 70 75 80

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<210> 1323
<211> 257
<212> Amino acid
<213> Homo sapiens
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<210> 1324
<211> 273
<212> Amino acid
<213> Homo sapiens
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824

Glu Thr Arg Val Lys Thr Ser Leu Glu Leu Leu Arg Thr Gln Leu Glu
 1 5 10 15
 Pro Thr Gly Thr Val Gly Asn Thr Ile Met Thr Ser Gln Pro Val Pro
 20 25 30
 Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
 35 40 45
 Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
 50 55 60
 His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
 65 70 75 80
 Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
 85 90 95
 Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
 100 105 110
 Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile
 115 120 125
 Ala Thr Glu Lys Arg Leu Thr Lys Leu Leu Val His Ser Ser Leu Val
 130 135 140
 Gly Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Ile Leu
 145 150 155 160
 Ser Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Gln Cys Glu Leu
 165 170 175
 Asp Lys Asn Asn Ile Pro Thr Arg Ser Tyr Val Ser Tyr Phe Tyr His
 180 185 190
 Asp Ser Leu Tyr Thr Thr Asp Cys Tyr Thr Ala Lys Ala Ser Leu Ala
 195 200 205
 Gly Thr Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Leu
 210 215 220
 Ala Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe
 225 230 235 240
 Pro Gly Ser Val Leu Phe Leu Pro His Ser Tyr Ile Gly Asn Ser Gly
 245 250 255
 Met Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr
 260 265 270
 Ser
 273

<210> 1325

<211> 477

<212> Amino acid

<213> Homo sapiens

<400> 1325

Glu Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu
 1 5 10 15
 Met Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val
 20 25 30
 Ser Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro
 35 40 45
 Tyr Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val
 50 55 60
 Gly Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr
 65 70 75 80
 Val Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala
 85 90 95
 Gln Ile Gln Pro Glu Asp Ala Pro Val Leu Trp Leu Gln Gly Gly
 100 105 110
 Pro Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr
 115 120 125

Val Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr
 130 135 140
 Thr Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe
 145 150 155 160
 Ser Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val
 165 170 175
 Ala Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro
 180 185 190
 Glu Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly
 195 200 205
 Lys Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val
 210 215 220
 Arg Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr
 225 230 235 240
 Ser Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln
 245 250 255
 Ile Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys
 260 265 270
 His Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe
 275 280 285
 Glu Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser
 290 295 300
 Tyr Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg
 305 310 315 320
 Cys Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu
 325 330 335
 Pro Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp
 340 345 350
 Gly Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val
 355 360 365
 Lys Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr
 370 375 380
 Asn Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser
 385 390 395 400
 Leu Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu
 405 410 415
 Lys Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr
 420 425 430
 Ile Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly
 435 440 445
 His Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn
 450 455 460
 Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475 477

<210> 1326

<211> 160

<212> Amino acid

<213> Homo sapiens

<400> 1326

Arg Asp Glu Arg Ala Lys Val Pro Phe Arg Ser Thr Glu Gly Gly Arg
 1 5 10 15
 Arg Arg Arg Arg Met Glu Ala Val Phe Val Phe Ser Leu Leu
 20 25 30
 Asp Cys Cys Ala Leu Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu
 35 40 45
 Ser Asp Leu Glu Cys Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys
 50 55 60

Leu Asn Lys Trp Val Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr
 65 70 75 80
 Val Leu Leu Leu Met Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu
 85 90 95
 Pro Val Ala Thr Trp Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly
 100 105 110
 Asn Met Gly Val Phe Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu
 115 120 125
 Lys Ser His Met Lys Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu
 130 135 140
 Cys Phe Phe Met Tyr Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
 145 150 155 160

<210> 1327
 <211> 131
 <212> Amino acid
 <213> Homo sapiens

<400> 1327
 Gln Ser Pro Gly His Gly Ala Pro Cys Gln Leu Ser Ser Ser His Ser
 1 5 10 15
 Arg Ser Asn Arg Leu Leu Ser Pro Met Ala Arg Ala Thr Leu Ser Ala
 20 25 30
 Ala Pro Ser Asn Pro Arg Leu Leu Arg Val Ala Leu Leu Leu Leu
 35 40 45
 Leu Val Ala Ala Ser Arg Arg Ala Ala Gly Ala Pro Leu Ala Thr Glu
 50 55 60
 Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln Gly Ile His Leu Lys Asn
 65 70 75 80
 Ile Gln Ser Val Lys Val Lys Ser Pro Gly Pro His Cys Ala Gln Thr
 85 90 95
 Glu Val Ile Ala Thr Leu Lys Asn Gly Gln Lys Ala Cys Leu Asn Pro
 100 105 110
 Ala Ser Pro Met Val Lys Lys Ile Ile Glu Lys Met Leu Lys Asn Gly
 115 120 125
 Lys Ser Asn
 130 131

<210> 1328
 <211> 44
 <212> Amino acid
 <213> Homo sapiens

<400> 1328
 His Pro Leu Ser Leu Val Phe Leu Ala Leu Asn Thr Gly Lys Glu Lys
 1 5 10 15
 Ser His Pro Gly Gly Gly Glu Arg Pro Gly Leu Ala Gly Gln Gly
 20 25 30
 Glu Pro Asp His Pro Ala Gly Ala Arg Asp Gly Arg
 35 40 44

<210> 1329
 <211> 525
 <212> Amino acid
 <213> Homo sapiens

<400> 1329
 Cys Thr Pro Val Ala Arg Ser Met Ala Thr Thr Ala Thr Cys Thr Arg
 1 5 10 15
 Phe Thr Asp Asp Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe
 20 25 30
 Ser Val Val Arg Arg Cys Val Lys Lys Thr Ser Thr Gln Glu Tyr Ala
 35 40 45
 Ala Lys Ile Ile Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys
 50 55 60
 Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu Lys His Pro Asn Ile
 65 70 75 80
 Val Arg Leu His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val
 85 90 95
 Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg
 100 105 110
 Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile His Gln Ile Leu
 115 120 125
 Glu Ser Val Asn His Ile His Gln His Asp Ile Val His Arg Asp Leu
 130 135 140
 Lys Pro Glu Asn Leu Leu Ala Ser Lys Cys Lys Gly Ala Ala Val
 145 150 155 160
 Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Glu Gln Gln
 165 170 175
 Ala Trp Phe Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val
 180 185 190
 Leu Arg Lys Asp Pro Tyr Gly Lys Pro Val Asp Ile Trp Ala Cys Gly
 195 200 205
 Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu
 210 215 220
 Asp Gln His Lys Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe
 225 230 235 240
 Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asn Leu Ile
 245 250 255
 Asn Gln Met Leu Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Asp Gln
 260 265 270
 Ala Leu Lys His Pro Trp Val Cys Gln Arg Ser Thr Val Ala Ser Met
 275 280 285
 Met His Arg Gln Glu Thr Val Glu Cys Leu Arg Lys Phe Asn Ala Arg
 290 295 300
 Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr Met Leu Val Ser Arg Asn
 305 310 315 320
 Phe Ser Ala Ala Lys Ser Leu Leu Asn Lys Lys Ser Asp Gly Gly Val
 325 330 335
 Lys Pro Gln Ser Asn Asn Lys Asn Ser Leu Val Ser Pro Ala Gln Glu
 340 345 350
 Pro Ala Pro Leu Gln Thr Ala Met Glu Pro Gln Thr Thr Val Val His
 355 360 365
 Asn Ala Thr Asp Gly Ile Lys Gly Ser Thr Glu Ser Cys Asn Thr Thr
 370 375 380
 Thr Glu Asp Glu Asp Leu Lys Val Arg Lys Gln Glu Ile Ile Lys Ile
 385 390 395 400
 Thr Glu Gln Leu Ile Glu Ala Ile Asn Asn Gly Asp Phe Glu Ala Tyr
 405 410 415
 Thr Lys Ile Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu
 420 425 430

Gly Asn Leu Val Glu Gly Met Asp Phe His Lys Phe Tyr Phe Glu Asn
 435 440 445
 Leu Leu Ser Lys Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn Pro
 450 455 460
 His Val His Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg
 465 470 475 480
 Leu Thr Gln Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser
 485 490 495
 Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Leu Asn Val
 500 505 510
 His Tyr His Cys Ser Gly Ala Pro Ala Ala Pro Leu Gln
 515 520 525

<210> 1330

<211> 205

<212> Amino acid

<213> Homo sapiens

<400> 1330

Asn Arg Arg Thr Val Lys Met Leu Leu Glu Leu Ser Glu Glu His Lys
 1 5 10 15
 Glu His Leu Ala Phe Leu Pro Gln Val Asp Ser Ala Val Val Ala Glu
 20 25 30
 Phe Gly Arg Ile Ala Val Glu Phe Leu Arg Arg Gly Ala Asn Pro Lys
 35 40 45
 Ile Tyr Glu Gly Ala Ala Arg Lys Leu Asn Val Ser Ser Asp Thr Val
 50 55 60
 Gln His Gly Val Glu Gly Leu Thr Tyr Leu Leu Thr Glu Ser Ser Lys
 65 70 75 80
 Leu Met Ile Ser Glu Leu Asp Phe Gln Asp Ser Val Phe Val Leu Gly
 85 90 95
 Phe Ser Glu Glu Leu Asn Lys Leu Leu Leu Gln Leu Tyr Leu Asp Asn
 100 105 110
 Arg Lys Glu Ile Arg Thr Ile Leu Ser Glu Leu Ala Pro Ser Leu Pro
 115 120 125
 Ser Tyr His Asn Leu Glu Trp Arg Leu Asp Val Gln Leu Ala Ser Arg
 130 135 140
 Ser Leu Arg Gln Gln Ile Lys Pro Ala Val Thr Ile Lys Leu His Leu
 145 150 155 160
 Asn Gln Asn Gly Asp His Asn Thr Lys Val Leu Gln Thr Asp Pro Ala
 165 170 175
 Thr Leu Leu His Leu Val Gln Gln Leu Glu Gln Ala Leu Glu Glu Met
 180 185 190
 Lys Thr Asn His Cys Arg Arg Val Val Arg Asn Ile Lys
 195 200 205

<210> 1331

<211> 78

<212> Amino acid

<213> Homo sapiens

<400> 1331

Gly Thr Ser Ile Tyr Leu Ala His Arg Val Ala Arg Ala Trp Glu Leu
 1 5 10 15

Ala Gln Phe Ile His His Thr Ser Lys Lys Ala Asp Val Val Leu Ala
 20 25 30
 Cys Gly Asp Ser Ile Val His Pro Glu Asp Leu Ile Cys Cys Pro Leu
 35 40 45
 Thr Gly Arg Ser Cys Leu Cys Asp Val His Leu Leu Ser Ser Leu Leu
 50 55 60
 Ala Arg Leu Gly Arg Gly Tyr Ala Val Ser Leu Thr Asn Leu
 65 70 75 78

<210> 1332

<211> 274

<212>Amino acid

<213> Homo sapiens

<400> 1332

Arg Gly Cys Gly Ser Cys Gly Tyr Lys Pro Ser Ala Gly Pro Ala Trp
 1 5 10 15
 Arg Pro Arg Pro Pro Pro Ala Val Ser Pro Leu Arg His Pro Glu Pro
 20 25 30
 Ala Lys Val Leu Ser Phe Ser Ser Cys Pro Leu Pro Ala Leu Gly Arg
 35 40 45
 Thr Gly Pro Ser Arg Ala Ala Arg Ala Gln Ser Leu Thr Met Ala Ser
 50 55 60
 Leu Phe Lys Lys Lys Thr Val Asp Asp Val Ile Lys Glu Gln Asn Arg
 65 70 75 80
 Glu Leu Arg Gly Thr Gln Arg Ala Ile Ile Arg Asp Arg Ala Ala Leu
 85 90 95
 Glu Lys Gln Glu Lys Gln Leu Glu Leu Glu Ile Lys Lys Met Ala Lys
 100 105 110
 Ile Gly Asn Lys Glu Ala Cys Lys Val Leu Ala Lys Gln Leu Val His
 115 120 125
 Leu Arg Lys Gln Lys Thr Arg Thr Phe Ala Val Ser Ser Lys Val Thr
 130 135 140
 Ser Met Ser Thr Gln Thr Lys Val Met Asn Ser Gln Met Lys Met Ala
 145 150 155 160
 Gly Ala Met Ser Thr Thr Ala Lys Thr Met Gln Ala Val Asn Lys Lys
 165 170 175
 Met Asp Pro Gln Lys Thr Leu Gln Thr Met Gln Asn Phe Gln Lys Glu
 180 185 190
 Asn Met Lys Met Glu Met Thr Glu Glu Met Ile Asn Asp Thr Leu Asp
 195 200 205
 Asp Ile Phe Asp Gly Ser Asp Asp Glu Glu Glu Ser Gln Asp Ile Val
 210 215 220
 Asn Gln Val Leu Asp Glu Ile Gly Ile Glu Ile Ser Gly Lys Met Ala
 225 230 235 240
 Lys Ala Pro Ser Ala Ala Arg Ser Leu Pro Ser Ala Ser Thr Ser Lys
 245 250 255
 Ala Thr Ile Ser Asp Glu Glu Ile Glu Arg Gln Leu Lys Ala Leu Gly
 260 265 270
 Val Asp
 274

<210> 1333

<211> 157

<212>Amino acid

<213> Homo sapiens


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<400> 1333
Ser Thr Asp Gly Asn Gly Ala Glu Arg Leu Phe Ala Glu Leu Arg Lys
 1           5           10           15
Met Asn Ala Arg Gly Leu Gly Ser Glu Leu Lys Asp Ser Ile Pro Val
          20           25           30
Thr Glu Leu Ser Ala Ser Gly Pro Phe Glu Ser His Asp Leu Leu Arg
          35           40           45
Lys Gly Phe Ser Cys Val Lys Asn Glu Leu Leu Pro Ser His Pro Leu
          50           55           60
Glu Leu Ser Glu Lys Asn Phe Gln Leu Asn Gln Asp Lys Met Asn Phe
          65           70           75           80
Ser Thr Leu Arg Asn Ile Gln Gly Leu Phe Ala Pro Leu Lys Leu Gln
          85           90           95
Met Glu Phe Lys Ala Val Gln Gln Val Gln Arg Leu Pro Phe Leu Ser
          100          105          110
Ser Ser Asn Leu Ser Leu Asp Val Leu Arg Gly Asn Asp Glu Thr Ile
          115          120          125
Gly Phe Glu Asp Ile Leu Asn Asp Pro Ser Gln Ser Glu Val Met Gly
          130          135          140
Glu Pro His Leu Met Val Glu Tyr Lys Leu Gly Leu Leu
          145          150          155          157

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<210> 1334

<211> 193

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(193)

<223> X = any amino acid or stop code

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<400> 1334
Arg Asn Met Lys Leu His Tyr Val Ala Val Leu Thr Leu Ala Ile Leu
 1           5           10           15
Met Phe Leu Thr Trp Leu Pro Glu Ser Leu Ser Cys Asn Lys Ala Leu
          20           25           30
Cys Ala Ser Asp Val Ser Lys Cys Leu Ile Gln Glu Leu Cys Gln Cys
          35           40           45
Arg Pro Gly Glu Gly Asn Cys Ser Cys Cys Lys Glu Cys Met Leu Cys
          50           55           60
Leu Gly Ala Leu Trp Asp Glu Cys Cys Asp Cys Val Gly Met Cys Asn
          65           70           75           80
Pro Arg Asn Tyr Ser Asp Thr Pro Pro Thr Ser Lys Ser Thr Val Glu
          85           90           95
Glu Leu His Glu Pro Ile Pro Ser Leu Phe Arg Ala Leu Thr Glu Gly
          100          105          110
Asp Thr Gln Leu Asn Trp Asn Ile Val Ser Phe Pro Val Ala Glu Glu
          115          120          125
Leu Ser His His Glu Asn Leu Val Ser Phe Leu Glu Thr Val Asn Gln
          130          135          140
Pro His His Gln Asn Val Ser Val Pro Ser Asn Asn Val His Ala Pro
          145          150          155          160
Tyr Ser Ser Asp Lys Glu Xaa Leu Pro Thr Val Asp Phe Phe His Ser
          165          170          175
Ala Pro Ser Cys Gly Leu Ser Met Xaa Ser Ile Ile Phe Phe Glu Glu

```

Thr 180 185 190
193

<210> 1335
<211> 179
<212> Amino acid
<213> Homo sapiens

<400> 1335
Val Gly Gly Val Pro Thr Trp Leu Glu Gly Cys Gly Ser Gly Asn Pro
1 5 10 15
Ser Pro Arg Ser Gly Gly Gly Pro Gly Ala Arg Leu Thr Leu Pro Ala
20 25 30
Leu Gln Met Thr Val His Asn Leu Tyr Leu Phe Asp Arg Asn Gly Val
35 40 45
Cys Leu His Tyr Ser Glu Trp His Arg Lys Lys Gln Ala Gly Ile Pro
50 55 60
Lys Glu Glu Glu Tyr Lys Leu Met Tyr Gly Met Leu Phe Ser Ile Arg
65 70 75 80
Ser Phe Val Ser Lys Met Ser Pro Leu Asp Met Lys Asp Gly Phe Leu
85 90 95
Ala Phe Gln Thr Ser Arg Tyr Lys Leu His Tyr Tyr Glu Thr Pro Thr
100 105 110
Gly Ile Lys Val Val Met Asn Thr Asp Leu Gly Val Gly Pro Ile Arg
115 120 125
Asp Val Leu His His Ile Tyr Ser Ala Leu Tyr Val Glu Leu Val Val
130 135 140
Lys Asn Pro Leu Cys Pro Leu Gly Gln Thr Val Gln Ser Glu Leu Phe
145 150 155 160
Arg Ser Arg Leu Asp Ser Tyr Val Arg Ser Leu Pro Phe Phe Ser Ala
165 170 175
Arg Ala Gly
179

<210> 1336
<211> 236
<212> Amino acid
<213> Homo sapiens

<400> 1336
Pro Gly Leu Ser Gln Glu Pro Ser Gly Ser Met Glu Thr Val Val Ile
1 5 10 15
Val Ala Ile Gly Val Leu Ala Thr Ile Phe Leu Ala Ser Phe Ala Ala
20 25 30
Leu Val Leu Val Cys Arg Gln Arg Tyr Cys Arg Pro Arg Asp Leu Leu
35 40 45
Gln Arg Tyr Asp Ser Lys Pro Ile Val Asp Leu Ile Gly Ala Met Glu
50 55 60
Thr Gln Ser Glu Pro Ser Glu Leu Glu Leu Asp Asp Val Val Ile Thr
65 70 75 80
Asn Pro His Ile Glu Ala Ile Leu Glu Asn Glu Asp Trp Ile Glu Asp
85 90 95
Ala Ser Gly Leu Met Ser His Cys Ile Ala Ile Leu Lys Ile Cys His

```

      100              105              110
Thr Leu Thr Glu Lys Leu Val Ala Met Thr Met Gly Ser Gly Ala Lys
      115              120              125
Met Lys Thr Ser Ala Ser Val Ser Asp Ile Ile Val Val Ala Lys Arg
      130              135              140
Ile Ser Pro Arg Val Asp Asp Val Val Lys Ser Met Tyr Pro Pro Leu
145              150              155              160
Asp Pro Lys Leu Leu Asp Ala Arg Thr Thr Ala Leu Leu Leu Ser Val
      165              170              175
Ser His Leu Val Leu Val Thr Arg Asn Ala Cys His Leu Thr Gly Gly
      180              185              190
Leu Asp Trp Ile Asp Gln Ser Leu Ser Ala Ala Glu Glu His Leu Glu
      195              200              205
Val Leu Arg Glu Ala Ala Leu Ala Ser Glu Pro Asp Lys Gly Leu Pro
      210              215              220
Gly Pro Glu Gly Phe Leu Gln Glu Gln Ser Ala Ile
225              230              235 236

```

<210> 1337

<211> 161

<212>Amino acid

<213> Homo sapiens

```

      <400> 1337
Val Gly Met Glu Leu Pro Ala Val Asn Leu Lys Val Ile Leu Leu Gly
  1              5              10              15
His Trp Leu Leu Thr Thr Trp Gly Cys Ile Val Phe Ser Gly Ser Tyr
      20              25              30
Ala Trp Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala
      35              40              45
Gln Arg Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu
      50              55              60
Ala Thr Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg
      65              70              75              80
Val Ser Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu
      85              90              95
Ser Leu Leu Leu Lys Pro Leu Ser Cys Cys Phe Val Tyr His Met Tyr
      100              105              110
Arg Glu Arg Gly Gly Glu Leu Leu Val His Thr Gly Phe Leu Gly Ser
      115              120              125
Ser Gln Asp Arg Ser Ala Tyr Gln Thr Ile Asp Ser Ala Glu Ala Pro
      130              135              140
Ala Asp Pro Phe Ala Val Pro Glu Gly Arg Ser Gln Asp Ala Arg Gly
145              150              155              160
Tyr
161

```

<210> 1338

<211> 200

<212>Amino acid

<213> Homo sapiens

```

      <400> 1338
Pro Ala Ser Arg Pro Leu Leu Gly Pro Asp Thr Gly Ser Val Ala Asn

```

```

1           5           10           15
Ile Phe Lys Gly Leu Val Ile Leu Pro Glu Met Ser Leu Val Ile Arg
20           25           30
Asn Leu Gln Arg Val Ile Pro Ile Arg Arg Ala Pro Leu Arg Ser Lys
35           40           45
Ile Glu Ile Val Arg Arg Ile Leu Gly Val Gln Lys Phe Asp Leu Gly
50           55           60
Ile Ile Cys Val Asp Asn Lys Asn Ile Gln His Ile Asn Arg Ile Tyr
65           70           75           80
Arg Asp Arg Asn Val Pro Thr Asp Val Leu Ser Phe Pro Phe His Glu
85           90           95
His Leu Lys Ala Gly Glu Phe Pro Gln Pro Asp Phe Pro Asp Asp Tyr
100          105          110
Asn Leu Gly Asp Ile Phe Leu Gly Val Glu Tyr Ile Phe His Gln Cys
115          120          125
Lys Glu Asn Glu Asp Tyr Asn Asp Val Leu Thr Val Thr Ala Thr His
130          135          140
Gly Leu Cys His Leu Leu Gly Phe Thr His Gly Thr Glu Ala Glu Trp
145          150          155          160
Gln Gln Met Phe Gln Lys Glu Lys Ala Val Leu Asp Glu Leu Gly Arg
165          170          175
Arg Thr Gly Thr Arg Leu Gln Pro Leu Thr Pro Gly Pro Leu Pro Glu
180          185          190
Gly Ala Glu Gly Arg Val Pro Phe
195          200

```

<210> 1339

<211> 267

<212>Amino acid

<213> Homo sapiens

<400> 1339

```

Leu Arg Asn Ala Leu Asp Val Leu His Arg Glu Val Pro Arg Val Leu
1           5           10           15
Val Asn Leu Val Asp Phe Leu Asn Pro Thr Ile Met Arg Gln Val Phe
20           25           30
Leu Gly Asn Pro Asp Lys Cys Pro Val Gln Gln Ala Met Leu Glu Pro
35           40           45
Leu Gly Ser Lys Thr Glu Thr Leu Asp Leu Arg Ala Glu Met Pro Ile
50           55           60
Thr Cys Pro Thr Gln Asn Glu Pro Phe Leu Arg Thr Pro Arg Asn Ser
65           70           75           80
Asn Tyr Thr Tyr Pro Ile Lys Pro Ala Ile Glu Asn Trp Gly Ser Asp
85           90           95
Phe Leu Cys Thr Glu Trp Lys Ala Ser Asn Ser Val Pro Thr Ser Val
100          105          110
His Gln Leu Arg Pro Ala Asp Ile Lys Val Val Ala Ala Leu Gly Asp
115          120          125
Ser Leu Thr Thr Ala Val Gly Ala Arg Pro Asn Asn Ser Ser Asp Leu
130          135          140
Pro Thr Ser Trp Arg Gly Leu Ser Trp Ser Ile Gly Gly Asp Gly Asn
145          150          155          160
Leu Glu Thr His Thr Thr Leu Pro Asn Ile Leu Lys Lys Phe Asn Pro
165          170          175
Tyr Leu Leu Gly Phe Ser Thr Ser Thr Trp Glu Gly Thr Ala Gly Leu
180          185          190
Asn Val Ala Ala Glu Gly Ala Arg Ala Arg Asp Met Pro Ala Gln Ala
195          200          205
Trp Asp Leu Val Glu Arg Met Lys Asn Ser Pro Asp Ile Asn Leu Glu

```

210	215	220
Lys Asp Trp Lys Leu Val Thr Leu Phe Ile Gly Gly Asn Asp Leu Cys		
225	230	235
His Tyr Cys Glu Asn Pro Glu Ala His Leu Ala Thr Glu Tyr Val Gln		240
	245	250
His Ile Gln Gln Ala Leu Asp Ile Leu Ser Glu		255
260	265	267

<210> 1340

<211> 286

<212>Amino acid

<213> Homo sapiens

<400> 1340																			
Val Val Glu Phe Leu Trp Ser Arg Arg Pro Ser Gly Ser Ser Asp Pro																			
1				5				10										15	
Arg Pro Arg Arg Pro Ala Ser Lys Cys Gln Met Met Glu Glu Arg Ala				20				25										30	
Asn Leu Met His Met Met Lys Leu Ser Ile Lys Val Leu Leu Gln Ser				35				40										45	
Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala Asp His Ala Pro Leu Gln				50				55										60	
Gln Phe Phe Val Val Met Glu His Cys Leu Lys His Gly Leu Lys Val				65				70										75	
Lys Lys Ser Phe Ile Gly Gln Asn Lys Ser Phe Phe Gly Pro Leu Glu				85				90										95	
Leu Val Glu Lys Leu Cys Pro Glu Ala Ser Asp Ile Ala Thr Ser Val				100				105										110	
Arg Asn Leu Pro Glu Leu Lys Thr Ala Val Gly Arg Gly Arg Ala Trp				115				120										125	
Leu Tyr Leu Ala Leu Met Gln Lys Lys Leu Ala Asp Tyr Leu Lys Val				130				135										140	
Leu Ile Asp Asn Lys His Leu Leu Ser Glu Phe Tyr Glu Pro Glu Ala				145				150										155	
Leu Met Met Glu Glu Gly Met Val Ile Val Gly Leu Leu Val Gly				165				170										175	
Leu Asn Val Leu Asp Ala Asn Leu Cys Leu Lys Gly Glu Asp Leu Asp				180				185										190	
Ser Gln Val Gly Val Ile Asp Phe Ser Leu Tyr Leu Lys Asp Val Gln				195				200										205	
Asp Leu Asp Gly Gly Lys Glu His Glu Arg Ile Thr Asp Val Leu Asp				210				215										220	
Gln Lys Asn Tyr Val Glu Glu Leu Asn Arg His Leu Ser Cys Thr Val				225				230										235	
Gly Asp Leu Gln Thr Lys Ile Asp Gly Leu Glu Lys Thr Asn Ser Lys				245				250										255	
Leu Gln Glu Arg Val Ser Ala Ala Thr Asp Arg Ile Cys Ser Leu Gln				260				265										270	
Glu Glu Gln Gln Gln Leu Arg Glu Gln Asn Glu Leu Ile Arg				275				280										285	286

<210> 1341

<211> 233

<212>Amino acid

<213> Homo sapiens

<400> 1341

Lys Pro Glu Gly Ala Arg Arg Val Gln Phe Val Met Gly Leu Phe Gly
 1 5 10 15
 Lys Thr Gln Glu Lys Pro Pro Lys Glu Leu Val Asn Glu Trp Ser Leu
 20 25 30
 Lys Ile Arg Lys Glu Met Arg Val Val Asp Arg Gln Ile Arg Asp Ile
 35 40 45
 Gln Arg Glu Glu Glu Lys Val Lys Arg Ser Val Lys Asp Ala Ala Lys
 50 55 60
 Lys Gly Gln Lys Asp Val Cys Ile Val Leu Ala Lys Glu Met Ile Arg
 65 70 75 80
 Ser Arg Lys Ala Val Ser Lys Leu Tyr Ala Ser Lys Ala His Met Asn
 85 90 95
 Ser Val Leu Met Gly Met Lys Asn Gln Leu Ala Val Leu Arg Val Ala
 100 105 110
 Gly Ser Leu Gln Lys Ser Thr Glu Val Met Lys Ala Met Gln Ser Leu
 115 120 125
 Val Lys Ile Pro Glu Ile Gln Ala Thr Met Arg Glu Leu Ser Lys Glu
 130 135 140
 Met Met Lys Ala Gly Ile Ile Glu Glu Met Leu Glu Asp Thr Phe Glu
 145 150 155 160
 Ser Met Asp Asp Gln Glu Glu Met Glu Glu Glu Ala Glu Met Glu Ile
 165 170 175
 Asp Arg Ile Leu Phe Glu Ile Thr Ala Gly Ala Leu Gly Lys Ala Pro
 180 185 190
 Ser Lys Val Thr Asp Ala Leu Pro Glu Pro Glu Pro Gly Ala Met
 195 200 205
 Ala Ala Ser Glu Asp Glu Glu Glu Glu Glu Ala Leu Glu Ala Met
 210 215 220
 Gln Ser Arg Leu Ala Thr Leu Arg Ser
 225 230 233

<210> 1342

<211> 150

<212> Amino acid

<213> Homo sapiens

<400> 1342

Arg Trp Asn Ser Ile Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val
 1 5 10 15
 Met Ala Gly Val Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys
 20 25 30
 Met Val Lys Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro
 35 40 45
 Tyr Gly Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala
 50 55 60
 Thr Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
 65 70 75 80
 Thr Gln Gly Cys Gly Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser
 85 90 95
 Gln Gly Asn Ile His Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln
 100 105 110
 Leu Cys Ala Cys Asp Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu
 115 120 125
 Asp Thr Tyr Gln Lys Arg Leu Arg Phe Tyr Trp Arg Pro His Cys Arg
 130 135 140
 Gly Gln Thr Pro Gly Cys

145

150

<210> 1343
 <211> 127
 <212> Amino acid
 <213> Homo sapiens

<400> 1343
 Lys Thr Val Ala Glu Glu Ala Ser Val Gly Asn Pro Glu Gly Ala Phe
 1 5 10 15
 Met Lys Met Leu Gln Ala Arg Lys Gln His Met Ser Thr Glu Leu Thr
 20 25 30
 Ile Glu Ser Glu Ala Pro Ser Asp Ser Ser Gly Ile Asn Leu Ser Gly
 35 40 45
 Phe Gly Ser Glu Gln Leu Asp Thr Asn Asp Glu Ser Asp Val Ser Ser
 50 55 60
 Ala Leu Ser Tyr Ile Leu Pro Tyr Leu Ser Leu Arg Asn Leu Gly Ala
 65 70 75 80
 Glu Ser Ile Leu Leu Pro Phe Thr Glu Gln Leu Phe Ser Asn Val Gln
 85 90 95
 Asp Gly Asp Arg Leu Leu Ser Ile Leu Lys Asn Asn Arg Lys Ser Pro
 100 105 110
 Ser Gln Ser Ser Leu Leu Gly Asn Lys Phe Lys Asn Lys Ile Phe
 115 120 125 127

<210> 1344
 <211> 126
 <212> Amino acid
 <213> Homo sapiens

<400> 1344
 Leu Pro Leu Thr Leu Leu Leu Ala Ala Pro Phe Ala His Leu Leu Leu
 1 5 10 15
 Pro Pro Gly His Asp Gln Ser Pro Cys Trp His Pro Gly Pro Ala Leu
 20 25 30
 Ser Pro Gly Thr Leu Gly Pro Leu Ser Trp Ala Met Ala Asn Ser Gly
 35 40 45
 Leu Gln Leu Leu Gly Tyr Phe Leu Ala Leu Gly Gly Trp Val Gly Ile
 50 55 60
 Ile Ala Ser Thr Ala Leu Pro Gln Trp Lys Gln Ser Ser Tyr Ala Gly
 65 70 75 80
 Asp Ala Ser Ile Gln Leu Arg Ser Lys Val Phe Val Leu Glu Ser Glu
 85 90 95
 Trp Gly Gly Asp Ser Leu Gly Leu Pro Arg Asp Cys Gly Trp Ser Cys
 100 105 110
 Leu Leu His Ser Ala Val Arg Ser Glu Lys Gly Phe Trp Ser
 115 120 125 126

<210> 1345
 <211> 328
 <212> Amino acid
 <213> Homo sapiens

<400> 1345

```

Asp Pro Arg Val Arg Pro Pro Leu Leu Gln Pro Pro Pro Pro Leu Leu
 1           5           10           15
Pro Arg Leu Val Ile Leu Lys Met Ala Pro Leu Asp Leu Asp Lys Tyr
          20          25          30
Val Glu Ile Ala Arg Leu Cys Lys Tyr Leu Pro Glu Asn Asp Leu Lys
        35          40          45
Arg Leu Cys Asp Tyr Val Cys Asp Leu Leu Leu Glu Glu Ser Asn Val
        50          55          60
Gln Pro Val Ser Thr Pro Val Thr Val Cys Gly Asp Ile His Gly Gln
        65          70          75          80
Phe Tyr Asp Leu Cys Glu Leu Phe Arg Thr Gly Gly Gln Val Pro Asp
          85          90          95
Thr Asn Tyr Ile Phe Met Gly Asp Phe Val Asp Arg Gly Tyr Tyr Ser
        100          105          110
Leu Glu Thr Phe Thr Tyr Leu Leu Ala Leu Lys Ala Lys Trp Pro Asp
        115          120          125
Arg Ile Thr Leu Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr Gln
        130          135          140
Val Tyr Gly Phe Tyr Asp Glu Cys Gln Thr Lys Tyr Gly Asn Ala Asn
        145          150          155          160
Ala Trp Arg Tyr Cys Thr Lys Val Phe Asp Met Leu Thr Val Ala Ala
        165          170          175
Leu Ile Asp Glu Gln Ile Leu Cys Val His Gly Gly Leu Ser Pro Asp
        180          185          190
Ile Lys Thr Leu Asp Gln Ile Arg Thr Ile Glu Arg Asn Gln Glu Ile
        195          200          205
Pro His Lys Gly Ala Phe Cys Asp Leu Val Trp Ser Asp Pro Glu Asp
        210          215          220
Val Asp Thr Trp Ala Ile Ser Pro Arg Gly Ala Gly Trp Leu Phe Gly
        225          230          235          240
Ala Lys Val Thr Asn Glu Phe Val His Ile Asn Asn Leu Lys Leu Ile
        245          250          255
Cys Arg Ala His Gln Leu Val His Glu Gly Tyr Lys Phe Met Phe Asp
        260          265          270
Glu Lys Leu Val Thr Val Trp Ser Ala Pro Asn Tyr Cys Tyr Arg Cys
        275          280          285
Gly Asn Ile Ala Ser Ile Met Val Phe Lys Asp Val Asn Thr Arg Glu
        290          295          300
Pro Lys Leu Phe Arg Ala Val Pro Asp Ser Glu Arg Val Ile Pro Pro
        305          310          315          320
Arg Thr Thr Thr Pro Tyr Phe Leu
          325          328

```

<210> 1346

<211> 253

<212> Amino acid

<213> Homo sapiens

<400> 1346

```

Ser Phe Ala Gly Ala Ala Ala Arg Pro Ser Thr Pro Pro Ala Ser Gly
 1           5           10           15
Arg Gly Ala Ala Pro Gly Arg Pro Gly Pro Ser Pro Met Asp Leu Arg
        20          25          30
Ala Gly Asp Ser Trp Gly Met Leu Ala Cys Leu Cys Thr Val Leu Trp

```



```

      35      40      45
His Leu Pro Ala Val Pro Ala Leu Asn Arg Thr Gly Asp Pro Gly Pro
  50      55      60
Gly Pro Ser Ile Gln Lys Thr Tyr Asp Leu Thr Arg Tyr Leu Glu His
  65      70      75      80
Gln Leu Arg Ser Leu Ala Gly Thr Tyr Leu Asn Tyr Leu Gly Pro Pro
      85      90      95
Phe Asn Glu Pro Asp Phe Asn Pro Pro Arg Leu Gly Ala Glu Thr Leu
      100      105      110
Pro Arg Ala Thr Val Asp Leu Glu Val Trp Arg Ser Leu Asn Asp Lys
      115      120      125
Leu Arg Leu Thr Gln Asn Tyr Glu Ala Tyr Ser His Leu Leu Cys Tyr
      130      135      140
Leu Arg Gly Leu Asn Arg Gln Ala Ala Thr Ala Glu Leu Arg Arg Ser
      145      150      155      160
Leu Ala His Phe Cys Thr Ser Leu Gln Gly Leu Leu Gly Ser Ile Ala
      165      170      175
Gly Val Met Ala Ala Leu Gly Tyr Pro Leu Pro Gln Pro Leu Pro Gly
      180      185      190
Thr Glu Pro Thr Trp Thr Pro Gly Pro Ala His Ser Asp Phe Leu Gln
      195      200      205
Lys Met Asp Asp Phe Trp Leu Leu Lys Glu Leu Gln Thr Trp Leu Trp
      210      215      220
Arg Ser Ala Lys Asp Phe Asn Arg Leu Lys Lys Lys Met Gln Pro Pro
      225      230      235      240
Ala Ala Ala Val Thr Leu His Leu Gly Ala His Gly Phe
      245      250      253

```

<210> 1347

<211> 195

<212> Amino acid

<213> Homo sapiens

<400> 1347

```

      5      10      15
Ile Lys Ile Ser Leu Lys Lys Arg Ser Met Ser Gly Ile Ser Gly Cys
  1      5      10      15
Pro Phe Phe Leu Trp Gly Leu Leu Ala Leu Leu Gly Leu Ala Leu Val
      20      25      30
Ile Ser Leu Ile Phe Asn Ile Ser His Tyr Val Glu Lys Gln Arg Gln
      35      40      45
Asp Lys Met Tyr Ser Tyr Ser Ser Asp His Thr Arg Val Asp Glu Tyr
      50      55      60
Tyr Ile Glu Asp Thr Pro Ile Tyr Gly Asn Leu Asp Asp Met Ile Ser
      65      70      75      80
Glu Pro Met Asp Glu Asn Cys Tyr Glu Gln Met Lys Ala Arg Pro Glu
      85      90      95
Lys Ser Val Asn Lys Met Gln Glu Ala Thr Pro Ser Ala Gln Ala Thr
      100      105      110
Asn Glu Thr Gln Met Cys Tyr Ala Ser Leu Asp His Ser Val Lys Gly
      115      120      125
Lys Arg Arg Lys Pro Arg Lys Gln Asn Thr His Phe Ser Asp Lys Asp
      130      135      140
Gly Asp Glu Gln Leu His Ala Ile Asp Ala Ser Val Ser Lys Thr Thr
      145      150      155      160
Leu Val Asp Ser Phe Ser Pro Glu Ser Gln Ala Val Glu Glu Asn Ile
      165      170      175
His Asp Asp Pro Ile Arg Leu Phe Gly Leu Ile Arg Ala Lys Arg Glu
      180      185      190
Pro Ile Asn

```

195

<210> 1348
 <211> 268
 <212> Amino acid
 <213> Homo sapiens

<400> 1348
 Val Glu Phe His Pro Gln Arg Ala Arg Ala Gly Ala Arg Ala Pro Ser
 1 5 10 15
 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 20 25 30
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Ala Ile Gly Ser Cys Ser
 35 40 45
 Lys Glu Tyr Arg Val Leu Leu Gly Gln Leu Gln Lys Gln Thr Asp Leu
 50 55 60
 Met Gln Asp Thr Ser Arg Leu Leu Asp Pro Tyr Ile Arg Ile Gln Gly
 65 70 75 80
 Leu Asp Val Pro Lys Leu Arg Glu His Cys Arg Glu Arg Pro Gly Ala
 85 90 95
 Phe Pro Ser Glu Glu Thr Leu Arg Gly Leu Gly Arg Arg Cys Phe Leu
 100 105 110
 Gln Thr Leu Asn Ala Thr Leu Gly Cys Val Leu His Arg Leu Ala Asp
 115 120 125
 Leu Glu Gln Arg Leu Pro Lys Ala Gln Asp Leu Glu Arg Ser Gly Leu
 130 135 140
 Asn Ile Glu Asp Leu Glu Lys Leu Gln Met Ala Arg Pro Asn Ile Leu
 145 150 155 160
 Gly Leu Arg Asn Asn Ile Tyr Cys Met Ala Gln Leu Leu Asp Asn Ser
 165 170 175
 Asp Thr Ala Glu Pro Thr Lys Ala Gly Arg Gly Ala Ser Gln Pro Pro
 180 185 190
 Thr Pro Thr Pro Ala Ser Asp Ala Phe Gln Arg Lys Leu Glu Gly Cys
 195 200 205
 Arg Phe Leu His Gly Tyr His Arg Phe Met His Ser Val Gly Arg Val
 210 215 220
 Phe Ser Lys Trp Gly Glu Ser Pro Asn Arg Ser Arg Arg His Ser Pro
 225 230 235 240
 His Gln Ala Leu Arg Lys Gly Val Arg Arg Thr Arg Pro Ser Arg Lys
 245 250 255
 Gly Lys Arg Leu Met Thr Arg Gly Gln Leu Pro Arg
 260 265 268

<210> 1349
 <211> 138
 <212> Amino acid
 <213> Homo sapiens

<400> 1349
 Asp Phe Pro Gly Arg Arg Phe Arg Leu Val Trp Leu Leu Val Leu Arg
 1 5 10 15
 Leu Pro Trp Arg Val Pro Gly Gln Leu Asp Pro Thr Thr Gly Arg Arg
 20 25 30
 Phe Ser Glu His Lys Leu Cys Ala Asp Asp Glu Cys Ser Met Leu Met

```

      35      40      45
Tyr Arg Gly Glu Ala Leu Glu Asp Phe Thr Gly Pro Asp Cys Arg Phe
  50      55      60
Val Asn Phe Lys Lys Gly Asp Pro Val Tyr Val Tyr Tyr Lys Leu Ala
  65      70      75      80
Arg Gly Trp Pro Glu Val Trp Ala Gly Ser Val Gly Arg Thr Phe Gly
      85      90      95
Tyr Phe Pro Lys Asp Leu Ile Gln Val Val His Glu Tyr Thr Lys Glu
      100      105      110
Glu Leu Gln Val Pro Thr Asn Glu Thr Asp Phe Val Cys Phe Asp Gly
      115      120      125
Gly Arg Asp Asp Phe His Asn Tyr Asn Val
  130      135      138

```

<210> 1350
 <211> 236
 <212> Amino acid
 <213> Homo sapiens

```

<400> 1350
Ser Pro Leu Gly Lys Glu Gly Gln Glu Glu Val Arg Val Lys Ile Lys
  1      5      10      15
Asp Leu Asn Glu His Ile Val Cys Cys Leu Cys Ala Gly Tyr Phe Val
      20      25      30
Asp Ala Thr Thr Ile Thr Glu Cys Leu His Thr Phe Cys Lys Ser Cys
      35      40      45
Ile Val Lys Tyr Leu Gln Thr Ser Lys Tyr Cys Pro Met Cys Asn Ile
  50      55      60
Lys Ile His Glu Thr Gln Pro Leu Leu Asn Leu Lys Leu Asp Arg Val
  65      70      75      80
Met Gln Asp Ile Val Tyr Lys Leu Val Pro Gly Leu Gln Asp Ser Glu
      85      90      95
Glu Lys Arg Ile Arg Glu Phe Tyr Gln Ser Arg Gly Leu Asp Arg Val
      100      105      110
Thr Gln Pro Thr Gly Glu Glu Pro Ala Leu Ser Asn Leu Gly Leu Pro
      115      120      125
Phe Ser Ser Phe Asp His Ser Lys Ala His Tyr Tyr Arg Tyr Asp Glu
  130      135      140
Gln Leu Asn Leu Cys Leu Glu Arg Leu Ser Ser Gly Lys Asp Lys Asn
  145      150      155      160
Lys Ser Val Leu Gln Asn Lys Tyr Val Arg Cys Ser Val Arg Ala Glu
      165      170      175
Val Arg His Leu Arg Arg Val Leu Cys His Arg Leu Met Leu Asn Pro
      180      185      190
Gln His Val Gln Leu Leu Phe Asp Asn Glu Val Leu Pro Asp His Met
      195      200      205
Thr Met Lys Gln Ile Trp Leu Ser Arg Trp Phe Gly Lys Pro Ser Pro
  210      215      220
Leu Leu Leu Gln Tyr Ser Val Lys Glu Lys Arg Arg
  225      230      235      236

```

<210> 1351
 <211> 178
 <212> Amino acid
 <213> Homo sapiens

<400> 1351

Leu Trp Trp Tyr Ser Ala His Ala Ala Val Asp Ala Met Met Asp Val
 1 5 10 15
 Phe Gly Val Gly Phe Pro Ser Lys Val Pro Trp Lys Lys Met Ser Ala
 20 25 30
 Glu Glu Leu Glu Asn Gln Tyr Cys Pro Ser Arg Trp Val Val Arg Leu
 35 40 45
 Gly Ala Glu Glu Ala Leu Arg Thr Tyr Ser Gln Ile Gly Ile Glu Ala
 50 55 60
 Thr Thr Arg Ala Arg Ala Thr Arg Lys Ser Leu Leu His Val Pro Tyr
 65 70 75 80
 Gly Asp Gly Glu Gly Glu Lys Val Asp Ile Tyr Phe Pro Asp Glu Ser
 85 90 95
 Ser Glu Ala Thr Thr Arg Ala Arg Ala Thr Arg Lys Ser Leu Leu His
 100 105 110
 Val Pro Tyr Gly Asp Gly Glu Gly Lys Val Asp Ile Tyr Phe Pro
 115 120 125
 Asp Glu Ser Ser Glu Ala Leu Pro Phe Phe Leu Phe Phe His Gly Gly
 130 135 140
 Tyr Trp Gln Ser Gly Arg His Pro Gly Pro His Gly Arg Pro Gly Asp
 145 150 155 160
 Pro Gln Arg Cys Val Cys Pro Glu Ala Val Ser Lys Gln Gln Ala Phe
 165 170 175
 Ser Trp
 178

<210> 1352

<211> 284

<212> Amino acid

<213> Homo sapiens

<400> 1352

Gly Val Arg Met Ala Ser Arg Gly Arg Arg Pro Glu His Gly Gly Pro
 1 5 10 15
 Pro Glu Leu Phe Tyr Asp Glu Thr Glu Ala Arg Lys Tyr Val Arg Asn
 20 25 30
 Ser Arg Met Ile Asp Ile Gln Thr Arg Met Ala Gly Arg Ala Leu Glu
 35 40 45
 Leu Leu Tyr Leu Pro Glu Asn Lys Pro Cys Tyr Leu Leu Asp Ile Gly
 50 55 60
 Cys Gly Thr Gly Leu Ser Gly Ser Tyr Leu Ser Asp Glu Gly His Tyr
 65 70 75 80
 Trp Val Gly Leu Asp Ile Ser Pro Ala Met Leu Asp Glu Ala Val Asp
 85 90 95
 Arg Glu Ile Glu Gly Asp Leu Leu Leu Gly Asp Met Gly Gln Gly Ile
 100 105 110
 Pro Phe Lys Pro Gly Thr Phe Asp Gly Cys Ile Ser Ile Ser Ala Val
 115 120 125
 Gln Trp Leu Cys Asn Ala Asn Lys Lys Ser Glu Asn Pro Ala Lys Arg
 130 135 140
 Leu Tyr Cys Phe Phe Ala Ser Leu Phe Ser Val Leu Val Arg Gly Ser
 145 150 155 160
 Arg Ala Val Leu Gln Leu Tyr Pro Glu Asn Ser Glu Gln Leu Glu Leu
 165 170 175
 Ile Thr Thr Gln Ala Thr Lys Ala Gly Phe Ser Gly Gly Met Val Val
 180 185 190
 Asp Tyr Pro Asn Ser Ala Lys Ala Lys Lys Phe Tyr Leu Cys Leu Phe

	195		200		205										
Ser	Gly	Pro	Ser	Thr	Phe	Ile	Pro	Glu	Gly	Leu	Ser	Glu	Asn	Gln	Asp
	210					215						220			
Glu	Val	Glu	Pro	Arg	Glu	Ser	Val	Phe	Thr	Asn	Glu	Arg	Phe	Pro	Leu
225					230					235				240	
Arg	Met	Ser	Arg	Arg	Gly	Met	Val	Arg	Lys	Ser	Arg	Ala	Trp	Val	Leu
			245						250					255	
Glu	Lys	Lys	Glu	Arg	His	Arg	Arg	Gln	Gly	Arg	Glu	Val	Arg	Pro	Asp
			260					265					270		
Thr	Gln	Tyr	Thr	Gly	Arg	Lys	Arg	Lys	Pro	Arg	Phe				
	275						280				284				

<210> 1353

<211> 363

<212> Amino acid

<213> Homo sapiens

<400> 1353

Thr	Leu	Ile	Cys	Arg	Met	Ala	Gly	Cys	Gly	Glu	Ile	Asp	His	Ser	Ile
1				5					10					15	
Asn	Met	Leu	Pro	Thr	Asn	Arg	Lys	Ala	Asn	Glu	Ser	Cys	Ser	Asn	Thr
			20					25					30		
Ala	Pro	Ser	Leu	Thr	Val	Pro	Glu	Cys	Ala	Ile	Cys	Leu	Gln	Thr	Cys
		35					40					45			
Val	His	Pro	Val	Ser	Leu	Pro	Cys	Lys	His	Val	Phe	Cys	Tyr	Leu	Cys
	50					55				60					
Val	Lys	Gly	Ala	Ser	Trp	Leu	Gly	Lys	Arg	Cys	Ala	Leu	Cys	Arg	Gln
65				70					75					80	
Glu	Ile	Pro	Glu	Asp	Phe	Leu	Asp	Lys	Pro	Thr	Leu	Leu	Ser	Pro	Glu
			85					90					95		
Glu	Leu	Lys	Ala	Ala	Ser	Arg	Gly	Asn	Gly	Glu	Tyr	Ala	Trp	Tyr	Tyr
		100					105					110			
Glu	Gly	Arg	Asn	Gly	Trp	Trp	Gln	Tyr	Asp	Glu	Arg	Thr	Ser	Arg	Glu
	115						120					125			
Leu	Glu	Asp	Ala	Phe	Ser	Lys	Gly	Lys	Lys	Asn	Thr	Glu	Met	Leu	Ile
	130					135					140				
Ala	Gly	Phe	Leu	Tyr	Val	Ala	Asp	Leu	Glu	Asn	Met	Val	Gln	Tyr	Arg
145				150					155					160	
Arg	Asn	Glu	His	Gly	Arg	Arg	Arg	Lys	Ile	Lys	Arg	Asp	Ile	Ile	Asp
			165					170					175		
Ile	Pro	Lys	Lys	Gly	Val	Ala	Gly	Leu	Arg	Leu	Asp	Cys	Asp	Ala	Asn
		180					185						190		
Thr	Val	Asn	Leu	Ala	Arg	Glu	Ser	Ser	Ala	Asp	Gly	Ala	Asp	Ser	Val
	195						200					205			
Ser	Ala	Gln	Ser	Gly	Ala	Ser	Val	Gln	Pro	Leu	Val	Ser	Ser	Val	Arg
	210						215					220			
Pro	Leu	Thr	Ser	Val	Asp	Gly	Gln	Leu	Thr	Ser	Pro	Ala	Thr	Pro	Ser
225					230					235				240	
Pro	Asp	Ala	Ser	Thr	Ser	Leu	Glu	Asp	Ser	Phe	Ala	His	Leu	Gln	Leu
			245						250					255	
Ser	Gly	Asp	Asn	Thr	Ala	Glu	Arg	Ser	His	Arg	Gly	Glu	Gly	Glu	Glu
		260					265					270			
Asp	His	Glu	Ser	Pro	Ser	Ser	Gly	Arg	Val	Pro	Ala	Pro	Asp	Thr	Ser
	275						280				285				
Ile	Glu	Glu	Thr	Glu	Ser	Asp	Ala	Ser	Ser	Asp	Ser	Glu	Asp	Val	Ser
	290					295					300				
Ala	Val	Val	Ala	Gln	His	Ser	Leu	Thr	Gln	Gln	Arg	Leu	Leu	Val	Ser
305				310						315					320
Asn	Ala	Asn	Gln	Thr	Val	Pro	Asp	Arg	Ser	Asp	Arg	Ser	Gly	Thr	Asp

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<210> 1354
<211> 368
<212>Amino acid
<213> Homo sapiens
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844

<210> 1355
 <211> 117
 <212>Amino acid
 <213> Homo sapiens

<400> 1355
 Pro Thr Thr Ser Asn Arg Ala Ile Thr Leu Thr Ala Trp Pro Lys Ile
 1 5 10 15
 Pro Phe Leu Gly Ile Cys Glu Ala Lys Asn Pro Arg Ser Glu Asn Met
 20 25 30
 Arg Leu Ala Thr Ile Leu Glu Val Ala Cys His His Leu Gly Ser Gly
 35 40 45
 Pro Pro Pro Ser Trp Glu Leu Trp Glu Gln Gly Pro Pro Gly Asn Ser
 50 55 60
 Ser Arg Tyr Ile Glu Phe Leu Asn Lys His Thr Tyr Ile Lys Gly Thr
 65 70 75 80
 Leu Arg Val Tyr Thr Lys Lys Phe Cys Met Leu Val Ile Lys Ser Phe
 85 90 95
 Glu Ser Lys Ser Cys Val Cys Val Tyr Asp Phe Asp Ser Lys Ser Ser
 100 105 110
 Val Asn Val Thr Val
 115 117

<210> 1356
 <211> 126
 <212>Amino acid
 <213> Homo sapiens

<400> 1356
 Pro Arg Val Arg Phe Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala
 1 5 10 15
 Trp Ile Leu Cys Gly Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile
 20 25 30
 Met Leu Leu Asp Ser Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys
 35 40 45
 Leu Glu Leu Asn Leu Tyr Lys Ile Ala Lys Leu Gln Thr Val Asn Tyr
 50 55 60
 Ile Ala Leu Val Val Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile
 65 70 75 80
 Cys Tyr Leu Leu Ile Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu
 85 90 95
 Ser Gly Leu Arg Val Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile
 100 105 110
 Thr Leu Ile Ile Phe Phe Leu Cys Phe Leu Pro Tyr His Thr
 115 120 125 126

<210> 1357
 <211> 222
 <212>Amino acid
 <213> Homo sapiens

<400> 1357

Gly Arg His Trp Leu Gly Ser Ala Gln Leu Thr Asp Gly Gly Ser Ala
 1 5 10 15
 Arg Lys Pro Lys Met Ala Val Pro Ala Ala Leu Ile Leu Arg Glu Ser
 20 25 30
 Pro Ser Met Lys Lys Ala Val Ser Leu Ile Asn Ala Ile Asp Thr Gly
 35 40 45
 Arg Phe Pro Arg Leu Leu Thr Arg Ile Leu Gln Lys Leu His Leu Lys
 50 55 60
 Ala Glu Ser Ser Phe Ser Glu Glu Glu Glu Lys Leu Gln Ala Ala
 65 70 75 80
 Phe Ser Leu Glu Lys Gln Asp Leu His Leu Val Leu Glu Thr Ile Ser
 85 90 95
 Phe Ile Leu Glu Gln Ala Val Tyr His Asn Val Lys Pro Ala Ala Leu
 100 105 110
 Gln Gln Gln Leu Glu Asn Ile His Leu Arg Gln Asp Lys Ala Glu Ala
 115 120 125
 Phe Val Asn Thr Trp Ser Ser Met Gly Gln Glu Thr Val Glu Lys Phe
 130 135 140
 Arg Gln Arg Ile Leu Ala Pro Cys Lys Leu Glu Thr Val Gly Trp Gln
 145 150 155 160
 Leu Asn Leu Gln Met Ala His Ser Ala Gln Ala Lys Leu Lys Ser Pro
 165 170 175
 Gln Ala Val Leu Gln Leu Gly Val Asn Asn Glu Asp Ser Lys Ser Leu
 180 185 190
 Glu Lys Val Leu Val Glu Phe Ser His Lys Glu Leu Phe Asp Phe Tyr
 195 200 205
 Asn Lys Leu Glu Thr Ile Gln Ala Gln Leu Asp Ser Leu Thr
 210 215 220 222

<210> 1358

<211> 116

<212> Amino acid

<213> Homo sapiens

<400> 1358

Glu Ala Ser Ser Ala Lys Thr Lys Arg Lys Glu Glu Lys Gly Pro Lys
 1 5 10 15
 Ala Lys Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu
 20 25 30
 Leu Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
 35 40 45
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val Ala
 50 55 60
 Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp Asp Gly
 65 70 75 80
 Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu Leu Leu Cys
 85 90 95
 Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser Phe Val Ile Pro
 100 105 110
 Cys Asn Asn Gln
 115 116

<210> 1359

<211> 466
 <212> Amino acid
 <213> Homo sapiens

<400> 1359

```

Lys Met Ala Glu Ala Val Phe His Ala Pro Lys Arg Lys Arg Arg Val
 1           5           10           15
Tyr Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His
      20           25           30
Gly Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn
      35           40           45
Asn Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys
      50           55           60
Gly Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr
      65           70           75           80
Ile Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn
      85           90           95
Met Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala
      100          105          110
Ala Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg
      115          120          125
Ile Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg
      130          135          140
Asn Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser
      145          150          155          160
Asn Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly
      165          170          175
Asp Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly
      180          185          190
Cys Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu
      195          200          205
Lys Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Cys
      210          215          220
Lys Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly
      225          230          235          240
Ser Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His
      245          250          255
Glu Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu
      260          265          270
Ala Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg
      275          280          285
Arg Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu
      290          295          300
Ala Phe Phe Leu Val Tyr Ala Leu Gly Cys Leu Ser Ile Tyr Tyr Glu
      305          310          315          320
Lys Glu Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val
      325          330          335
Gln Pro Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser
      340          345          350
Lys Gly Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu
      355          360          365
Leu Tyr Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile
      370          375          380
Ile Glu Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu
      385          390          395          400
Ser Trp Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser
      405          410          415
Lys Glu Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp
      420          425          430
Lys Glu Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu

```

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<210> 1360
<211> 419
<212> Amino acid
<213> Homo sapiens
```

848

```

      370              375              380
Ser Pro Asp Asp Ser Asp Ser Ser Tyr Gly Ser His Ser Thr Asp Ser
385              390              395              400
Leu Met Gly Ser Ser Pro Val Phe Asn Gln Arg Cys Lys Lys Arg Met
      405              410              415
Arg Lys Ile
      419

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<210> 1361
<211> 220
<212>Amino acid
<213> Homo sapiens

```

```

<400> 1361
Arg Glu Gln Ile Leu Phe Ile Glu Ile Arg Asp Thr Ala Lys Gly Gly
 1              5              10              15
Glu Thr Glu Gln Pro Pro Ser Leu Ser Pro Leu His Gly Gly Arg Met
      20              25              30
Pro Glu Met Gly Glu Gly Ile Gln Ser Leu Ala Arg Glu Thr Gln Ser
      35              40              45
His Arg Gly Arg Arg Gln Gly Trp Asp Ala Thr Trp Val Thr Arg Cys
      50              55              60
Arg Glu Ser Leu Asn Arg Gly Gly Ala Gly Ala Gly Lys Arg Ala Gly
      65              70              75              80
Ala Leu Ala His His Val Phe Leu Ala Leu Ile Glu Pro Asn Leu Ala
      85              90              95
Glu Arg Glu Ala Ser Glu Glu Glu Val Lys Ala Cys Ser Asp Glu Thr
      100             105             110
Val Val Ala Asp Leu Leu Val Lys Val Val Tyr Val Leu Gly Ala Ile
      115             120             125
Leu Lys Ile Phe Leu Arg Glu Gly Asn Val Leu Asn Gln His Ser Gly
      130             135             140
Met Asp Ile Glu Lys Tyr Ser Glu His Tyr Gln His Asp His Ser Pro
      145             150             155             160
Gly Ala Glu Asp Asp Ala Ala Gly Gly Gln Leu Arg Pro Thr Ala Gln
      165             170             175
Glu Arg Arg His Lys Glu Gly Ser Arg Gly Ser Pro Arg Cys Lys Arg
      180             185             190
Ala Arg Lys Ala Val Gly Glu Ser Pro Gly Cys Pro Arg Pro Arg Val
      195             200             205
Arg Pro Arg Val Arg Pro Arg Val Arg Pro Arg Val
      210             215             220

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<210> 1362
<211> 82
<212>Amino acid
<213> Homo sapiens

```

```

<400> 1362
Gly Thr Arg Gly Cys Cys Arg Glu Gly Thr Ala Tyr Ala Lys Ala Tyr
 1              5              10              15
Gln Phe Met Ala Ser His Leu Ser Leu Gly Lys Pro Val Ser Thr Gly
      20              25              30
Ser Ile Pro Arg Phe Asn Lys Ala Leu Phe Asn Lys Gln Ala Lys Cys

```

```

          35          40          45
Lys Pro Asn His Tyr Ser Phe Ile Gly Leu Ser Met Leu Ser Pro Glu
          50          55          60
Asn Phe Ser Ile Gly Cys Lys Tyr Ser Val Trp Phe Ser Glu Thr Lys
          65          70          75          80
Gly Phe
          82

```

<210> 1363
 <211> 143
 <212> Amino acid
 <213> Homo sapiens

```

          <400> 1363
Gly Ala Gln Gly Val Arg Val Gly Ile Gly Glu Val Gly Arg Val Gln
 1          5          10          15
Ala Pro Arg Val Ser Leu Leu His Ser Gln Gly Val Pro Arg Gly Gly
          20          25          30
Thr Gly Glu Ala Val Lys Glu Glu Gly Arg Gly Ser Ser Leu His Pro
          35          40          45
Pro Leu Pro Pro Gln Gly Leu Gly Glu Tyr Ala Ala Cys Gln Ser His
          50          55          60
Ala Phe Met Lys Gly Val Phe Thr Phe Val Thr Gly Thr Gly Met Ala
          65          70          75          80
Phe Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro Leu Gln
          85          90          95
Trp Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser Tyr Gly
          100          105          110
Val Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu Phe Leu
          115          120          125
Glu Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Arg Ser
          130          135          140          143

```

<210> 1364
 <211> 194
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(194)
 <223> X = any amino acid or stop code

```

          <400> 1364
Gly Thr Ser Glu Leu Leu Cys Ile Gln Arg Trp Asn Trp Gly Pro Ala
 1          5          10          15
Phe Pro Pro Arg Pro Gly Leu Ala Leu Ala Pro Thr Leu Gln Leu Leu
          20          25          30
Val Glu Met Gly Ser Ala Lys Ser Val Pro Val Thr Pro Ala Arg Pro
          35          40          45
Pro Pro His Asn Lys His Leu Ala Arg Val Ala Asp Pro Arg Ser Pro
          50          55          60
Ser Ala Gly Ile Leu Arg Thr Pro Ile Gln Val Glu Ser Ser Pro Gln
          65          70          75          80

```

```

Pro Gly Leu Pro Ala Gly Glu Gln Leu Glu Gly Leu Lys His Ala Gln
      85                      90                      95
Asp Ser Asp Pro Arg Ser Pro Leu Gly Lys Asn Xaa Gly His Gly Trp
      100                    105                    110
Gln Val Gly Gln Gly Ser Asp Leu Gly Ser Pro Gln Pro Leu Pro Pro
      115                    120                    125
Ser Ala Ser His Leu Tyr Ser Ser Arg Ala Ser Arg Cys Ser Gln Pro
      130                    135                    140
Pro Cys Leu Ser Leu Pro Trp Phe Gly Val Arg Ser Ser Pro Ala Asn
      145                    150                    155                    160
Thr Tyr His Val Pro Val Thr Ser Leu Cys Pro Ser Pro Ala Leu His
      165                    170                    175
Tyr Thr Ala Leu Gln Ala Gly Ile Ile Ser Thr Ser Gln Ala Arg Ala
      180                    185                    190
Pro Arg
      194

```

```

<210> 1365
<211> 114
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)...(114)
<223> X = any amino acid or stop code

```

```

<400> 1365
Pro Leu Leu Leu Pro Arg Phe Ile Asp Ile Pro Cys Leu Leu Cys Tyr
  1          5          10          15
Leu Thr Gln Val Thr Pro Asp Asp Met Tyr Ala Lys Ala Phe Leu Ile
      20          25          30
Lys Pro Asn Thr Ala Ile Thr Gly Thr Asp Arg Arg Lys Leu Arg Ala
      35          40          45
Asp Glu Thr Thr Asp Phe Pro Thr Leu Gly Thr Asp Gln Ile Tyr Glu
      50          55          60
Leu Leu Pro Gly Lys Asp Glu Leu Asn Ile Val Lys Ser Asn Ala His
      65          70          75          80
Lys Arg Asp Ala Xaa Thr Ala Tyr Val Ser Gly Glu Asn His Ile Leu
      85          90          95
Ser Glu Pro Xaa Lys Asn Leu Tyr Pro Ala Val Asn Thr Leu Ser Ser
      100          105          110
Tyr Pro
      114

```

```

<210> 1366
<211> 80
<212>Amino acid
<213> Homo sapiens

```

```

<400> 1366
Ser Arg Gln Pro Pro Leu Leu Thr Met Val Phe Leu Leu Glu Phe
  1          5          10          15
Leu Phe Leu Val Phe Phe Pro Gly Cys Val Asn Gln Leu Leu Leu Ser

```

```

      20      25      30
Tyr Pro Trp Gln Gly Gln Gly Thr Ser Leu Trp Ser Ser Leu Ser Phe
      35      40      45
His Trp Leu Leu Pro Gln Glu Asp Ser Ser Arg Leu Ser Ile Phe Pro
      50      55      60
Leu Arg Ala Gly Ser Pro Pro Gln Pro Ala Gln Ala Pro Gln Arg Ile
      65      70      75      80

```

<210> 1367
 <211> 301
 <212>Amino acid
 <213> Homo sapiens

```

      <400> 1367
Lys Ser Arg Glu Gln Ser Ser Leu Phe Ala Ala Asp Ala Glu Arg Ser
  1      5      10      15
Trp Gly Gly Lys Ser Cys Cys Leu Leu Arg Trp Arg Phe Val Gly Lys
      20      25      30
Ala Ser His Phe Pro Arg Leu Leu Pro Leu Pro Gly Glu Glu Arg Pro
      35      40      45
Glu Thr Lys Glu Arg Ala Trp Lys Met Glu Gln Thr Trp Thr Arg Asp
      50      55      60
Tyr Phe Ala Glu Asp Asp Gly Glu Met Val Pro Arg Thr Ser His Thr
      65      70      75      80
Ala Ala Ser Val Ser Leu Thr Ala Phe Leu Ser Asp Thr Lys Asp Arg
      85      90      95
Gly Pro Pro Val Gln Ser Gln Ile Trp Arg Ser Gly Glu Lys Val Pro
      100      105      110
Phe Val Gln Thr Tyr Ser Leu Arg Ala Phe Glu Lys Pro Pro Gln Val
      115      120      125
Gln Thr Gln Ala Leu Arg Asp Phe Glu Lys His Leu Asn Asp Leu Lys
      130      135      140
Lys Glu Asn Phe Ser Leu Lys Leu Leu Ile Tyr Phe Leu Glu Glu Arg
      145      150      155      160
Met Gln Gln Lys Tyr Glu Ala Ser Arg Glu Asp Ile Tyr Lys Arg Asn
      165      170      175
Thr Glu Leu Lys Val Glu Val Glu Ser Leu Lys Arg Glu Leu Gln Asp
      180      185      190
Lys Lys Gln His Leu Asp Lys Thr Trp Ala Asp Val Glu Asn Leu Asn
      195      200      205
Ser Gln Asn Glu Ala Glu Leu Arg Arg Gln Phe Glu Glu Arg Gln Gln
      210      215      220
Glu Met Glu His Val Tyr Glu Leu Leu Glu Asn Lys Met Gln Leu Leu
      225      230      235      240
Gln Glu Glu Ser Arg Leu Ala Lys Asn Glu Ala Ala Arg Met Ala Ala
      245      250      255
Leu Val Glu Ala Glu Lys Glu Cys Asn Leu Glu Leu Ser Glu Lys Leu
      260      265      270
Lys Gly Val Thr Lys Asn Trp Glu Asp Val Pro Gly Asp Gln Val Lys
      275      280      285
Pro Asp Gln Tyr Thr Glu Ala Leu Ala Gln Arg Asp Lys
      290      295      300 301

```

<210> 1368
 <211> 308
 <212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(308)

<223> X = any amino acid or stop code

<400> 1368

```

Thr Arg Arg Arg Gly Thr Thr Trp Arg Ser Pro Arg Pro Arg Arg Ala
 1          5          10          15
Ser Thr Ser Arg Pro Ser Thr Arg Pro Arg Gly Val Ala Ser Trp Pro
          20          25          30
Trp Glu Thr Ala Gly Thr Ala Thr Thr Gly Pro Gly Pro Ser Ala Arg
          35          40          45
Thr Arg Arg Arg Ala Ala Arg Arg Arg Ser Arg Pro Arg Arg Arg
          50          55          60
Ala His Gly Gly Leu Ser Gln Pro Ala Gly Trp Gln Ser Leu Leu Ser
          65          70          75          80
Phe Thr Ile Leu Phe Leu Ala Trp Leu Ala Gly Phe Ser Ser Arg Leu
          85          90          95
Phe Ala Val Ile Arg Phe Glu Ser Ile Ile His Glu Phe Asp Pro Trp
          100          105          110
Phe Asn Tyr Arg Ser Thr His His Leu Ala Ser His Gly Phe Tyr Glu
          115          120          125
Phe Leu Asn Trp Phe Asp Glu Arg Ala Trp Tyr Pro Leu Gly Arg Ile
          130          135          140
Val Gly Gly Thr Val Tyr Pro Gly Leu Met Ile Thr Ala Gly Leu Ile
          145          150          155          160
His Trp Ile Leu Asn Thr Leu Asn Ile Thr Val His Ile Arg Asp Val
          165          170          175
Cys Val Phe Leu Ala Pro Thr Phe Ser Gly Leu Thr Ser Ile Ser Thr
          180          185          190
Phe Leu Leu Thr Arg Glu Leu Trp Asn Gln Gly Ala Gly Leu Leu Ala
          195          200          205
Ala Cys Phe Ile Ala Ile Val Pro Gly Tyr Ile Ser Arg Ser Val Ala
          210          215          220
Gly Ser Phe Asp Asn Glu Gly Ile Ala Ile Phe Ala Leu Gln Phe Thr
          225          230          235          240
Tyr Tyr Leu Trp Val Lys Ser Val Lys Thr Gly Ser Val Phe Trp Thr
          245          250          255
Met Cys Cys Cys Leu Ser Tyr Phe Tyr Met Val Ser Ala Trp Gly Gly
          260          265          270
Tyr Val Phe Ile Ile Asn Leu Ile Pro Leu His Ala Phe Val Leu Val
          275          280          285
Leu Met Gln Arg Tyr Ser Lys Arg Val Tyr Ile Xaa Tyr Ser Thr Phe
          290          295          300
Tyr Ile Val Gly
          305          308

```

<210> 1369

<211> 212

<212> Amino acid

<213> Homo sapiens

<400> 1369

Arg Arg Leu Ile Val Val Leu Ser Asp Ala Phe Leu Ser Arg Ala Trp
 1 5 10 15
 Cys Ser His Ser Phe Arg Val Gly Pro Ala Arg Gly Trp Val Gly Pro
 20 25 30
 Ser Val Ala Pro Thr Pro Leu Thr Val Pro Pro Arg Arg Glu Gly Leu
 35 40 45
 Cys Arg Leu Leu Glu Leu Thr Arg Arg Pro Ile Phe Ile Thr Phe Glu
 50 55 60
 Gly Gln Arg Arg Asp Pro Ala His Pro Ala Leu Arg Leu Leu Arg Gln
 65 70 75 80
 His Arg His Leu Val Thr Leu Leu Leu Trp Arg Pro Gly Ser Val Thr
 85 90 95
 Pro Ser Ser Asp Phe Trp Lys Glu Val Gln Leu Ala Leu Pro Arg Lys
 100 105 110
 Val Arg Tyr Arg Pro Val Glu Gly Asp Pro Gln Thr Gln Leu Gln Asp
 115 120 125
 Asp Lys Asp Pro Met Leu Ile Leu Arg Gly Arg Val Pro Glu Gly Arg
 130 135 140
 Ala Leu Asp Ser Glu Val Asp Pro Asp Pro Glu Gly Asp Leu Gly Val
 145 150 155 160
 Arg Gly Pro Val Phe Gly Glu Pro Ser Ala Pro Pro His Thr Ser Gly
 165 170 175
 Val Ser Leu Gly Glu Ser Arg Ser Ser Glu Val Asp Val Ser Asp Leu
 180 185 190
 Gly Ser Arg Asn Tyr Ser Ala Arg Thr Asp Phe Tyr Cys Leu Val Ser
 195 200 205
 Lys Asp Asp Met
 210 212

<210> 1370

<211> 281

<212> Amino acid

<213> Homo sapiens

<400> 1370

Leu Ser His Glu Gly Trp Arg Arg Gly Arg Glu Gly Glu Arg Ile Asn
 1 5 10 15
 Ser Ser Val Ala Ser Leu Ala Pro Leu Cys Ile Leu Pro Asp Leu Pro
 20 25 30
 Ser Asn Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu
 35 40 45
 Leu Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
 50 55 60
 Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg Glu
 65 70 75 80
 Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His Ala Gly
 85 90 95
 Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met Gly Ser His
 100 105 110
 Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu Asn His Gly Met
 115 120 125
 Asp Lys Val Ala His Glu Ile Asn His Gly Ile Gly Gln Ala Gly Lys
 130 135 140
 Glu Ala Glu Lys Leu Gly His Gly Val Asn Asn Ala Ala Gly Gln Ala
 145 150 155 160
 Gly Lys Glu Ala Asp Lys Ala Val Gln Gly Phe His Thr Gly Val His
 165 170 175
 Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly Gln Gly Val Asn His Ala
 180 185 190

Ala	Asp	Gln	Ala	Gly	Lys	Glu	Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His
	195						200					205			
His	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly
	210					215					220				
Val	Asn	Gln	Ala	Ser	Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His
	225				230					235					240
Gln	Ser	Gly	Ser	Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu
			245						250					255	
Ala	Ser	Gly	Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu
		260						265						270	
Trp	Arg	Ser	Val	Ala	Asn	Ile	Met	Pro							
		275					280	281							

<210> 1371
 <211> 119
 <212> Amino acid
 <213> Homo sapiens

<400> 1371

Ser	Ala	Ser	Gly	Gly	Leu	Gly	Met	Thr	Val	Glu	Gly	Pro	Glu	Gly	Ser
1				5					10					15	
Glu	Arg	Glu	His	Arg	Pro	Pro	Glu	Lys	Pro	Pro	Arg	Pro	Pro	Arg	Pro
			20					25					30		
Leu	His	Leu	Ser	Asp	Arg	Ser	Phe	Arg	Arg	Lys	Lys	Asp	Ser	Val	Glu
		35					40					45			
Ser	His	Pro	Thr	Trp	Val	Asp	Asp	Thr	Arg	Ile	Asp	Ala	Asp	Ala	Ile
	50					55					60				
Val	Glu	Lys	Ile	Val	Gln	Ser	Gln	Asp	Phe	Thr	Asp	Gly	Ser	Asn	Thr
	65				70					75				80	
Glu	Asp	Ser	Asn	Leu	Arg	Leu	Phe	Val	Ser	Arg	Asp	Gly	Ser	Ala	Thr
			85					90						95	
Leu	Ser	Gly	Ile	Gln	Leu	Ala	Thr	Arg	Val	Ser	Ser	Gly	Val	Tyr	Glu
		100						105					110		
Pro	Val	Val	Ile	Glu	Ser	His									
		115				119									

<210> 1372
 <211> 108
 <212> Amino acid
 <213> Homo sapiens

<400> 1372

Glu	Arg	Ser	Gly	Trp	Pro	Gln	Pro	Glu	Gly	Thr	Val	Thr	Ala	Gln	Gly
1				5					10					15	
Pro	Leu	Phe	Trp	Glu	Arg	Leu	Ser	Gly	Ala	Val	Thr	Val	Ser	Ser	Gly
			20					25					30		
Tyr	Lys	Ala	Asp	Met	Trp	Pro	Ser	Phe	Pro	Gln	Val	Arg	Val	Gly	Ser
	35					40						45			
Phe	Leu	Phe	Gly	Ile	Leu	Phe	Ser	Phe	Gly	Ser	Ser	Ser	Ser	Leu	Pro
	50				55					60					
Pro	Gly	Leu	Pro	Pro	Pro	Ala	Ser	Leu	Leu	Cys	Cys	Ala	Val	Gln	Trp
	65				70				75					80	
Gly	Ala	Arg	Ala	Leu	Phe	Leu	Pro	Cys	Leu	Lys	Glu	Arg	Ala	Leu	Gly
			85					90						95	

Met Glu Met Arg Asn Asn Thr Leu Ser Phe Arg Gln
 100 105 108

<210> 1373
 <211> 209
 <212>Amino acid
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)...(209)
 <223> X = any amino acid or stop code

<400> 1373
 Ser Ser Ser Asn Leu Arg Leu Ser Phe Leu Ile Asn Glu Asn Ile Leu
 1 5 10 15
 Gly Lys Cys Phe Arg Ser Gly Pro Ser Cys Ala Gly Pro Arg Ile Ser
 20 25 30
 Pro Leu Ala Ala Gln Tyr Glu Cys Pro Arg Pro Ser Leu Leu Ile Met
 35 40 45
 Ala Ser Val Pro Lys Thr Asn Lys Ile Glu Pro Arg Ser Tyr Ser Ile
 50 55 60
 Ile Pro Ser Cys Gly Ile Arg Arg Leu Gly Pro Ala Leu Asn Thr Leu
 65 70 75 80
 Ile Phe Gln Ser Lys Arg Phe Gly Pro Arg Gly His Ser Ala Lys Ser
 85 90 95
 Ile Glu Gly Ala Pro Arg Gly Lys Gly Arg Gly Arg Ala Val Ala Arg
 100 105 110
 Leu Ala Ala Asp Arg Pro Pro Ala Pro Lys Ile Gln Leu Arg Ala Phe
 115 120 125
 Xaa Leu Gln Gln Leu Xaa Tyr Thr Leu Leu Glu Leu Glu Leu Pro Arg
 130 135 140
 Leu Leu Ala Pro Asp Leu Pro Ser Asn Gly Ser Ser Leu Lys Asp Leu
 145 150 155 160
 Lys Trp Thr His Ser Asn Tyr Arg Ala Ser Lys Glu Ser Cys Ile Val
 165 170 175
 Ile Phe Val Thr Thr Ser Pro Gly Arg Glu Trp Val Ile Cys Ala Leu
 180 185 190
 Ala Ala Phe Leu Gly Cys Gly Ser Leu Ser Gln Ala Pro Ser Pro Glu
 195 200 205
 Ser
 209

<210> 1374
 <211> 153
 <212>Amino acid
 <213> Homo sapiens

<400> 1374
 Leu Arg Ile Ile Asn Thr Tyr Phe Cys Phe Lys Phe Leu Ile Val Asn
 1 5 10 15
 Tyr Ile His Gly Thr Thr Lys Ala Arg Lys Pro His Val Leu Gly Glu
 20 25 30
 Ser Leu Ile Ser Ala Met Ser Arg Gln Glu Pro Lys Met Phe Val Leu

```

      35      40      45
Leu Tyr Val Thr Ser Phe Ala Ile Cys Ala Ser Gly Gln Pro Arg Gly
  50      55      60
Asn Gln Leu Lys Gly Glu Asn Tyr Ser Pro Arg Tyr Ile Cys Ser Ile
  65      70      75      80
Pro Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Ala Asn Gly Ser Pro
      85      90      95
Gly Pro His Gly Arg Ile Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly
      100      105      110
Arg Lys Gly Glu Lys Gly Glu Lys Gly Thr Ala Gly Leu Arg Gly Lys
      115      120      125
Thr Gly Pro Leu Gly Leu Ala Gly Glu Lys Gly Asp Gln Gly Glu Thr
      130      135      140
Gly Lys Lys Gly Pro Ile Gly Pro Glu
145      150      153

```

<210> 1375
 <211> 149
 <212>Amino acid
 <213> Homo sapiens

```

<400> 1375
Phe Ala Ser Ala Met Leu Gly Ser Arg Val Asp Arg Pro Lys Leu Ser
  1      5      10      15
Val Ala Pro Ser Val Val Leu Glu Glu Asp Gln Val Leu Val Ser Pro
      20      25      30
Ala Val Asp Leu Glu Ala Gly Cys Arg Leu Arg Asp Phe Thr Glu Lys
      35      40      45
Ile Met Asn Val Lys Gly Lys Val Ile Leu Ser Met Leu Val Val Ser
      50      55      60
Thr Val Ile Ile Val Phe Trp Glu Phe Ile Asn Ser Thr Glu Gly Ser
      65      70      75      80
Phe Leu Trp Ile Tyr His Ser Lys Asn Pro Glu Val Asp Asp Ser Ser
      85      90      95
Ala Gln Lys Gly Trp Trp Phe Leu Ser Trp Phe Asn Asn Gly Ile His
      100      105      110
Asn Tyr Gln Gln Gly Glu Glu Asp Ile Asp Lys Glu Lys Gly Arg Glu
      115      120      125
Glu Thr Lys Gly Arg Lys Met Thr Gln Gln Ser Phe Gly Tyr Gly Thr
      130      135      140
Gly Leu Ile Gln Thr
145      149

```

<210> 1376
 <211> 416
 <212>Amino acid
 <213> Homo sapiens

```

<400> 1376
Gly Ser His Arg Phe Ser Leu Ala Ser Pro Leu Asp Pro Glu Val Gly
  1      5      10      15
Pro Tyr Cys Asp Thr Pro Thr Met Arg Thr Leu Phe Asn Leu Leu Trp
      20      25      30
Leu Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp

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```

      35      40      45
Ala Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser
  50      55      60
Asp Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala
  65      70      75      80
Glu Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg
      85      90      95
Asp Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn
      100      105      110
Ser His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln
      115      120      125
Ile Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe
      130      135      140
Glu Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val
      145      150      155      160
Arg Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu
      165      170      175
Asp Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu
      180      185      190
Ile Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His
      195      200      205
Phe Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys
      210      215      220
Arg Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His
      225      230      235      240
Gln Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro
      245      250      255
Gly Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu
      260      265      270
Ala Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr
      275      280      285
Ala His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys
      290      295      300
Val Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu
      305      310      315      320
Gly Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg
      325      330      335
Glu Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp His Arg
      340      345      350
Pro Arg Met Val Trp Asp Ser Gln Val Ser Glu His Phe Phe Glu Tyr
      355      360      365
Lys Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr Leu Lys
      370      375      380
Ser Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val
      385      390      395      400
Ser Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
      405      410      415      416

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<210> 1377

<211> 316

<212> Amino acid

<213> Homo sapiens

<400> 1377

```

Gly Arg Glu Gly Thr Gly Trp Gly Pro Ala Met Ser Glu Val Thr Arg
  1      5      10      15
Ser Leu Leu Gln Arg Trp Gly Ala Ser Phe Arg Arg Gly Ala Asp Phe

```

```

      20      25      30
Asp Ser Trp Gly Gln Leu Val Glu Ala Ile Asp Glu Tyr Gln Ile Leu
      35      40      45
Ala Arg His Leu Gln Lys Glu Ala Gln Ala Gln His Asn Asn Ser Glu
      50      55      60
Phe Thr Glu Glu Gln Lys Lys Thr Ile Gly Lys Ile Ala Thr Cys Leu
      65      70      75      80
Glu Leu Arg Ser Ala Ala Leu Gln Ser Thr Gln Ser Gln Glu Glu Phe
      85      90      95
Lys Leu Glu Asp Leu Lys Lys Leu Glu Pro Ile Leu Lys Asn Ile Leu
      100      105      110
Thr Tyr Asn Lys Glu Phe Pro Phe Asp Val Gln Pro Val Pro Leu Arg
      115      120      125
Arg Ile Leu Ala Pro Gly Glu Glu Glu Asn Leu Glu Phe Glu Glu Asp
      130      135      140
Glu Glu Glu Gly Gly Ala Gly Ala Gly Ser Pro Asp Ser Phe Pro Ala
      145      150      155      160
Arg Val Pro Gly Thr Leu Leu Pro Arg Leu Pro Ser Glu Pro Gly Met
      165      170      175
Thr Leu Leu Thr Ile Arg Ile Glu Lys Ile Gly Leu Lys Asp Ala Gly
      180      185      190
Gln Cys Ile Asn Pro Tyr Ile Thr Val Ser Val Lys Asp Leu Asn Gly
      195      200      205
Ile Asp Leu Thr Pro Val Gln Asp Thr Pro Val Ala Ser Arg Lys Glu
      210      215      220
Asp Thr Tyr Val His Phe Asn Val Asp Ile Glu Leu Gln Lys His Val
      225      230      235      240
Glu Lys Leu Thr Lys Gly Ala Ala Ile Phe Phe Glu Phe Lys His Tyr
      245      250      255
Lys Pro Lys Lys Arg Phe Thr Ser Thr Lys Cys Phe Ala Phe Met Glu
      260      265      270
Met Asp Glu Ile Lys Leu Gly Pro Ile Val Ile Glu Leu Tyr Lys Lys
      275      280      285
Pro Thr Asp Phe Lys Arg Lys Gln Leu Gln Leu Leu Thr Lys Lys Pro
      290      295      300
Leu Tyr Leu His Leu His Gln Thr Leu His Lys Glu
      305      310      315      316

```

<210> 1378

<211> 90

<212> Amino acid

<213> Homo sapiens

<400> 1378

```

Gly Ser Ile Thr Ser Glu Pro Ser Leu Asp Ser Leu Gln Pro Leu Pro
  1      5      10      15
Pro Gly Phe Lys Arg Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp
      20      25      30
Tyr Arg Arg Pro Pro Pro Gly Leu Ala Tyr Phe Cys Ile Phe Ser Arg
      35      40      45
Asp Glu Val Ser Pro Cys Trp Pro Gly Cys Ser Pro Ser Pro Asp Leu
      50      55      60
Met Ile Arg Leu Pro Arg Pro Pro Ser Val Gly Ile Thr Gly Val Ser
      65      70      75      80
His Arg Ala Trp Pro Thr Ile Asp Asn Phe
      85      90

```

<210> 1379

<211> 332
 <212> Amino acid
 <213> Homo sapiens

<400> 1379
 Lys Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser
 1 5 10 15
 Pro Val Val Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr
 20 25 30
 His Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu
 35 40 45
 Cys Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro
 50 55 60
 Thr His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp
 65 70 75 80
 Cys Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His
 85 90 95
 Trp Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser
 100 105 110
 Gly Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu
 115 120 125
 Ser Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln
 130 135 140
 Val Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val
 145 150 155 160
 Tyr Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser
 165 170 175
 Tyr Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu
 180 185 190
 Pro Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp
 195 200 205
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu
 210 215 220
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp
 225 230 235 240
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Val
 245 250 255
 Arg Pro Pro Pro Ser Gln Val His Ser His Cys Arg Pro Cys Leu Cys
 260 265 270
 Lys Asp Ala Val Pro Tyr Gln Arg Gly Ser Leu Lys Arg Thr His Pro
 275 280 285
 Lys Gln Gly Lys Ile Gly Gly Gly Thr Ser Ala Phe Leu Val Ser Leu
 290 295 300
 Thr Leu Ala Ser Ser Ser Ser Leu Ser Ser Pro Thr Ser Phe Leu
 305 310 315 320
 Tyr Leu Phe His Arg Leu Asp Arg Arg Ser Leu Pro
 325 330 332

<210> 1380
 <211> 117
 <212> Amino acid
 <213> Homo sapiens

<400> 1380
 Leu Arg Leu Trp Asn Arg Asn Gln Met Met His Asn Ile Ile Val Lys

```

      1           5           10           15
Glu Leu Ile Val Thr Phe Phe Leu Gly Ile Thr Val Val Gln Met Leu
      20           25           30
Ile Ser Val Thr Gly Leu Lys Gly Val Glu Ala Gln Asn Gly Ser Glu
      35           40           45
Ser Glu Val Phe Val Gly Lys Tyr Glu Thr Leu Val Phe Tyr Trp Pro
      50           55           60
Ser Leu Leu Cys Leu Ala Phe Leu Leu Gly Arg Phe Leu His Met Phe
      65           70           75           80
Val Lys Ala Leu Arg Val His Leu Gly Trp Glu Leu Gln Val Glu Glu
      85           90           95
Lys Ser Val Leu Glu Val His Gln Gly Glu His Val Lys Gln Leu Leu
      100           105           110
Arg Ile Pro Arg Pro
      115           117

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<210> 1381
<211> 216
<212>Amino acid
<213> Homo sapiens

```

```

      <400> 1381
Lys Val Asn Arg Lys Leu Arg Lys Lys Gly Lys Ile Ser His Asp Lys
      1           5           10           15
Arg Lys Lys Ser Arg Ser Lys Ala Ile Gly Ser Asp Thr Ser Asp Ile
      20           25           30
Val His Ile Trp Cys Pro Glu Gly Met Lys Thr Ser Asp Ile Lys Glu
      35           40           45
Leu Asn Ile Val Leu Pro Glu Phe Glu Lys Thr His Leu Glu His Gln
      50           55           60
Gln Arg Ile Glu Ser Lys Val Cys Lys Ala Ala Ile Ala Thr Phe Tyr
      65           70           75           80
Val Asn Val Lys Glu Gln Phe Ile Lys Met Leu Lys Glu Ser Gln Met
      85           90           95
Leu Thr Asn Leu Lys Arg Lys Asn Ala Lys Met Ile Ser Asp Ile Glu
      100           105           110
Lys Lys Arg Gln Arg Met Ile Glu Val Gln Asp Glu Leu Leu Arg Leu
      115           120           125
Glu Pro Gln Leu Lys Gln Leu Gln Thr Lys Tyr Asp Glu Leu Lys Glu
      130           135           140
Arg Lys Ser Ser Leu Arg Asn Ala Ala Tyr Phe Leu Ser Asn Leu Lys
      145           150           155           160
Gln Leu Tyr Gln Asp Tyr Ser Asp Val Gln Ala Gln Glu Pro Asn Val
      165           170           175
Lys Glu Thr Tyr Asp Ser Ser Ser Leu Pro Ala Leu Leu Phe Lys Ala
      180           185           190
Arg Thr Leu Leu Gly Ala Glu Ser His Leu Arg Asn Ile Asn His Gln
      195           200           205
Leu Glu Lys Leu Leu Asp Gln Gly
      210           215 216

```

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<210> 1382
<211> 137
<212>Amino acid
<213> Homo sapiens

```

```

<220>
<221> misc_feature

```

<222> (1)...(137)

<223> X = any amino acid or stop code

<400> 1382

```

Val Trp Val Ala Met Glu Glu Pro Pro Val Arg Glu Glu Glu Xaa Glu
 1          5          10          15
Glu Gly Glu Glu Asp Glu Glu Arg Asp Glu Val Gly Pro Glu Gly Ala
      20          25          30
Leu Gly Lys Ser Pro Phe Gln Leu Thr Ala Glu Asp Val Tyr Asp Ile
      35          40          45
Ser Tyr Leu Leu Gly Arg Glu Leu Met Ala Leu Gly Ser Asp Pro Arg
      50          55          60
Val Thr Gln Leu Gln Phe Lys Val Val Arg Val Leu Glu Met Leu Glu
      65          70          75          80
Ala Leu Val Asn Glu Gly Ser Leu Ala Leu Glu Glu Leu Lys Met Glu
      85          90          95
Arg Asp His Leu Arg Lys Glu Val Glu Gly Leu Arg Arg Gln Ser Pro
      100          105          110
Pro Ala Ser Gly Glu Trp Pro Asp Ser Thr Lys Arg Arg Pro Arg Arg
      115          120          125
Lys Lys Arg Lys Arg Cys Cys Gly Tyr
      130          135          137

```

<210> 1383

<211> 90

<212>Amino acid

<213> Homo sapiens

<400> 1383

```

Pro Arg Asn Asp His Arg Leu Thr Gln Ser Arg Arg Asp Ser Ser Ser
 1          5          10          15
Lys Thr Arg Ala Phe Leu Val Pro Arg Phe Leu Pro Ala His Ala Gly
      20          25          30
Val Thr Ser Glu Glu Arg Thr Ala Met Lys Arg Glu Gly Gly Ala Ala
      35          40          45
His Leu Cys Ser Asp Ser Leu Pro Glu Ser Gln Gln Gln Asp Gly Asn
      50          55          60
His Ala Pro Asn Phe Ser Ser His Gly Ser Cys Arg Arg Arg Gln Arg
      65          70          75          80
Arg Arg His Asp Lys Ala Leu His Ala Arg
      85          90

```

<210> 1384

<211> 166

<212>Amino acid

<213> Homo sapiens

<400> 1384

```

Thr His Ala Ser Glu Lys Ser Arg Ala Thr Met Ser Ser Trp Ser Arg
 1          5          10          15

```


Gln Arg Pro Lys Ser Pro Gly Gly Ile Gln Pro His Val Ser Arg Thr
 20 25 30
 Leu Phe Leu Leu Leu Leu Leu Ala Ala Ser Ala Trp Gly Val Thr Leu
 35 40 45
 Ser Pro Lys Asp Cys Gln Val Phe Arg Ser Asp His Gly Ser Ser Ile
 50 55 60
 Ser Cys Gln Pro Pro Ala Glu Ile Pro Gly Tyr Leu Pro Ala Asp Thr
 65 70 75 80
 Val His Leu Ala Val Glu Phe Phe Asn Leu Thr His Leu Pro Ala Asn
 85 90 95
 Leu Leu Gln Gly Ala Ser Lys Leu Gln Glu Leu His Leu Ser Ser Asn
 100 105 110
 Gly Leu Glu Ser Leu Ser Pro Glu Phe Leu Arg Pro Val Pro Gln Leu
 115 120 125
 Arg Val Leu Asp Leu Thr Arg Asn Ala Leu Thr Gly Leu Pro Pro Gly
 130 135 140
 Leu Phe Gln Ala Ser Ala Thr Leu Asp Thr Leu Val Leu Lys Glu Asn
 145 150 155 160
 Gln Leu Glu Val Leu Glu
 165 166

<210> 1385

<211> 164

<212>Amino acid

<213> Homo sapiens

<400> 1385

Glu Arg Pro Arg Ile Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe
 1 5 10 15
 Leu Cys His Leu Val Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile
 20 25 30
 Ile Asn Thr Ile Gln Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys
 35 40 45
 Gln Leu Phe Arg Lys Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser
 50 55 60
 Gln Leu Val Met Leu Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile
 65 70 75 80
 Phe Thr Asp Pro Arg Ala Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile
 85 90 95
 Val Val Leu Asn His Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser
 100 105 110
 Leu Ser Glu Arg Phe Gly Leu Leu Gly Val Ser Gln Lys Cys Ile Pro
 115 120 125
 Pro Cys Leu Thr His Phe Phe Gly Ser Ala Pro Pro Leu Val Phe Leu
 130 135 140
 Leu Leu Val Ile Gln Asn Leu Gln Lys Asn Gln Gln Ser Phe Tyr Leu
 145 150 155 160
 Met Lys Trp Ser
 164

<210> 1386

<211> 289

<212>Amino acid

<213> Homo sapiens

<400> 1386

Met Ile Val Phe Gly Trp Ala Val Phe Leu Ala Ser Arg Ser Leu Gly
 1 5 10 15
 Gln Gly Leu Leu Thr Leu Glu Glu His Ile Ala His Phe Leu Gly
 20 25 30
 Thr Gly Gly Ala Ala Thr Thr Met Gly Asn Ser Cys Ile Cys Arg Asp
 35 40 45
 Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln Gln Ala Glu
 50 55 60
 Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser Gln Pro Arg Asp Pro
 65 70 75 80
 Val Arg Pro Pro Arg Arg Gly Arg Gly Pro His Glu Pro Arg Arg Lys
 85 90 95
 Lys Gln Asn Val Asp Gly Leu Val Leu Asp Thr Leu Ala Val Ile Arg
 100 105 110
 Thr Leu Val Asp Asn Asp Gln Glu Pro Pro Tyr Ser Met Ile Thr Leu
 115 120 125
 His Glu Met Ala Glu Thr Asp Glu Gly Trp Leu Asp Val Val Gln Ser
 130 135 140
 Leu Ile Arg Val Ile Pro Leu Glu Asp Pro Leu Gly Pro Ala Val Ile
 145 150 155 160
 Thr Leu Leu Leu Asp Glu Cys Pro Leu Pro Thr Lys Asp Ala Leu Gln
 165 170 175
 Lys Leu Thr Glu Ile Leu Asn Leu Asn Gly Glu Val Ala Cys Gln Asp
 180 185 190
 Ser Ser His Pro Ala Lys His Arg Asn Thr Ser Ala Val Leu Gly Cys
 195 200 205
 Leu Ala Glu Lys Leu Ala Gly Pro Ala Ser Ile Gly Leu Leu Ser Pro
 210 215 220
 Gly Ile Leu Glu Tyr Leu Leu Gln Cys Leu Leu Gln Ser His Pro Thr
 225 230 235 240
 Val Met Leu Phe Ala Leu Ile Ala Leu Glu Lys Phe Ala Gln Thr Ser
 245 250 255
 Glu Asn Lys Leu Thr Ile Ser Glu Ser Ser Ile Ser Asp Arg Leu Val
 260 265 270
 Thr Leu Glu Ser Trp Ala Asn Asp Pro Asp Tyr Leu Lys Arg Gln Val
 275 280 285
 Gly
 289

<210> 1387

<211> 320

<212> Amino acid

<213> Homo sapiens

<400> 1387

Arg Phe Gly Thr Arg Gly Leu Ala Lys Ser Lys Gly Val Val Leu Met
 1 5 10 15
 Ala Leu Cys Ala Leu Thr Arg Ala Leu Arg Ser Leu Asn Leu Ala Pro
 20 25 30
 Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln Met
 35 40 45
 Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu Pro
 50 55 60
 Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val Ser
 65 70 75 80
 Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg Lys
 85 90 95

Ser Gly Gly Arg Asp His Thr Gly Arg Ile Arg Val His Gly Ile Gly
 100 105 110
 Gly Gly His Lys Gln Arg Tyr Arg Met Ile Asp Phe Leu Arg Phe Arg
 115 120 125
 Pro Glu Glu Thr Lys Ser Gly Pro Phe Glu Glu Lys Val Ile Gln Val
 130 135 140
 Arg Tyr Asp Pro Cys Arg Ser Ala Asp Ile Ala Leu Val Ala Gly Gly
 145 150 155 160
 Ser Arg Lys Arg Trp Ile Ile Ala Thr Glu Asn Met Gln Ala Gly Asp
 165 170 175
 Thr Ile Leu Asn Ser Asn His Ile Gly Arg Met Ala Val Ala Ala Arg
 180 185 190
 Glu Gly Asp Ala His Pro Leu Gly Ala Leu Pro Val Gly Thr Leu Ile
 195 200 205
 Asn Asn Val Glu Ser Glu Pro Gly Arg Gly Ala Gln Tyr Ile Arg Ala
 210 215 220
 Ala Gly Thr Cys Gly Val Leu Leu Arg Lys Val Asn Gly Thr Ala Ile
 225 230 235 240
 Ile Gln Leu Pro Ser Lys Arg Gln Met Gln Val Leu Glu Thr Cys Val
 245 250 255
 Ala Thr Val Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile
 260 265 270
 Gly Lys Ala Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly
 275 280 285
 Arg Trp His Arg Lys Gly Gly Trp Ala Gly Arg Lys Ile Arg Pro Leu
 290 295 300
 Pro Pro Met Lys Ser Tyr Val Lys Leu Pro Ser Ala Ser Ala Gln Ser
 305 310 315 320

<210> 1388

<211> 140

<212> Amino acid

<213> Homo sapiens

<400> 1388

Pro Val Gln Gly Ala Arg Cys Trp Leu Asp Ala Arg Arg Asn Val Arg
 1 5 10 15
 Val Phe Ser Gly Val Cys Cys Gly Cys Gly Ile His Gly Tyr Trp Ala
 20 25 30
 Glu Pro Cys Gly Gly Cys Gly Ala Met Glu Gly Leu Arg Ser Ser Val
 35 40 45
 Glu Leu Asp Pro Glu Leu Thr Pro Gly Lys Leu Asp Glu Glu Met Val
 50 55 60
 Gly Leu Pro Pro His Asp Ala Ser Pro Gln Val Thr Phe His Ser Leu
 65 70 75 80
 Asp Gly Lys Thr Val Val Cys Pro His Phe Met Gly Leu Leu Leu Gly
 85 90 95
 Leu Leu Leu Leu Leu Thr Leu Ser Val Arg Asn Gln Leu Cys Val Arg
 100 105 110
 Gly Glu Arg Gln Leu Ala Glu Thr Leu His Ser Gln Val Lys Glu Lys
 115 120 125
 Ser Gln Leu Ile Gly Lys Lys Thr Asp Cys Arg Asp
 130 135 140

<210> 1389

<211> 448

<212>Amino acid

<213> Homo sapiens

<400> 1389

Gly Ala Arg Gly Arg Pro Leu Ala Glu Thr Trp Pro Phe Leu Thr Ala
 1 5 10 15
 Pro Val Leu Pro Gly Gln Leu Gln Ile Thr Glu Pro Thr Met Ala Glu
 20 25 30
 Lys Gly Asp Cys Ile Ala Ser Val Tyr Gly Tyr Asp Leu Gly Gly Arg
 35 40 45
 Phe Val Asp Phe Gln Pro Leu Gly Phe Gly Val Asn Gly Leu Val Leu
 50 55 60
 Ser Ala Val Asp Ser Arg Ala Cys Arg Lys Val Ala Val Lys Lys Ile
 65 70 75 80
 Ala Leu Ser Asp Ala Arg Ser Met Lys His Ala Leu Arg Glu Ile Lys
 85 90 95
 Ile Ile Arg Arg Leu Asp His Asp Asn Ile Val Lys Val Tyr Glu Val
 100 105 110
 Leu Gly Pro Lys Gly Thr Asp Leu Gln Gly Glu Leu Phe Lys Phe Ser
 115 120 125
 Val Ala Tyr Ile Val Gln Glu Tyr Met Glu Thr Asp Leu Ala Arg Leu
 130 135 140
 Leu Glu Gln Gly Thr Leu Ala Glu Glu His Ala Lys Leu Phe Met Tyr
 145 150 155 160
 Gln Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu His
 165 170 175
 Arg Asp Leu Lys Pro Ala Asn Ile Phe Ile Ser Thr Glu Asp Leu Val
 180 185 190
 Leu Lys Ile Gly Asp Phe Gly Leu Ala Arg Ile Val Asp Gln His Tyr
 195 200 205
 Ser His Lys Gly Tyr Leu Ser Glu Gly Leu Val Thr Lys Trp Tyr Arg
 210 215 220
 Ser Pro Arg Leu Leu Leu Ser Pro Asn Asn Tyr Thr Lys Ala Ile Asp
 225 230 235 240
 Met Trp Ala Ala Gly Cys Ile Leu Ala Glu Met Leu Thr Gly Arg Met
 245 250 255
 Leu Phe Ala Gly Ala His Glu Leu Glu Gln Met Gln Leu Ile Leu Glu
 260 265 270
 Thr Ile Pro Val Ile Arg Glu Glu Asp Lys Asp Glu Leu Leu Arg Val
 275 280 285
 Met Pro Ser Phe Val Ser Ser Thr Trp Glu Val Lys Arg Pro Leu Arg
 290 295 300
 Lys Leu Leu Pro Glu Val Asn Ser Glu Ala Ile Asp Phe Leu Glu Lys
 305 310 315 320
 Ile Leu Thr Phe Asn Pro Met Asp Arg Leu Thr Ala Glu Met Gly Leu
 325 330 335
 Gln His Pro Tyr Met Ser Pro Tyr Ser Cys Pro Glu Asp Glu Pro Thr
 340 345 350
 Ser Gln His Pro Phe Arg Ile Glu Asp Glu Ile Asp Asp Ile Val Leu
 355 360 365
 Met Ala Ala Asn Gln Ser Gln Leu Ser Asn Trp Asp Thr Cys Ser Ser
 370 375 380
 Arg Tyr Pro Val Ser Leu Ser Ser Asp Leu Glu Trp Arg Pro Asp Arg
 385 390 395 400
 Cys Gln Asp Ala Ser Glu Val Gln Arg Asp Pro Arg Ala Gly Ser Ala
 405 410 415
 Pro Leu Ala Glu Asn Val Gln Val Asp Pro Arg Lys Asp Ser His Ser
 420 425 430
 Ser Ser Ala Ser Cys Gln Ala Gly Arg Asn Gly Val Ser Arg Tyr Gln
 435 440 445 448

<210> 1390
 <211> 815
 <212> Amino acid
 <213> Homo sapiens

<400> 1390
 Met Arg Thr Leu Gly Thr Cys Leu Ala Thr Leu Ala Gly Leu Leu Leu
 1 5 10 15
 Thr Ala Ala Gly Glu Thr Phe Ser Gly Gly Cys Leu Phe Asp Glu Pro
 20 25 30
 Tyr Ser Thr Cys Gly Tyr Ser Gln Ser Glu Gly Asp Asp Phe Asn Trp
 35 40 45
 Glu Gln Val Asn Thr Leu Thr Lys Pro Thr Ser Asp Pro Trp Met Pro
 50 55 60
 Ser Gly Ser Phe Met Leu Val Asn Ala Ser Gly Arg Pro Glu Gly Gln
 65 70 75 80
 Arg Ala His Leu Leu Leu Pro Gln Leu Lys Glu Asn Asp Thr His Cys
 85 90 95
 Ile Asp Phe His Tyr Phe Val Ser Ser Lys Ser Asn Ser Pro Pro Gly
 100 105 110
 Leu Leu Asn Val Tyr Val Lys Val Asn Asn Gly Pro Leu Gly Asn Pro
 115 120 125
 Ile Trp Asn Ile Ser Gly Asp Pro Thr Arg Thr Trp Asn Arg Ala Glu
 130 135 140
 Leu Ala Ile Ser Thr Phe Trp Pro Asn Phe Tyr Gln Val Ile Phe Glu
 145 150 155 160
 Val Ile Thr Ser Gly His Gln Gly Tyr Leu Ala Ile Asp Glu Val Lys
 165 170 175
 Val Leu Gly His Pro Cys Thr Arg Thr Pro His Phe Leu Arg Ile Gln
 180 185 190
 Asn Val Glu Val Asn Ala Gly Gln Phe Ala Thr Phe Gln Cys Ser Ala
 195 200 205
 Ile Gly Arg Thr Val Ala Gly Asp Arg Leu Trp Leu Gln Gly Ile Asp
 210 215 220
 Val Arg Asp Ala Pro Leu Lys Glu Ile Lys Val Thr Ser Ser Arg Arg
 225 230 235 240
 Phe Ile Ala Ser Phe Asn Val Val Asn Thr Thr Lys Arg Asp Ala Gly
 245 250 255
 Lys Tyr Arg Cys Met Ile Arg Thr Glu Gly Gly Val Gly Ile Ser Asn
 260 265 270
 Tyr Ala Glu Leu Val Val Lys Glu Pro Pro Val Pro Ile Ala Pro Pro
 275 280 285
 Gln Leu Ala Ser Val Gly Ala Thr Tyr Leu Trp Ile Gln Leu Asn Ala
 290 295 300
 Asn Ser Ile Asn Gly Asp Gly Pro Ile Val Ala Arg Glu Val Glu Tyr
 305 310 315 320
 Cys Thr Ala Ser Gly Ser Trp Asn Asp Arg Gln Pro Val Asp Ser Thr
 325 330 335
 Ser Tyr Lys Ile Gly His Leu Asp Pro Asp Thr Glu Tyr Glu Ile Ser
 340 345 350
 Val Leu Leu Thr Arg Pro Gly Glu Gly Gly Thr Gly Ser Pro Gly Pro
 355 360 365
 Ala Leu Arg Thr Arg Thr Lys Cys Ala Asp Pro Met Arg Gly Pro Arg
 370 375 380
 Lys Leu Glu Val Val Glu Val Lys Ser Arg Gln Ile Thr Ile Arg Trp
 385 390 395 400

Glu Pro Phe Gly Tyr Asn Val Thr Arg Cys His Ser Tyr Asn Leu Thr
 405 410 415
 Val His Tyr Cys Tyr Gln Val Gly Gly Gln Glu Gln Val Arg Glu Glu
 420 425 430
 Val Ser Trp Asp Thr Glu Asn Ser His Pro Gln His Thr Ile Thr Asn
 435 440 445
 Leu Ser Pro Tyr Thr Asn Val Ser Val Lys Leu Ile Leu Met Asn Pro
 450 455 460
 Glu Gly Arg Lys Glu Ser Gln Glu Leu Ile Val Gln Thr Asp Glu Asp
 465 470 475 480
 Leu Pro Gly Ala Val Pro Thr Glu Ser Ile Gln Gly Ser Thr Phe Glu
 485 490 495
 Glu Lys Ile Phe Leu Gln Trp Arg Glu Pro Thr Gln Thr Tyr Gly Val
 500 505 510
 Ile Thr Leu Tyr Glu Ile Thr Tyr Lys Ala Val Ser Ser Phe Asp Pro
 515 520 525
 Glu Ile Asp Leu Ser Asn Gln Ser Gly Arg Val Ser Lys Leu Gly Asn
 530 535 540
 Glu Thr His Phe Leu Phe Phe Gly Leu Tyr Pro Gly Thr Thr Tyr Ser
 545 550 555 560
 Phe Thr Ile Arg Ala Ser Thr Ala Lys Gly Phe Gly Pro Pro Ala Thr
 565 570 575
 Asn Gln Phe Thr Thr Lys Ile Ser Ala Pro Ser Met Pro Ala Tyr Glu
 580 585 590
 Leu Glu Thr Pro Leu Asn Gln Thr Asp Asn Thr Val Thr Val Met Leu
 595 600 605
 Lys Pro Ala His Ser Arg Gly Ala Pro Val Ser Val Tyr Gln Ile Val
 610 615 620
 Val Glu Glu Glu Arg Pro Arg Arg Thr Lys Lys Thr Thr Glu Ile Leu
 625 630 635 640
 Lys Cys Tyr Pro Val Pro Ile His Phe Gln Asn Ala Ser Leu Leu Asn
 645 650 655
 Ser Gln Tyr Tyr Phe Ala Ala Glu Phe Pro Ala Asp Ser Leu Gln Ala
 660 665 670
 Ala Gln Pro Phe Thr Ile Gly Asp Asn Lys Thr Tyr Asn Gly Tyr Trp
 675 680 685
 Asn Thr Pro Leu Leu Pro Tyr Lys Ser Tyr Arg Ile Tyr Phe Gln Ala
 690 695 700
 Ala Ser Arg Ala Asn Gly Glu Thr Lys Ile Asp Cys Val Gln Val Ala
 705 710 715 720
 Thr Lys Gly Ala Ala Thr Pro Lys Pro Val Pro Glu Pro Glu Lys Gln
 725 730 735
 Thr Asp His Thr Val Lys Ile Ala Gly Val Ile Ala Gly Ile Leu Leu
 740 745 750
 Phe Val Ile Ile Phe Leu Gly Val Val Leu Val Met Lys Lys Arg Leu
 755 760 765
 Tyr Lys His Gly Ala Ser Ile Cys Ser Ala Ser Gly Glu Ala Ser Gly
 770 775 780
 Ser Phe Gln Ser Trp Arg Lys Ala Lys His Lys Gln Ala Cys Pro Met
 785 790 795 800
 Ala Arg Ala Gly Ala Arg Glu Arg Ala Gly Gly Cys Leu Lys Leu
 805 810 815

<210> 1391

<211> 142

<212> Amino acid

<213> Homo sapiens

<400> 1391

Gly Ile Arg Gln Leu Leu Gln Leu Ser Arg Ala Ser Met Ala Ala Arg
 1 5 10 15
 Lys Ser Trp Thr Ala Leu Arg Leu Cys Ala Thr Val Val Val Leu Asp
 20 25 30
 Met Val Val Cys Lys Gly Phe Val Gln Asp Leu Asp Glu Ser Phe Lys
 35 40 45
 Glu Asn Arg Asn Asp Asp Ile Trp Leu Val His Phe Tyr Ala Pro Trp
 50 55 60
 Cys Gly His Cys Lys Lys Leu Glu Pro Ile Trp Asn Glu Ala Gly Leu
 65 70 75 80
 Glu Met Lys Ser Ile Gly Ser Pro Val Lys Ala Gly Lys Met Asp Ala
 85 90 95
 Thr Ser Tyr Ser Ser Ile Ala Ser Glu Phe Gly Val Arg Gly Tyr Pro
 100 105 110
 Thr Ile Lys Leu Ala Leu Ile Arg Pro Leu Pro Ser Gln Gln Met Phe
 115 120 125
 Glu His Met His Lys Arg His Arg Val Phe Phe Val Tyr Val
 130 135 140 142

<210> 1392

<211> 282

<212> Amino acid

<213> Homo sapiens

<400> 1392
 Gly Leu Val Ile Val Ile Ser His Phe Ser Pro Ser Pro Gly Leu Leu
 1 5 10 15
 Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro Ile Thr Leu Asn Val
 20 25 30
 Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr Leu Thr Ser Phe Pro
 35 40 45
 Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys Met Pro Thr Lys Arg
 50 55 60
 Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp Gly Lys Val Phe Arg
 65 70 75 80
 Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu Asp Leu Pro Glu Asp
 85 90 95
 Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala Asp Phe Tyr Gln Val
 100 105 110
 Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu Val Glu Leu Ser Lys
 115 120 125
 Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu Asn Gln Arg Val Gln
 130 135 140
 Thr Val His Phe Thr Val Arg Glu Ala Pro Gln Ile Tyr Ser Leu Ser
 145 150 155 160
 Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile Phe Ser Thr Ser Cys
 165 170 175
 Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe Tyr Cys Ser Asn Gly
 180 185 190
 Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp Pro Asn His Leu Thr
 195 200 205
 Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro Glu Glu Glu Tyr Thr
 210 215 220
 Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro Ala Asn Lys Gln Ile
 225 230 235 240
 Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu Lys Ile Ala Leu Ser
 245 250 255
 Asp Gly Phe Cys Ile Asp Ser Ser His Pro His Ala Leu Asp Phe Met
 260 265 270

<210> 1393
 <211> 308
 <212> Amino acid
 <213> Homo sapiens

<400> 1393
 Ser Cys Ala Asp Asn Leu Val Ala Ala Ser Gly Gly Cys Trp Phe Val
 1 5 10 15
 Leu Gly Glu Arg Arg Ala Gly Ser Leu Leu Ser Ala Ser Tyr Gly Thr
 20 25 30
 Phe Ala Met Pro Gly Met Val Leu Phe Gly Arg Arg Trp Ala Ile Ala
 35 40 45
 Ser Asp Asp Leu Val Phe Pro Gly Phe Phe Glu Leu Val Val Arg Val
 50 55 60
 Leu Trp Trp Ile Gly Ile Leu Thr Leu Tyr Leu Met His Arg Gly Lys
 65 70 75 80
 Leu Asp Cys Ala Gly Gly Ala Leu Leu Ser Ser Tyr Leu Ile Val Leu
 85 90 95
 Met Ile Leu Leu Ala Val Val Ile Cys Thr Val Ser Ala Ile Met Cys
 100 105 110
 Val Ser Met Arg Gly Thr Ile Cys Asn Pro Gly Pro Arg Lys Ser Met
 115 120 125
 Ser Lys Leu Leu Tyr Ile Arg Leu Ala Leu Phe Phe Pro Glu Met Val
 130 135 140
 Trp Ala Ser Leu Gly Ala Ala Trp Val Ala Asp Gly Val Gln Cys Asp
 145 150 155 160
 Arg Thr Val Val Asn Gly Ile Ile Ala Thr Val Val Val Ser Trp Ile
 165 170 175
 Ile Ile Ala Ala Thr Val Val Ser Ile Ile Ile Val Phe Asp Pro Leu
 180 185 190
 Gly Gly Lys Met Ala Pro Tyr Ser Ser Ala Gly Pro Ser His Leu Asp
 195 200 205
 Ser His Asp Ser Ser Gln Leu Leu Asn Gly Leu Lys Thr Ala Ala Thr
 210 215 220
 Ser Val Trp Glu Thr Arg Ile Lys Leu Leu Cys Cys Cys Ile Gly Lys
 225 230 235 240
 Asp Asp His Thr Arg Val Ala Phe Ser Ser Thr Ala Glu Leu Phe Ser
 245 250 255
 Thr Tyr Phe Ser Asp Thr Asp Leu Val Pro Ser Asp Ile Ala Ala Gly
 260 265 270
 Leu Ala Leu Leu His Gln Gln Gln Asp Asn Ile Arg Asn Asn Gln Asp
 275 280 285
 Leu Pro Arg Trp Ser Ala Met Pro Gln Gly Ala Pro Arg Lys Leu Ile
 290 295 300
 Trp Met Gln Asn
 305 308

<210> 1394
 <211> 238
 <212> Amino acid
 <213> Homo sapiens

<400> 1394

Phe Arg Ala Ala Thr Ala Ala Ala Lys Gly Asn Gly Gly Gly Gly Gly
 1 5 10 15
 Arg Ala Gly Ala Gly Asp Ala Ser Gly Thr Arg Lys Lys Lys Gly Pro
 20 25 30
 Gly Pro Leu Ala Thr Ala Tyr Leu Val Ile Tyr Asn Val Val Met Thr
 35 40 45
 Ala Gly Trp Leu Val Ile Ala Val Gly Leu Val Arg Ala Tyr Leu Ala
 50 55 60
 Lys Gly Ser Tyr His Ser Leu Tyr Tyr Ser Ile Glu Lys Pro Leu Lys
 65 70 75 80
 Phe Phe Gln Thr Gly Ala Leu Leu Glu Ile Leu His Cys Ala Ile Gly
 85 90 95
 Ile Val Pro Ser Ser Val Val Leu Thr Ser Phe Gln Val Met Ser Arg
 100 105 110
 Val Phe Leu Ile Trp Ala Val Thr His Ser Val Lys Glu Val Gln Ser
 115 120 125
 Glu Asp Ser Val Leu Phe Val Ile Ala Trp Thr Ile Thr Glu Ile Ile
 130 135 140
 Arg Tyr Ser Phe Tyr Thr Phe Ser Leu Leu Asn His Leu Pro Tyr Leu
 145 150 155 160
 Ile Lys Arg Ala Arg Tyr Thr Leu Phe Ile Val Leu Tyr Pro Met Gly
 165 170 175
 Val Ser Gly Glu Leu Leu Thr Ile Tyr Ala Ala Leu Pro Phe Val Arg
 180 185 190
 Gln Ala Gly Leu Tyr Ser Ile Ser Leu Pro Asn Ser Thr Lys Lys Ile
 195 200 205
 Phe Leu Ile Ser Gln Val Trp Trp His Met Leu Ala Val Ser Ala Asp
 210 215 220
 Ala Lys Ala Ala Glu Met Pro Ala Val Leu Lys Pro Gly Pro
 225 230 235 238

<210> 1395

<211> 231

<212> Amino acid

<213> Homo sapiens

<400> 1395

Met Leu Thr Gly Val Gly Cys Leu Val Ser Ser Glu Ser Leu Ser Cys
 1 5 10 15
 Val Gln Cys Asn Ser Trp Glu Lys Ser Cys Val Asn Ser Ile Ala Ser
 20 25 30
 Glu Cys Pro Ser His Ala Asn Thr Ser Cys Ile Ser Ser Ala Ser
 35 40 45
 Ser Ser Leu Glu Thr Pro Val Arg Leu Tyr Gln Asn Met Phe Cys Ser
 50 55 60
 Ala Glu Asn Cys Ser Glu Glu Thr His Ile Thr Ala Phe Thr Val His
 65 70 75 80
 Val Ser Ala Glu Glu His Phe His Phe Val Ser Gln Cys Cys Glu Gly
 85 90 95
 Lys Glu Cys Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro Leu Lys Asn
 100 105 110
 Val Ser Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser Asn Gly Thr
 115 120 125
 Ser Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu Gln Cys Val
 130 135 140
 Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys Ser Leu Val
 145 150 155 160

Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln Phe Leu Ser
 165 170 175
 Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys Phe Glu Cys
 180 185 190
 Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro Thr Thr Ser His
 195 200 205
 Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu Ala Leu Ala Ser Leu
 210 215 220
 Leu Leu Arg Gly Leu Leu Pro
 225 230 231

<210> 1396
 <211> 216
 <212> Amino acid
 <213> Homo sapiens

<400> 1396
 Val Pro Ala Arg Arg Arg Ala Met Glu Ile Gly Thr Glu Ile Ser Arg
 1 5 10 15
 Lys Ile Arg Ser Ala Ile Lys Gly Lys Leu Gln Glu Leu Gly Ala Tyr
 20 25 30
 Val Asp Glu Glu Leu Pro Asp Tyr Ile Met Val Met Val Ala Asn Lys
 35 40 45
 Lys Ser Gln Asp Gln Met Thr Glu Asp Leu Ser Leu Phe Leu Gly Asn
 50 55 60
 Asn Thr Ile Arg Phe Thr Val Trp Leu His Gly Val Leu Asp Lys Leu
 65 70 75 80
 Arg Ser Val Thr Thr Glu Pro Ser Ser Leu Lys Ser Ser Asp Thr Asn
 85 90 95
 Ile Phe Asp Ser Asn Val Pro Ser Asn Lys Ser Asn Phe Ser Arg Gly
 100 105 110
 Asp Glu Arg Arg His Glu Ala Ala Val Pro Pro Leu Ala Ile Pro Ser
 115 120 125
 Ala Arg Pro Glu Lys Arg Asp Ser Arg Val Ser Thr Ser Ser Gln Glu
 130 135 140
 Ser Lys Thr Thr Asn Val Arg Gln Thr Tyr Asp Asp Gly Ala Ala Thr
 145 150 155 160
 Arg Leu Met Ser Thr Val Lys Pro Leu Arg Glu Pro Ala Pro Ser Glu
 165 170 175
 Asp Val Ile Asp Ile Lys Pro Glu Pro Asp Asp Leu Ile Asp Glu Asp
 180 185 190
 Leu Asn Phe Val Gln Glu Lys Pro Leu Ser Gln Lys Lys Pro Thr Val
 195 200 205
 Thr Leu Thr Tyr Gly Ser Ser Arg
 210 215 216

<210> 1397
 <211> 135
 <212> Amino acid
 <213> Homo sapiens

<400> 1397
 Ala Ser Arg Val Leu Ala Ala Val Met Gly Leu Pro Trp Gly Gln Pro
 1 5 10 15

His Leu Gly Leu Gln Met Leu Leu Leu Ala Leu Asn Trp Leu Arg Pro
 20 25 30
 Ser Leu Ser Leu Glu Leu Val Pro Tyr Thr Pro Gln Ile Thr Ala Trp
 35 40 45
 Asp Leu Glu Gly Lys Val Thr Ala Thr Thr Phe Ser Leu Glu Gln Pro
 50 55 60
 Arg Cys Val Phe Asp Gly Leu Ala Ser Ala Ser Asp Thr Val Trp Leu
 65 70 75 80
 Val Val Ala Phe Ser Asn Ala Ser Arg Gly Phe Gln Asn Pro Glu Thr
 85 90 95
 Leu Ala Asp Ile Pro Ala Ser Pro Gln Leu Leu Thr Asp Gly His Tyr
 100 105 110
 Met Thr Leu Pro Leu Ser Pro Asp Gln Leu Pro Cys Gly Asp Pro Met
 115 120 125
 Ala Gly Ser Gly Ser Ala Pro
 130 135

<210> 1398

<211> 41

<212> Amino acid

<213> Homo sapiens

<400> 1398

Asn Ser Leu Asn Asn Phe Phe Phe Glu Thr Glu Ser Cys Cys Val Ala
 1 5 10 15
 Gln Ala Gly Val Gln Trp Arg Asp Leu Gly Ser Leu Gln Ala Pro Pro
 20 25 30
 Pro Gly Phe Lys Arg Phe Ser Cys Leu
 35 40 41

<210> 1399

<211> 151

<212> Amino acid

<213> Homo sapiens

<400> 1399

Lys Ser Leu Pro Leu Gln Lys His Pro Lys Pro Ser Cys Gln Glu Asp
 1 5 10 15
 Gln Gly Leu Gly Arg Gly Ser Leu Ser Gly His Ser Pro Leu Thr Leu
 20 25 30
 Leu Thr Phe Leu Thr Ser Cys Ala Leu Gly Asp Gln Gln Leu Leu Pro
 35 40 45
 Pro Arg Thr Ser Gly Ser Leu Cys Gln Glu Ser Met Ser Glu Gln Ser
 50 55 60
 Cys Gln Met Ser Glu Leu Arg Leu Leu Leu Leu Gly Lys Cys Arg Ser
 65 70 75 80
 Gly Lys Ser Ala Thr Gly Asn Ala Ile Leu Gly Lys His Val Phe Lys
 85 90 95
 Ser Lys Phe Ser Asp Gln Thr Val Ile Lys Met Cys Gln Arg Glu Ser
 100 105 110
 Trp Val Leu Arg Glu Arg Lys Val Val Val Ile Asp Thr Pro Asp Leu
 115 120 125
 Phe Ser Ser Ile Ala Cys Ala Glu Asp Lys Gln Arg Asn Ile Gln His
 130 135 140

Leu Leu Glu Leu Ser Ala Pro
145 150 151

<210> 1400
<211> 324
<212> Amino acid
<213> Homo sapiens

<400> 1400
Phe Val Glu Thr Thr Val Ser Val Gln Ser Ala Glu Ser Ser Asp Ala
1 5 10 15
Leu Ser Trp Ser Arg Leu Pro Arg Ala Leu Ala Ser Val Gly Pro Glu
20 25 30
Glu Ala Arg Ser Gly Ala Pro Val Gly Gly Gly Arg Trp Gln Leu Ser
35 40 45
Asp Arg Val Glu Gly Gly Ser Pro Thr Leu Gly Leu Leu Gly Gly Ser
50 55 60
Pro Ser Ala Gln Pro Gly Thr Gly Asn Val Glu Ala Gly Ile Pro Ser
65 70 75 80
Gly Arg Met Leu Glu Pro Leu Pro Cys Trp Asp Ala Ala Lys Asp Leu
85 90 95
Lys Glu Pro Gln Cys Pro Pro Gly Asp Arg Val Gly Val Gln Pro Gly
100 105 110
Asn Ser Arg Val Trp Gln Gly Thr Met Glu Lys Ala Gly Leu Ala Trp
115 120 125
Thr Arg Gly Thr Gly Val Gln Ser Glu Gly Thr Trp Glu Ser Gln Arg
130 135 140
Gln Asp Ser Asp Ala Leu Pro Ser Pro Glu Leu Leu Pro Gln Asp Gln
145 150 155 160
Asp Lys Pro Phe Leu Arg Lys Ala Cys Ser Pro Ser Asn Ile Pro Ala
165 170 175
Val Ile Ile Thr Asp Met Gly Thr Gln Glu Asp Gly Ala Leu Glu Glu
180 185 190
Thr Gln Gly Ser Pro Arg Gly Asn Leu Pro Leu Arg Lys Leu Ser Ser
195 200 205
Ser Ser Ala Ser Ser Thr Gly Phe Ser Ser Ser Tyr Glu Asp Ser Glu
210 215 220
Glu Asp Ile Ser Ser Asp Pro Glu Arg Thr Leu Asp Pro Asn Ser Ala
225 230 235 240
Phe Leu His Thr Leu Asp Gln Gln Lys Pro Arg Val Val Glu Ser Arg
245 250 255
Ser Val Thr Gln Ala Gly Val Gln Trp His Asp Ile Gly Ser Leu Gln
260 265 270
Pro Leu Pro Pro Trp Ile Gln Ala Ile Leu His Ala Ser Ala Phe Arg
275 280 285
Ile Ala Gly Thr Thr Gly Ala Cys His His Ala Arg Ile Ile Phe Gly
290 295 300
Phe Leu Val Glu Arg Gly Phe His His Val Gly Gln Asp Gly Leu Tyr
305 310 315 320
Leu Leu Ile Leu
324

<210> 1401
<211> 76
<212> Amino acid
<213> Homo sapiens

<220>

<221> misc_feature
 <222> (1)...(76)
 <223> X = any amino acid or stop code

<400> 1401
 Lys Ile Cys Ser Ser Tyr Phe Leu Arg Ile Ile Cys Ile Leu Gln Lys
 1 5 10 15
 Glu Ala Gln Glu Ala Ser Asn Leu Tyr Thr Ser Cys Asp Phe Phe Ser
 20 25 30
 Pro Ala Phe Tyr Phe Val Ile Tyr Arg Leu Tyr Asn Phe Lys Ile His
 35 40 45
 Trp Pro Gly Ala Val Ala His Thr Tyr Ser Pro Ser Thr Leu Gly Gly
 50 55 60
 Arg Gly Arg Trp Val Thr Xaa Gly Arg Glu Phe Met
 65 70 75 76

<210> 1402
 <211> 102
 <212> Amino acid
 <213> Homo sapiens

<400> 1402
 Leu Ile Leu Ser Leu Pro Leu Leu Tyr Gly His Leu Lys Ser Tyr Thr
 1 5 10 15
 Phe Pro Ser Glu His Tyr Leu His Leu Leu Gln Thr Phe Ala Thr Phe
 20 25 30
 Asn Lys Tyr Leu Asn Val Cys Val Leu Ile Phe Ile His His Lys Pro
 35 40 45
 Val Val Pro Ala Ile Gln Gly Thr Asn Val Gly Gly Ser Leu Glu Pro
 50 55 60
 Arg Arg Leu Arg Leu Gln Ala Met Ile Val Pro Leu His Phe Gly
 65 70 75 80
 Leu Gly Asn Arg Val Arg Pro Cys Leu Lys Lys Gln Gln Gln Gln Gln
 85 90 95
 Gln Gln Gln Gln Lys Lys
 100 102

<210> 1403
 <211> 124
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(124)
 <223> X = any amino acid or stop code

<400> 1403
 Arg Met Glu Thr Lys Pro Val Ile Thr Cys Leu Lys Thr Leu Leu Ile
 1 5 10 15

```

Ile Tyr Ser Phe Val Phe Trp Ile Thr Gly Val Ile Leu Leu Ala Ala
      20              25              30
Gly Val Trp Gly Lys Leu Thr Leu Gly Ser Tyr Ile Ser Leu Ile Ala
      35              40              45
Glu Asn Ser Thr Tyr Ala Pro Tyr Val Leu Ile Val Thr Gly Thr Thr
      50              55              60
Ile Val Ala Tyr Pro Leu Val Xaa Phe Phe Phe Ser Tyr Ser Ser Gly
      65              70              75              80
Phe Ser Tyr Ile Leu Ala Val Arg Leu Ile Ala Gly Ile Ala Leu Val
      85              90              95
Tyr Asn Tyr Ile Pro Arg Ser Ser Ser Arg Ala Leu Val Arg Leu Val
      100             105             110
Val Leu Leu Arg Phe Leu Leu Ser Arg His Pro Ser
      115             120             124

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<210> 1404

<211> 136

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(136)

<223> X = any amino acid or stop code

<400> 1404

```

Asn Ala Glu His Pro Gly Met Asp Arg His Asp Leu Cys Gln Lys Ala
  1              5              10              15
Lys Leu Ala Glu His Ala Glu Arg Asp Asp Asp Met Ala Ala Cys Met
      20              25              30
Lys Thr Val Thr Asp Gln Gly Ala Glu Leu Ser Asn Glu Glu Arg Asn
      35              40              45
Leu Leu Ser Asp Ala His Thr Asn Ala Val Xaa Ala Arg Arg Ser Ser
      50              55              60
Trp Met Gly Ala Xaa Arg Ile Glu Gln Lys Thr Glu Gly Ala Asp Thr
      65              70              75              80
Gln Gln Gln Met Ala Pro Asp Cys Arg Glu Ile Phe Ala Thr Glu Leu
      85              90              95
Arg Asp Ile Cys Asp Asp Val Leu Ser Leu Leu Glu Lys Leu Leu Ile
      100             105             110
Pro Asn Ala Ser His Ala Xaa Ser Leu Val Tyr Tyr Leu His Met Ile
      115             120             125
Gly Asp Tyr Tyr Arg Tyr Trp Leu
      130             135 136

```

<210> 1405

<211> 110

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(110)

<223> X = any amino acid or stop code

MISSING AT THE TIME OF PUBLICATION

Gly Asn Asp Tyr Ser Leu Gly Leu Thr Pro Thr Gly Val Leu Val Phe
 85 90 95
 Glu Gly Asp Thr Lys Ile Gly Leu Phe Phe Trp Pro Lys Ile Thr Arg
 100 105 110
 Leu Asp Phe Lys Lys Asn Lys Leu Thr Leu Val Val Val Glu Asp Asp
 115 120 125
 Asp Gln Gly Lys Glu Gln Glu His Thr Phe Val Phe Arg Leu Asp His
 130 135 140
 Pro Lys Ala Cys Lys His Leu Trp Lys Cys Ala Val Glu His His Ala
 145 150 155 160
 Phe Phe Arg Leu Arg Gly Pro Val Gln Lys Ser Ser His Arg Ser Gly
 165 170 175
 Phe Ile Arg Leu Gly Ser Arg Phe Arg Tyr Ser Gly Lys Thr Glu Tyr
 180 185 190
 Gln Thr Thr Lys Thr Asn Lys Ala Arg Arg Ser Thr Ser Phe Glu Arg
 195 200 205
 Arg Pro Ser Lys Arg Tyr Ser Arg Arg Thr Leu Gln Met Lys Ala Cys
 210 215 220
 Ala Thr Lys Pro Glu Glu Leu Ser Val His Asn Asn Val Ser Thr Gln
 225 230 235 240
 Ser Asn Gly Ser Gln Gln Ala Trp Gly Met Arg Ser Ala Leu Pro Val
 245 250 255
 Ser Pro Ser Ile Ser Ser Ala Pro Val Pro Val Glu Ile Glu Asn Leu
 260 265 270
 Pro Gln Ser Pro Gly Thr Asp Gln His Asp Arg Lys Trp Leu Ser Ala
 275 280 285
 Ala Ser Asp Cys Cys Gln Arg Gly Gly Asn Gln Trp Asn Thr Arg Ala
 290 295 300
 Leu
 305

<210> 1408

<211> 92

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(92)

<223> X = any amino acid or stop code

<400> 1408

Ala Thr Ala Pro Gly Leu Phe Asn Phe Phe Xaa Phe Leu Phe Gln Cys
 1 5 10 15
 Arg Glu Glu His Lys Lys Lys Asn Pro Glu Val Pro Val Asn Phe Ala
 20 25 30
 Glu Phe Ser Lys Lys Cys Ser Gly Arg Trp Lys Thr Met Ser Ser Lys
 35 40 45
 Glu Lys Phe Lys Phe Gly Glu Met Ala Lys Ala Asp Glu Val Cys Tyr
 50 55 60
 Asp Arg Glu Met Lys Asp Tyr Gly Pro Ala Lys Gly Gly Lys Lys Lys
 65 70 75 80
 Asp Pro Asn Ala Pro Lys Arg Pro Pro Ser Gly Phe
 85 90 92

<210> 1409

<211> 169

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(169)

<223> X = any amino acid or stop code

<400> 1409

```

Ala Glu Gly Leu Gly Ser Trp Ala Val Trp Ala Gly Leu Gly Trp Ala
 1          5          10          15
Gly Arg His Met Glu Ala Gly Gly Ala Thr Gly Ala Leu Gly Val Gly
          20          25          30
Ser Lys Leu Pro Ser Ala Phe Cys Phe Pro Gly Ser Ser Val Ala Met
          35          40          45
Asp Met Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly Val
          50          55          60
Val Tyr Lys Ala Lys Asn Arg Glu Thr Gly Gln Leu Val Ala Leu Lys
          65          70          75          80
Lys Ile Arg Leu Asp Leu Xaa Val Leu Gly Arg Pro Leu Ser Tyr Pro
          85          90          95
Pro Trp Ala Ile Thr Thr Trp Ala Leu Pro Asp Pro Phe Pro Leu Ser
          100          105          110
Trp Ser Pro Arg Leu Thr Pro Leu Gly Ala Ala Gln Gln Pro Leu Pro
          115          120          125
Val Leu Ser Pro Val His Cys Leu Leu Thr Ser Leu Cys Arg Gly Pro
          130          135          140
Asp Cys Gly Val Trp Trp Met Thr Cys Gln Gly Ala Gln Val Ser Ile
145          150          155          160
Ala Gly Ala Leu Val Ile Leu Trp Gly
          165          169

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<210> 1410

<211> 146

<212> Amino acid

<213> Homo sapiens

<400> 1410

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Leu Cys Val Ser Val Leu Cys Ser Phe Ser Tyr Leu Gln Asn Gly Trp
 1          5          10          15
Thr Ala Ser Asp Pro Val His Gly Tyr Trp Phe Arg Ala Gly Asp His
          20          25          30
Val Ser Arg Asn Ile Pro Val Ala Thr Asn Asn Pro Val Arg Ala Val
          35          40          45
Gln Glu Glu Thr Arg Asp Arg Phe His Leu Leu Gly Asp Pro Gln Asn
          50          55          60
Lys Asp Cys Thr Leu Ser Ile Arg Asp Thr Arg Glu Ser Asp Ala Gly
          65          70          75          80
Thr Tyr Val Phe Cys Val Glu Arg Gly Asn Met Lys Trp Asn Tyr Lys
          85          90          95
Tyr Asp Gln Leu Ser Val Asn Val Thr Ala Ser Gln Asp Leu Leu Ser
          100          105          110
Arg Tyr Arg Leu Glu Val Pro Glu Ser Val Thr Val Gln Glu Gly Leu
          115          120          125
Cys Val Ser Val Pro Trp Gln Cys Pro Leu Pro Pro Leu Gln Leu Asp
130          135          140

```

Cys Leu
145 146

<210> 1411
<211> 250
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(250)
<223> X = any amino acid or stop code

<400> 1411
Gln Leu Gln Leu Cys Gln Asn Cys Thr Lys Arg Gly Glu Cys His Cys
1 5 10 15
Val Pro Phe Asp Thr Tyr Ile Lys Thr Lys Lys Glu Lys Lys Arg Leu
20 25 30
Ser Val Leu Pro Pro Thr Arg Leu Met Glu Ala Arg Phe Ser Pro Ile
35 40 45
Asn Gln Ile Leu Pro Trp Cys Arg Gln Asp Leu Ala Ile Ser Ile Ser
50 55 60
Lys Ala Ile Asn Thr Gln Glu Ala Pro Val Lys Glu Lys His Ala Arg
65 70 75 80
Arg Ile Ile Leu Gly Thr His His Glu Lys Gly Ala Phe Thr Phe Trp
85 90 95
Ser Tyr Ala Ile Gly Leu Pro Leu Pro Ser Ser Ser Ile Leu Ser Trp
100 105 110
Lys Phe Cys His Val Leu His Lys Val Leu Arg Asp Gly His Pro Asn
115 120 125
Val Leu His Asp Cys Gln Arg Tyr Arg Ser Asn Ile Arg Glu Ile Gly
130 135 140
Asp Leu Trp Gly His Leu His Asp Arg Tyr Gly Gln Leu Val Asn Val
145 150 155 160
Tyr Thr Lys Leu Leu Thr Lys Ile Ser Phe His Leu Lys His Pro
165 170 175
Gln Phe Pro Ala Gly Leu Glu Val Thr Asp Glu Val Leu Glu Lys Ala
180 185 190
Ala Gly Thr Asp Val Asn Asn Met Xaa Val Thr Leu His Gly Tyr Met
195 200 205
Ala Ser Ser Pro Arg Leu Pro His Ser Phe Leu Pro Arg Leu Thr Pro
210 215 220
Arg Arg Pro His Gly Ala Val Gly Leu Asn Glu Ser Val Ala Leu Leu
225 230 235 240
Val Asp Ala His Ala Pro Arg Asp Arg Gly
245 250

<210> 1412
<211> 169
<212>Amino acid
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(169)
<223> X = any amino acid or stop code

<400> 1412

Ala	Ala	Pro	His	Arg	Met	Pro	Arg	Ala	Pro	His	Phe	Met	Pro	Leu	Leu
1				5					10					15	
Leu	Leu	Leu	Leu	Leu	Leu	Ser	Leu	Pro	His	Thr	Gln	Ala	Ala	Phe	Pro
			20					25					30		
Gln	Asp	Pro	Leu	Pro	Leu	Leu	Ile	Ser	Asp	Leu	Gln	Gly	Thr	Ser	Pro
		35					40					45			
Leu	Ser	Trp	Leu	Pro	Ser	Leu	Glu	Asp	Asp	Ala	Val	Ala	Ala	Xaa	Leu
	50					55					60				
Gly	Leu	Asp	Phe	Gln	Arg	Phe	Leu	Thr	Leu	Asn	Arg	Thr	Leu	Leu	Val
65					70					75					80
Ala	Ala	Arg	Asp	His	Val	Phe	Ser	Phe	Asp	Leu	Gln	Ala	Glu	Glu	Glu
				85					90					95	
Gly	Glu	Gly	Leu	Val	Pro	Asn	Lys	Tyr	Leu	Thr	Trp	Arg	Ser	Gln	Asp
			100					105					110		
Val	Glu	Asn	Cys	Ala	Val	Arg	Xaa	Lys	Leu	Thr	Leu	Asn	Arg	Thr	Leu
		115					120					125			
Leu	Val	Ala	Ala	Arg	Asp	His	Val	Phe	Ser	Phe	Asp	Leu	Gln	Ala	Glu
	130					135					140				
Glu	Glu	Gly	Glu	Gly	Leu	Val	Pro	Asn	Lys	Tyr	Leu	Thr	Trp	Arg	Ser
145					150					155					160
Gln	Asp	Val	Glu	Asn	Cys	Ala	Val	Arg							
				165				169							

<210> 1413

<211> 131

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(131)

<223> X = any amino acid or stop code

<400> 1413

His	Leu	Val	Pro	Lys	Thr	Arg	Gly	Arg	Gly	Thr	Pro	Ser	Gly	Asp	Gln
1				5					10					15	
Ser	Pro	Val	Leu	Thr	Leu	Thr	Pro	Xaa	Gly	Asp	Pro	Pro	Thr	Ile	Leu
			20					25					30		
Gly	Pro	Gln	Thr	Asn	Gln	Pro	Lys	Glu	His	Leu	Thr	Asn	Phe	Lys	Ser
		35					40					45			
Gly	Lys	Arg	Ser	Phe	His	Ser	Leu	Leu	Gln	Pro	Leu	Leu	Leu	Leu	Leu
	50					55					60				
His	Pro	Ser	Ile	Ser	Pro	Phe	Leu	Asn	Phe	Gly	Ser	Phe	Pro	Phe	Leu
65					70					75					80
Val	Glu	Thr	Glu	Glu	Thr	Cys	Phe	Ile	His	Lys	Leu	Lys	Thr	Pro	Ala
				85					90					95	
Leu	Val	Thr	Pro	Asp	Ser	Leu	Pro	Leu	Val	Phe	Asn	His	Cys	Gly	Asp
			100					105					110		
Ala	Cys	Leu	Ile	Ile	His	Pro	His	Phe	Arg	Asp	Val	Glu	Phe	His	His
		115					120					125			
Thr	Gly	Asn													
			130	131											

<210> 1414

<211> 365
 <212>Amino acid
 <213> Homo sapiens

<400> 1414
 Cys Cys Ser Thr Lys Asn Ile Ser Gly Asp Lys Ala Cys Asn Leu Met
 1 5 10 15
 Ile Phe Asp Thr Arg Lys Thr Ala Arg Gln Pro Asn Cys Tyr Leu Phe
 20 25 30
 Phe Cys Pro Asn Glu Glu Ala Cys Pro Leu Lys Pro Ala Lys Gly Leu
 35 40 45
 Met Ser Tyr Arg Ile Ile Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu
 50 55 60
 Pro Ser Gln Glu Leu Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe
 65 70 75 80
 Ser Gln Ala Val Thr Pro Leu Ala His His Thr Asp Tyr Ser Lys
 85 90 95
 Pro Thr Asp Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser
 100 105 110
 Ser Asp His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln
 115 120 125
 Leu Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser
 130 135 140
 Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala Leu
 145 150 155 160
 Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala Thr Pro
 165 170 175
 Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr Pro Ser Gly
 180 185 190
 Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro Val Thr Thr Val
 195 200 205
 Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr Val Phe Thr Arg Ala
 210 215 220
 Ala Ala Thr Leu Gln Ala Met Ala Thr Thr Ala Val Leu Thr Thr Thr
 225 230 235 240
 Phe Gln Ala Pro Thr Asp Ser Lys Gly Ser Leu Glu Thr Ile Pro Phe
 245 250 255
 Thr Glu Ile Ser Asn Leu Thr Leu Asn Thr Gly Asn Val Tyr Asn Pro
 260 265 270
 Thr Ala Leu Ser Met Ser Asn Val Glu Ser Ser Thr Met Asn Lys Thr
 275 280 285
 Ala Ser Trp Glu Gly Arg Glu Ala Ser Pro Gly Ser Ser Ser Gln Gly
 290 295 300
 Ser Val Pro Glu Asn Gln Tyr Gly Leu Pro Phe Glu Lys Trp Leu Leu
 305 310 315 320
 Ile Gly Ser Leu Leu Phe Gly Val Leu Phe Leu Val Ile Gly Leu Val
 325 330 335
 Leu Leu Gly Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg Tyr Ser
 340 345 350
 Arg Leu Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile
 355 360 365

<210> 1415
 <211> 148
 <212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1)...(148)

<223> X = any amino acid or stop code

<400> 1415

```

Ile Phe Ala Gly Ser Gly Val Met Arg Leu Lys Ile Ser Leu Leu Lys
 1           5           10           15
Glu Pro Lys His Gln Glu Leu Val Ser Cys Val Gly Trp Thr Thr Ala
          20           25           30
Glu Glu Leu Tyr Ser Cys Ser Asp Asp His His Ile Val Lys Trp Asn
          35           40           45
Leu Leu Thr Ser Glu Thr Thr Gln Ile Val Lys Leu Pro Asp Asp Ile
          50           55           60
Tyr Pro Ile Asp Phe His Trp Phe Pro Lys Ser Leu Gly Val Lys Lys
          65           70           75           80
Gln Thr His Ala Glu Ser Phe Val Leu Thr Ser Ser Asp Gly Lys Phe
          85           90           95
His Leu Ile Ser Lys Leu Gly Arg Val Glu Lys Ser Val Glu Ala His
          100          105          110
Cys Gly Ala Val Leu Ala Gly Arg Trp Asn Tyr Glu Gly Thr Ala Leu
          115          120          125
Val Thr Val Gly Glu Asp Gly Gln Ile Xaa Ile Trp Ser Lys Thr Gly
          130          135          140
Met Leu Ile Ser
145          148

```

<210> 1416

<211> 122

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(122)

<223> X = any amino acid or stop code

<400> 1416

```

Ala Arg Ala Thr Thr Lys Arg His Phe Ile Leu Leu Phe Leu Phe Phe
 1           5           10           15
Leu Arg Arg Cys Leu Phe Leu Ser Pro Arg Met Glu Cys Asn Gly Ala
          20           25           30
Ile Leu Ala His Cys Asn Leu His Leu Pro Gly Ser Ser Ser Ser
          35           40           45
Ala Ser Ala Ser Xaa Val Ala Gly Ile Thr Asp Val Arg His His Ala
          50           55           60
Gln Leu Ile Leu Phe Val Phe Leu Val Glu Thr Gly Phe His Arg Val
          65           70           75           80
Gly Gln Ala Gly Leu Lys Leu Leu Thr Ser Gly Asp Leu Leu Thr Ser
          85           90           95
Ala Ser Gln Ser Ala Gly Ile Ile Met Gly Ile Ser His Cys Ala Gln
          100          105          110
Pro Lys Lys Ala Phe Xaa Thr Lys Thr Phe
          115          120          122

```

<210> 1417

<211> 138
 <212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(138)
 <223> X = any amino acid or stop code

<400> 1417
 Glu Ala Gly Ser Asn Asp Asp Leu Ala Thr Xaa Lys Thr Cys Gly Arg
 1 5 10 15
 Ala Arg Pro Ser Ser Arg Ser Arg Gln Phe Gly Ser Arg Val Trp Asn
 20 25 30
 His Arg Gln Gly Val Arg Ser Ser Pro Gly Glu Gly Ala Gly Ser Arg
 35 40 45
 Ser Pro Cys Arg Arg Arg His Arg Arg Lys His Arg Arg Asn Val Gln
 50 55 60
 Ser Pro Xaa Arg Arg Arg Ser Arg Ser Cys Ser Arg Arg Ser Gly Arg
 65 70 75 80
 Cys Ser Val Ala Leu Leu Gly Ala Cys Pro Val Ala Gly His Ser Arg
 85 90 95
 Gly Lys Val Val Cys Arg Arg Ala His Ala Ile Thr Gln Arg Arg Arg
 100 105 110
 Cys Cys Gly Phe Asp Pro Met Val His Pro Lys Glu His Arg Gly Xaa
 115 120 125
 Arg Glu Arg Ser Arg Lys Trp Ser Arg Ser
 130 135 138

<210> 1418
 <211> 92
 <212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(92)
 <223> X = any amino acid or stop code

<400> 1418
 Ala Thr Ala Pro Gly Leu Phe Asn Phe Phe Xaa Phe Leu Phe Gln Cys
 1 5 10 15
 Arg Glu Glu His Lys Lys Lys Asn Pro Glu Val Pro Val Asn Phe Ala
 20 25 30
 Glu Phe Ser Lys Lys Cys Ser Gly Arg Trp Lys Thr Met Ser Ser Lys
 35 40 45
 Glu Lys Phe Lys Phe Gly Glu Met Ala Lys Ala Asp Glu Val Cys Tyr
 50 55 60
 Asp Arg Glu Met Lys Asp Tyr Gly Pro Ala Lys Gly Gly Lys Lys Lys
 65 70 75 80
 Asp Pro Asn Ala Pro Lys Arg Pro Pro Ser Gly Phe
 85 90 92

<210> 1419

<211> 44
 <212>Amino acid
 <213> Homo sapiens

<400> 1419
 Leu Thr Val Asn Tyr Val Leu Val Phe Ser Arg Asp Ser Gly Leu Arg
 1 5 10 15
 Ala Ile Glu Asn Leu Met Gln Lys Lys Gly Lys Phe Asp Tyr Ile Leu
 20 25 30
 Leu Glu Thr Thr Gly Leu Ala Asp Pro Gly Lys Lys
 35 40 44

<210> 1420
 <211> 91
 <212>Amino acid
 <213> Homo sapiens

<400> 1420
 His Glu Ala Ala Leu Cys Arg Thr Arg Ala Val Ala Ala Glu Arg His
 1 5 10 15
 Phe Leu Arg Val Phe Leu Phe Phe Arg Pro Phe Arg Gly Val Gly Thr
 20 25 30
 Glu Ser Gly Ser Glu Ser Gly Ser Ser Lys Ala Lys Glu Pro Arg Thr
 35 40 45
 Pro Ser Ser Ser Tyr Gly Thr Ala Gln Tyr Arg Arg Trp Pro Ile Ala
 50 55 60
 Gln Glu Tyr Lys His Cys Thr Ala His Asn Asp Thr Gly Thr Leu Cys
 65 70 75 80
 Ser Glu Leu Arg Glu Pro Trp Arg Arg Pro Gln
 85 90 91

<210> 1421
 <211> 190
 <212>Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(190)
 <223> X = any amino acid or stop code

<400> 1421
 Glu Gly Ser Ser Gln Ala Asn Thr Leu Arg Ser Arg Lys Glu Asn Arg
 1 5 10 15
 Asn Asn Leu Leu Ala Cys Leu Glu Ser His Val Leu Arg Xaa Gln Phe
 20 25 30
 Thr Glu Ser His Leu Cys Ser Leu Met Gly Asp Asn Pro Phe Gln Pro
 35 40 45
 Lys Ser Asn Ser Lys Met Ala Glu Leu Phe Met Glu Cys Glu Glu Glu
 50 55 60

Glu Leu Glu Pro Trp Gln Lys Lys Val Lys Glu Val Glu Asp Asp Asp
 65 70 75 80
 Asp Asp Glu Pro Ile Phe Val Gly Glu Ile Ser Ser Ser Lys Pro Ala
 85 90 95
 Ile Ser Asn Ile Leu Asn Arg Val Asn Pro Ser Ser Tyr Ser Arg Gly
 100 105 110
 Leu Lys Asn Gly Ala Leu Ser Arg Gly Ile Thr Ala Ala Phe Lys Pro
 115 120 125
 Thr Ser Gln His Tyr Thr Asn Pro Thr Ser Asn Pro Val Pro Ala Ser
 130 135 140
 Pro Ile Asn Phe His Pro Glu Ser Arg Ser Ser Asp Ser Ser Val Ile
 145 150 155 160
 Gly Gln Pro Phe Ser Lys Pro Val Ser Val Ser Lys Thr Ile Arg Pro
 165 170 175
 Ala Gln Gly Ser Ile Gly Cys Cys Leu Ser Ile Ser Thr Val
 180 185 190

<210> 1422
 <211> 207
 <212> Amino acid
 <213> Homo sapiens

<400> 1422
 Cys Phe Ser Leu Glu Asp Ile Leu Asn Phe Phe Leu Gln Gly Phe Ser
 1 5 10 15
 Ala Gly Leu Phe Ala Phe Tyr His Asp Lys Asp Gly Asn Pro Leu Thr
 20 25 30
 Ser Arg Phe Ala Asp Gly Leu Pro Pro Phe Asn Tyr Ser Leu Gly Leu
 35 40 45
 Tyr Gln Trp Ser Asp Lys Val Val Arg Lys Val Glu Arg Leu Trp Asp
 50 55 60
 Val Arg Asp Asn Lys Ile Val Arg His Thr Val Tyr Leu Leu Val Thr
 65 70 75 80
 Pro Arg Val Val Glu Ala Arg Lys His Phe Asp Cys Pro Val Leu
 85 90 95
 Glu Gly Met Glu Leu Glu Asn Gln Gly Gly Val Gly Thr Glu Leu Asn
 100 105 110
 His Trp Glu Lys Arg Leu Leu Glu Asn Glu Ala Met Thr Gly Ser His
 115 120 125
 Thr Gln Asn Arg Val Leu Ser Arg Ile Thr Leu Ala Leu Met Glu Asp
 130 135 140
 Thr Gly Arg Gln Met Leu Ser Pro Tyr Cys Asp Thr Leu Arg Ser Asn
 145 150 155 160
 Pro Leu Gln Leu Thr Cys Arg Gln Asp Gln Arg Ala Val Ala Val Cys
 165 170 175
 Asn Leu Gln Lys Phe Pro Lys Pro Leu Pro Gln Glu Tyr Gln Tyr Phe
 180 185 190
 Asp Glu Leu Ser Gly Ile Pro Ala Glu Asp Leu Pro Tyr Tyr Gly
 195 200 205 207

<210> 1423
 <211> 423
 <212> Amino acid
 <213> Homo sapiens

<400> 1423

Ala Ala Arg Arg Arg Arg Gln Leu Val Ser Arg Arg Arg Thr Ala Glu
 1 5 10 15
 Tyr Pro Arg Arg Arg Ser Ser Pro Ser Ala Arg Pro Pro Asp Val
 20 25 30
 Pro Gly Gln Gln Pro Lys Ala Ala Lys Ser Pro Ser Pro Val Gln Gly
 35 40 45
 Lys Lys Ser Pro Arg Leu Leu Cys Ile Glu Lys Val Thr Thr Asp Lys
 50 55 60
 Asp Pro Lys Glu Glu Lys Glu Glu Glu Asp Asp Ser Ala Leu Pro Gln
 65 70 75 80
 Glu Val Ser Ile Ala Ala Ser Arg Pro Ser Arg Gly Trp Arg Ser Ser
 85 90 95
 Arg Thr Ser Val Ser Arg His Arg Asp Thr Glu Asn Thr Arg Ser Ser
 100 105 110
 Arg Ser Lys Thr Gly Ser Leu Gln Leu Ile Cys Lys Ser Glu Pro Asn
 115 120 125
 Thr Asp Gln Leu Asp Tyr Asp Val Gly Glu Glu His Gln Ser Pro Gly
 130 135 140
 Gly Ile Ser Ser Glu Glu Glu Glu Glu Glu Glu Glu Met Leu Ile
 145 150 155 160
 Ser Glu Glu Glu Ile Pro Phe Lys Asp Asp Pro Arg Asp Glu Thr Tyr
 165 170 175
 Lys Pro His Leu Glu Arg Glu Thr Pro Lys Pro Arg Arg Lys Ser Gly
 180 185 190
 Lys Val Lys Glu Glu Lys Glu Lys Lys Glu Ile Lys Val Glu Val Glu
 195 200 205
 Val Glu Val Lys Glu Glu Glu Asn Glu Ile Arg Glu Asp Glu Glu Pro
 210 215 220
 Pro Arg Lys Arg Gly Arg Arg Arg Lys Asp Asp Lys Ser Pro Arg Leu
 225 230 235 240
 Pro Lys Arg Arg Lys Lys Pro Pro Ile Gln Tyr Val Arg Cys Glu Met
 245 250 255
 Glu Gly Cys Gly Thr Val Leu Ala His Pro Arg Tyr Leu Gln His His
 260 265 270
 Ile Lys Tyr Gln His Leu Leu Lys Lys Lys Tyr Val Cys Pro His Pro
 275 280 285
 Ser Cys Gly Arg Leu Phe Arg Leu Gln Lys Gln Leu Leu Arg His Ala
 290 295 300
 Lys His His Thr Asp Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala Arg
 305 310 315 320
 Ala Phe Lys Ser Ser His Asn Leu Ala Val His Arg Met Ile His Thr
 325 330 335
 Gly Glu Lys Pro Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln
 340 345 350
 Lys Ala Ser Leu Asn Trp His Met Lys Lys His Asp Ala Asp Ser Phe
 355 360 365
 Tyr Gln Phe Ser Cys Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp
 370 375 380
 Ser Val Val Ala His Lys Ala Lys Ser His Pro Glu Val Leu Ile Ala
 385 390 395 400
 Glu Ala Leu Ala Ala Asn Ala Gly Ala Leu Ile Thr Ser Thr Asp Ile
 405 410 415
 Leu Gly Thr Asn Pro Glu Ser
 420 423

<210> 1424

<211> 158

<212> Amino acid

<213> Homo sapiens

<400> 1424

```

Met Thr Ala Asn Arg Leu Ala Glu Ser Leu Leu Ala Leu Ser Gln Gln
 1           5           10           15
Glu Glu Leu Ala Asp Leu Pro Lys Asp Tyr Leu Leu Ser Glu Ser Glu
          20           25           30
Asp Glu Gly Asp Asn Asp Gly Glu Arg Lys His Gln Lys Leu Leu Glu
          35           40           45
Ala Ile Ser Ser Leu Asp Gly Lys Asn Arg Arg Lys Leu Ala Glu Arg
          50           55           60
Ser Glu Ala Ser Leu Lys Val Ser Glu Phe Asn Val Ser Ser Glu Gly
          65           70           75           80
Ser Gly Glu Lys Leu Val Leu Ala Asp Leu Leu Glu Pro Val Lys Thr
          85           90           95
Ser Ser Ser Leu Ala Thr Val Lys Lys Gln Leu Ser Arg Val Lys Ser
          100          105          110
Lys Lys Thr Val Glu Leu Pro Leu Asn Lys Glu Glu Ile Glu Arg Ile
          115          120          125
His Arg Glu Val Ala Phe Asn Lys Thr Ala Gln Val Leu Ser Lys Trp
          130          135          140
Asp Pro Val Val Leu Lys Asn Arg Gln Ala Glu Gln Leu *
145           150           155           157

```

<210> 1425

<211> 286

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (286)

<223> X = any amino acid or stop code

<400> 1425

```

Arg Ile Asp Phe Met Phe His Ser Ser Ala Met Val Asn Ser His Arg
 1           5           10           15
Lys Pro Met Phe Asn Ile His Arg Gly Phe Tyr Cys Leu Thr Ala Ile
          20           25           30
Leu Pro Gln Ile Cys Ile Cys Ser Gln Phe Ser Val Pro Ser Ser Tyr
          35           40           45
His Phe Thr Glu Asp Pro Gly Ala Phe Pro Val Ala Thr Asn Gly Glu
          50           55           60
Arg Phe Pro Trp Gln Glu Leu Arg Leu Pro Ser Val Val Ile Pro Leu
          65           70           75           80
His Tyr Asp Leu Phe Val His Pro Asn Leu Thr Ser Leu Asp Phe Val
          85           90           95
Ala Ser Glu Lys Ile Glu Val Leu Val Ser Asn Ala Thr Gln Leu Ile
          100          105          110
Ile Leu His Ser Lys Asp Leu Glu Ile Thr Asn Ala Thr Leu Gln Ser
          115          120          125
Glu Glu Asp Ser Arg Tyr Met Lys Pro Gly Lys Glu Leu Lys Val Leu
          130          135          140
Ser Tyr Pro Ala His Glu Gln Ile Ala Leu Leu Val Pro Glu Lys Leu
145           150           155           160
Thr Pro His Leu Lys Tyr Tyr Val Ala Met Asp Phe Gln Ala Lys Leu
          165          170          175
Gly Asp Gly Phe Glu Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Leu Gly

```

```
<210> 1426
<211> 224
<212> Amino acid
<213> Homo sapiens
```

```
<210> 1427
<211> 133
<212> Amino acid
<213> Homo sapiens
```

<400> 1427

```

Arg Leu Gln Asn Ser Ser Leu Met Asp Pro Lys Leu Gly Arg Met Ala
 1              5              10              15
Ala Ser Leu Leu Ala Val Leu Leu Leu Leu Leu Glu Arg Gly Met
      20              25              30
Phe Ser Ser Pro Ser Pro Pro Pro Ala Leu Leu Glu Lys Val Phe Gln
      35              40              45
Tyr Ile Asp Leu His Gln Asp Glu Phe Val Gln Thr Leu Lys Glu Trp
      50              55              60
Val Ala Ile Glu Ser Asp Ser Val Gln Pro Val Pro Arg Phe Arg Gln
      65              70              75              80
Glu Leu Phe Arg Met Met Ala Val Ala Ala Asp Thr Leu Gln Arg Leu
      85              90              95
Gly Ala Arg Val Ala Ser Val Asp Met Gly Pro Gln Gln Leu Pro Asp
      100              105              110
Gly Gln Ser Leu Pro Ile Pro Pro Val Ile Leu Ala Glu Leu Gly Ser
      115              120              125
Asp Pro Thr Lys Gly
      130              133

```

<210> 1428

<211> 38

<212> Amino acid

<213> Homo sapiens

<400> 1428

```

Phe Phe Phe Phe Glu Met Glu Ser Cys Ser Val Thr Gln Ala Gly Val
 1              5              10              15
Pro Trp His Asp Leu Ser Ser Leu Gln Pro Pro Pro Pro Arg Phe Lys
      20              25              30
Arg Phe Ser Cys Leu Ser
      35              38

```

<210> 1429

<211> 145

<212> Amino acid

<213> Homo sapiens

<400> 1429

```

Asp Pro Lys Ala Gln Leu Pro Glu Pro Leu Arg Val Leu Trp Thr Ala
 1              5              10              15
His Leu Val Ala Met Ala Pro Gly Ser Arg Thr Ser Leu Leu Leu Ala
      20              25              30
Phe Ala Leu Leu Cys Leu Pro Trp Leu Gln Glu Ala Gly Ala Val Gln
      35              40              45
Thr Val Pro Leu Ser Arg Leu Phe Asp His Ala Met Leu Gln Ala His
      50              55              60
Arg Ala His Gln Leu Ala Ile Asp Thr Tyr Gln Glu Phe Glu Glu Thr
      65              70              75              80
Tyr Ile Pro Lys Asp Gln Lys Tyr Ser Phe Leu His Asp Ser Gln Thr
      85              90              95
Ser Phe Cys Phe Ser Asp Ser Ile Pro Thr Pro Ser Asn Met Glu Glu

```

100 105 110
 Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu
 115 120 125
 Ile Glu Ser Trp Leu Glu Pro Val Arg Ile Leu Met Ser Ile Val Pro
 130 135 140
 Asn
 145

<210> 1430
 <211> 453
 <212> Amino acid
 <213> Homo sapiens

<400> 1430
 Phe Val Lys Leu Ile Lys Lys His Gln Ala Ala Met Glu Lys Glu Ala
 1 5 10 15
 Lys Val Met Ser Asn Glu Glu Lys Lys Phe Gln Gln His Ile Gln Ala
 20 25 30
 Gln Gln Lys Lys Glu Leu Asn Ser Phe Leu Glu Ser Gln Lys Arg Glu
 35 40 45
 Tyr Lys Leu Arg Lys Glu Gln Leu Lys Glu Glu Leu Asn Glu Asn Gln
 50 55 60
 Ser Thr Pro Lys Lys Glu Lys Gln Glu Trp Leu Ser Lys Gln Lys Glu
 65 70 75 80
 Asn Ile Gln His Phe Gln Ala Glu Glu Glu Ala Asn Leu Leu Arg Arg
 85 90 95
 Gln Arg Gln Tyr Leu Glu Leu Glu Cys Arg Arg Phe Lys Arg Arg Met
 100 105 110
 Leu Leu Gly Arg His Asn Leu Glu Gln Asp Leu Val Arg Glu Glu Leu
 115 120 125
 Asn Lys Arg Gln Thr Gln Lys Asp Leu Glu His Ala Met Leu Leu Arg
 130 135 140
 Gln His Glu Ser Met Gln Glu Leu Glu Phe Arg His Leu Asn Thr Ile
 145 150 155 160
 Gln Lys Met Arg Cys Glu Leu Ile Arg Leu Gln His Gln Thr Glu Leu
 165 170 175
 Thr Asn Gln Leu Glu Tyr Asn Lys Arg Arg Glu Arg Glu Leu Arg Arg
 180 185 190
 Lys His Val Met Glu Val Arg Gln Gln Pro Lys Ser Leu Lys Ser Lys
 195 200 205
 Glu Leu Gln Ile Lys Lys Gln Phe Gln Asp Thr Cys Lys Ile Gln Thr
 210 215 220
 Arg Gln Tyr Lys Ala Leu Arg Asn His Leu Leu Glu Thr Thr Pro Lys
 225 230 235 240
 Ser Glu His Lys Ala Val Leu Lys Arg Leu Lys Glu Glu Gln Thr Arg
 245 250 255
 Lys Leu Ala Ile Leu Ala Glu Gln Tyr Asp His Ser Ile Asn Glu Met
 260 265 270
 Leu Ser Thr Gln Ala Leu Arg Leu Asp Glu Ala Gln Glu Ala Glu Cys
 275 280 285
 Gln Val Leu Lys Met Gln Leu Gln Gln Glu Leu Glu Leu Leu Asn Ala
 290 295 300
 Tyr Gln Ser Lys Ile Lys Met Gln Ala Glu Ala Gln His Asp Arg Glu
 305 310 315 320
 Leu Arg Glu Leu Glu Gln Arg Val Ser Leu Arg Arg Ala Leu Leu Glu
 325 330 335
 Gln Lys Ile Glu Glu Met Leu Ala Leu Gln Asn Glu Arg Thr Glu
 340 345 350
 Arg Ile Arg Ser Leu Leu Glu Arg Gln Ala Arg Glu Ile Glu Ala Phe

355 360 365
 Asp Ser Glu Ser Met Arg Leu Gly Phe Ser Asn Met Val Leu Ser Asn
 370 375 380
 Leu Ser Pro Glu Ala Phe Ser His Ser Tyr Pro Gly Ala Ser Gly Trp
 385 390 395 400
 Ser His Asn Pro Thr Gly Gly Pro Gly Pro His Trp Gly His Pro Met
 405 410 415
 Gly Gly Pro Pro Gln Ala Trp Gly His Pro Met Gln Gly Gly Pro Gln
 420 425 430
 Pro Trp Gly His Pro Ser Gly Pro Met Gln Gly Val Pro Arg Gly Ser
 435 440 445
 Ser Met Gly Val Arg
 450 453

<210> 1431
 <211> 151
 <212> Amino acid
 <213> Homo sapiens

<400> 1431
 Leu Ala His Gly Ser Phe Gly Val Ser Asp Phe Pro Ala Pro Ala Ala
 1 5 10 15
 Ala Pro Ala His Thr Leu Thr Ser Phe Ser Gly Ser Leu Ser Pro Gln
 20 25 30
 Phe Arg Lys Pro Leu Gly Arg Ala Pro Ala Met Pro Leu Val Arg Tyr
 35 40 45
 Arg Lys Val Val Ile Leu Gly Tyr Arg Cys Val Gly Lys Thr Ser Leu
 50 55 60
 Ala His Gln Phe Val Glu Gly Glu Phe Ser Glu Gly Tyr Asp Pro Thr
 65 70 75 80
 Val Glu Asn Thr Tyr Ser Lys Ile Val Thr Leu Gly Lys Asp Glu Phe
 85 90 95
 His Leu His Leu Val Asp Thr Ala Gly Gln Asp Glu Tyr Ser Ile Leu
 100 105 110
 Pro Tyr Ser Phe Ile Ile Gly Val His Gly Tyr Val Leu Val Tyr Ser
 115 120 125
 Val Thr Ser Leu His Ser Phe Gln Val Ile Glu Ser Leu Tyr Gln Lys
 130 135 140
 Leu His Glu Gly His Gly Lys
 145 150 151

<210> 1432
 <211> 514
 <212> Amino acid
 <213> Homo sapiens

<400> 1432
 Ser Ser Pro Ser Arg Glu Leu Cys Phe Tyr Gly Phe Trp Ile Ala Ser
 1 5 10 15
 Ser Trp Trp Ser Arg Trp Val Gly Ser Leu Gly Pro Gly Ile Leu Pro
 20 25 30
 Ser Pro Pro Ala Arg Gly Arg Thr Phe Ala Ser Val Ser Arg Leu Pro
 35 40 45
 Pro Pro Trp Ser Ala Gly Ile Thr Leu Thr Pro Phe Leu Ile Cys Gln

50	55	60
Ser Gly Ser Val Cys Pro Gly Leu Gly Ala Gly Phe Gly Val Arg Ser		
65	70	75
Phe His His Pro Val Ala Arg Ser Ala Val Leu Leu Leu Pro Leu Ala		80
	85	90
Pro Ala Ala Ala Gln Asp Ser Thr Gln Ala Ser Thr Pro Gly Ser Pro		95
	100	105
Leu Ser Pro Thr Glu Tyr Glu Arg Phe Phe Ala Leu Leu Thr Pro Thr		110
	115	120
Trp Lys Ala Glu Thr Thr Cys Arg Leu Arg Ala Thr His Gly Cys Arg		125
	130	135
Asn Pro Thr Leu Val Gln Leu Asp Gln Tyr Glu Asn His Gly Leu Val		140
145	150	155
Pro Asp Gly Ala Val Cys Ser Asn Leu Pro Tyr Ala Ser Trp Phe Glu		160
	165	170
Ser Phe Cys Gln Phe Thr His Tyr Arg Cys Ser Asn His Val Tyr Tyr		175
	180	185
Ala Lys Arg Val Leu Cys Ser Gln Pro Val Ser Ile Leu Ser Pro Asn		190
	195	200
Thr Leu Lys Glu Ile Glu Ala Ser Ala Glu Val Ser Pro Thr Thr Met		205
	210	215
Thr Ser Pro Ile Ser Pro His Phe Thr Val Thr Glu Arg Gln Thr Phe		220
225	230	235
Gln Pro Trp Pro Glu Arg Leu Ser Asn Asn Val Glu Glu Leu Leu Gln		240
	245	250
Ser Ser Leu Ser Leu Gly Gly Gln Glu Gln Ala Pro Glu His Lys Gln		255
	260	265
Glu Gln Gly Val Glu His Arg Gln Glu Pro Thr Gln Glu His Lys Gln		270
	275	280
Glu Glu Gly Gln Lys Gln Glu Glu Gln Glu Glu Gln Glu Glu Glu		285
	290	295
Gly Lys Gln Glu Glu Gly Gln Gly Thr Lys Glu Gly Arg Glu Ala Val		300
305	310	315
Ser Gln Leu Gln Thr Asp Ser Glu Pro Lys Phe His Ser Glu Ser Leu		320
	325	330
Ser Ser Asn Pro Ser Ser Phe Ala Pro Arg Val Arg Glu Val Glu Ser		335
	340	345
Thr Pro Met Ile Met Glu Asn Ile Gln Glu Leu Ile Arg Ser Ala Gln		350
	355	360
Glu Ile Asp Glu Met Asn Glu Ile Tyr Asp Glu Asn Ser Tyr Trp Arg		365
	370	375
Asn Gln Asn Pro Gly Ser Leu Leu Gln Leu Pro His Thr Glu Ala Leu		380
385	390	395
Leu Val Leu Cys Tyr Ser Ile Val Glu Asn Thr Cys Ile Ile Thr Pro		400
	405	410
Thr Ala Lys Ala Trp Lys Tyr Met Glu Glu Glu Ile Leu Gly Phe Gly		415
	420	425
Lys Ser Val Cys Asp Ser Leu Gly Arg Arg His Met Ser Thr Cys Ala		430
	435	440
Leu Cys Asp Phe Cys Ser Leu Lys Leu Glu Gln Cys His Ser Glu Ala		445
	450	455
Ser Leu Gln Arg Gln Gln Cys Asp Thr Ser His Lys Thr Pro Phe Val		460
465	470	475
Ser Pro Leu Leu Ala Ser Gln Ser Leu Ser Ile Gly Asn Gln Val Gly		480
	485	490
Ser Pro Glu Ser Gly Arg Phe Tyr Gly Leu Asp Leu Tyr Gly Gly Leu		495
	500	505
His Met		510
514		

<210> 1433

<211> 241

<212> Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(241)

<223> X = any amino acid or stop code

<400> 1433

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Val Ser Trp Val Pro Ser Lys Asp Gly Asp Val Glu Gly Ala Arg Arg
 1           5           10           15
Pro Phe Thr Arg Leu Asn Thr Ser Leu Gly Pro Gly Leu Gln Glu Gly
 20           25           30
Arg Arg Arg Thr Trp Leu Val Pro Ile Pro Gly Ala Val Leu Pro Gly
 35           40           45
Arg Thr Gln Glu Gln Pro Arg Ala Ser Pro Leu Tyr Xaa Pro Gly Ala
 50           55           60
Pro Pro Cys Gln Pro Gln Gly Leu Val Ala Gly Pro Trp Ala Gln Xaa
 65           70           75           80
Ala Gly Leu Arg Ser Asp Gly Phe Gly Pro Trp Pro Trp Arg Leu Val
 85           90           95
Gly Thr Ala Gly Pro Arg Glu Lys Lys Val Gln Lys Ser Lys Cys Trp
100           105           110
His Phe Arg Cys Gly Arg His Pro Ala Arg Arg Ser Gly Trp Ala Gly
115           120           125
Arg His Ala Ser Leu Leu Ala Thr Gly Arg Pro Cys Ser Ser Ala Pro
130           135           140
Ser Gln Gln Pro Leu Gly Thr Ala Gly Asp Ser Arg Gln Glu Leu Leu
145           150           155           160
Arg Pro Pro Leu Val Xaa Val Asn Gly Ala Gln Ser Ser Ala Ala Gly
165           170           175
Asp Trp Gly Ser Ser Pro Arg Thr Ala Gln Ala Leu Ala Arg Pro His
180           185           190
Arg Leu Gly His His Pro Ala Ala Val Ala Pro Ala Ala Arg Leu Arg
195           200           205
Thr Gln Ser Gly His Ser Pro Arg Gly Pro Leu Cys Arg Ser Pro Gly
210           215           220
Ser Pro Arg Arg Met Gly Thr Trp Arg Gly Pro Ala Gly His Ser His
225           230           235           240
Asp
241

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<210> 1434

<211> 127

<212>Amino acid

<213> Homo sapiens

<400> 1434

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Lys Thr Val Ala Glu Glu Ala Ser Val Gly Asn Pro Glu Gly Ala Phe
 1           5           10           15
Met Lys Met Leu Gln Ala Arg Lys Gln His Met Ser Thr Glu Leu Thr
 20           25           30
Ile Glu Ser Glu Ala Pro Ser Asp Ser Ser Gly Ile Asn Leu Ser Gly
 35           40           45
Phe Gly Ser Glu Gln Leu Asp Thr Asn Asp Glu Ser Asp Val Ser Ser
 50           55           60

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Ala Leu Ser Tyr Ile Leu Pro Tyr Leu Ser Leu Arg Asn Leu Gly Ala
 65 70 75 80
 Glu Ser Ile Leu Leu Pro Phe Thr Glu Gln Leu Phe Ser Asn Val Gln
 85 90 95
 Asp Gly Asp Arg Leu Leu Ser Ile Leu Lys Asn Asn Arg Lys Ser Pro
 100 105 110
 Ser Gln Ser Ser Leu Leu Gly Asn Lys Phe Lys Asn Lys Ile Phe
 115 120 125 127

<210> 1435
 <211> 182
 <212> Amino acid
 <213> Homo sapiens

<400> 1435
 Gly Glu Cys Phe Ile Met Ala Ala Val Val Gln Gln Asn Asp Leu Val
 1 5 10 15
 Phe Glu Phe Ala Ser Asn Val Met Glu Asp Glu Arg Gln Leu Gly Asp
 20 25 30
 Pro Ala Ile Phe Pro Ala Val Ile Val Glu His Val Pro Gly Ala Asp
 35 40 45
 Ile Leu Asn Ser Tyr Ala Gly Leu Ala Cys Val Glu Glu Pro Asn Asp
 50 55 60
 Met Ile Thr Glu Ser Ser Leu Asp Val Ala Glu Glu Ile Ile Asp
 65 70 75 80
 Asp Asp Asp Asp Asp Ile Thr Leu Thr Val Glu Ala Ser Cys His Asp
 85 90 95
 Gly Asp Glu Thr Ile Glu Thr Ile Glu Ala Ala Glu Ala Leu Leu Asn
 100 105 110
 Met Asp Ser Pro Gly Pro Met Leu Asp Glu Lys Arg Ile Asn Asn Asn
 115 120 125
 Ile Phe Ser Ser Pro Glu Asp Asp Met Val Val Ala Pro Val Thr His
 130 135 140
 Val Ser Val Thr Leu Asp Gly Ile Pro Glu Val Met Glu Thr Gln Gln
 145 150 155 160
 Val Gln Glu Lys Tyr Ala Asp Ser Pro Gly Ala Ser Ser Pro Glu Gln
 165 170 175
 Pro Lys Arg Lys Lys Lys
 180 182

<210> 1436
 <211> 154
 <212> Amino acid
 <213> Homo sapiens

<400> 1436
 His Glu Ala Ser Gly Val Ser Arg Ala Leu Leu Gln Ser Ala Pro Gly
 1 5 10 15
 Thr Pro Ala Thr Val Gly Ile Ser Val Gly Glu Leu Trp Pro Phe Ala
 20 25 30
 Arg Cys Cys Ser His Ser Tyr Val Arg Ser Leu Arg Gly Leu Ser Val
 35 40 45
 Ser Thr His Leu Leu Cys Phe Thr Ile Tyr Ile Met Asn Pro Ser Met
 50 55 60

Lys Gln Lys Gln Glu Glu Ile Lys Glu Asn Ile Lys Thr Ser Ser Val
 65 70 75 80
 Pro Arg Arg Thr Leu Lys Met Ile Gln Pro Ser Ala Ser Gly Ser Leu
 85 90 95
 Val Gly Arg Glu Asn Glu Leu Ser Ala Gly Leu Ser Lys Arg Lys His
 100 105 110
 Arg Asn Asp His Leu Thr Ser Thr Thr Ser Ser Pro Gly Val Ile Val
 115 120 125
 Pro Glu Ser Ser Glu Asn Lys Asn Leu Gly Gly Val Thr Gln Glu Ser
 130 135 140
 Phe Asp Leu Met Ile Lys Gly Met Lys Lys
 145 150 154

<210> 1437
 <211> 63
 <212> Amino acid
 <213> Homo sapiens

<400> 1437
 Pro Leu Pro Ala Arg Gly Lys Ser Thr Leu Pro Ala Thr Phe Cys Ser
 1 5 10 15
 Pro Ser Ala Pro Glu Leu Ala Ser Met Ser Val Val Pro Pro Asn Arg
 20 25 30
 Ser Gln Thr Gly Trp Pro Arg Gly Val Thr Gln Phe Gly Asn Lys Tyr
 35 40 45
 Ile Gln Gln Thr Lys Pro Leu Thr Leu Glu Arg Thr Ile Asn Leu
 50 55 60 63

<210> 1438
 <211> 140
 <212> Amino acid
 <213> Homo sapiens

<400> 1438
 Ala Glu Gly Glu Asp Val Pro Pro Leu Pro Thr Ser Ser Gly Asp Gly
 1 5 10 15
 Trp Glu Lys Asp Leu Glu Glu Ala Leu Glu Ala Gly Gly Cys Asp Leu
 20 25 30
 Glu Thr Leu Arg Asn Ile Ile Gln Gly Arg Pro Leu Pro Ala Asp Leu
 35 40 45
 Arg Ala Lys Val Trp Lys Ile Ala Leu Asn Val Ala Gly Lys Gly Asp
 50 55 60
 Ser Leu Ala Ser Trp Asp Gly Ile Leu Asp Leu Pro Glu Gln Asn Thr
 65 70 75 80
 Ile His Lys Asp Cys Leu Gln Phe Ile Asp Gln Leu Ser Val Pro Glu
 85 90 95
 Glu Lys Ala Ala Glu Leu Leu Leu Asp Ile Glu Ser Val Ile Thr Phe
 100 105 110
 Tyr Cys Lys Ser Arg Asn Ile Lys Tyr Ser Thr Ser Leu Ser Trp Ile
 115 120 125
 His Leu Leu Lys Pro Leu Val His Leu Gln Leu Pro
 130 135 140

<210> 1439
 <211> 84
 <212> Amino acid
 <213> Homo sapiens

<400> 1439
 Ala Leu Pro Lys Phe Leu Thr His Gly Val Lys Ser Asn Glu Arg Val
 1 5 10 15
 Val Val Trp Leu Phe Pro Pro Ser Phe Arg Ala Ala Thr Met Val His
 20 25 30
 Met Asn Val Leu Pro Asp Ala Leu Lys Ser Ile Asn Asn Ala Glu Arg
 35 40 45
 Arg Gly Lys Pro Gln Val Leu Ile Arg Leu Cys Ser Lys Ile Ile Ile
 50 55 60
 Trp Phe Leu Thr Val Met Val Lys Tyr Gly Tyr Ile Gly Lys Phe Glu
 65 70 75 80
 Pro Thr Arg Pro
 84

<210> 1440
 <211> 255
 <212> Amino acid
 <213> Homo sapiens

<400> 1440
 Ala Met Ala Gln Tyr Gly His Pro Ser Pro Leu Gly Met Ala Ala Arg
 1 5 10 15
 Glu Glu Leu Tyr Ser Lys Val Thr Pro Arg Arg Asn Arg Gln Gln Arg
 20 25 30
 Pro Gly Thr Ile Lys His Gly Ser Ala Leu Asp Val Leu Leu Ser Met
 35 40 45
 Gly Phe Pro Arg Ala Arg Ala Gln Lys Ala Leu Ala Ser Thr Gly Gly
 50 55 60
 Arg Ser Val Gln Ala Ala Cys Asp Trp Leu Phe Ser His Val Gly Asp
 65 70 75 80
 Pro Phe Leu Asp Asp Pro Leu Pro Arg Glu Tyr Val Leu Tyr Leu Arg
 85 90 95
 Pro Thr Gly Pro Leu Ala Gln Lys Leu Ser Asp Phe Trp Gln Gln Ser
 100 105 110
 Lys Gln Ile Cys Gly Lys Asn Lys Ala His Asn Ile Phe Pro His Ile
 115 120 125
 Thr Leu Cys Gln Phe Phe Met Cys Glu Asp Ser Lys Val Asp Ala Leu
 130 135 140
 Gly Glu Ala Leu Gln Thr Thr Val Ser Arg Trp Lys Cys Lys Phe Ser
 145 150 155 160
 Ala Pro Leu Pro Leu Glu Leu Tyr Thr Ser Ser Asn Phe Ile Gly Leu
 165 170 175
 Phe Val Lys Glu Asp Ser Ala Glu Val Leu Lys Lys Phe Ala Ala Asp
 180 185 190
 Phe Ala Ala Glu Ala Ala Ser Lys Thr Glu Val His Val Glu Pro His
 195 200 205
 Lys Lys Gln Leu His Val Thr Leu Ala Tyr His Phe Gln Ala Ser His
 210 215 220
 Leu Pro Thr Leu Glu Lys Leu Ala Gln Asn Ile Asp Val Lys Leu Gly
 225 230 235 240

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<210> 1441
<211> 134
<212> Amino acid
<213> Homo sapiens
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<210> 1442
<211> 155
<212> Amino acid
<213> Homo sapiens
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898

<210> 1443
 <211> 157
 <212>Amino acid
 <213> Homo sapiens

<400> 1443
 Pro Ala Pro Ala Ala Arg Ser Arg Glu Leu Leu Lys Glu Leu Arg Asn
 1 5 10 15
 Gly Gln Asp Met Asp Thr Val Val Phe Glu Asp Val Val Val Asp Phe
 20 25 30
 Thr Leu Glu Trp Ala Leu Leu Asn Pro Ala Gln Arg Lys Leu Tyr
 35 40 45
 Arg Asp Val Met Leu Glu Thr Phe Lys His Leu Ala Ser Val Asp Asn
 50 55 60
 Glu Ala Gln Leu Lys Ala Ser Gly Ser Ile Ser Gln Gln Asp Thr Ser
 65 70 75 80
 Gly Glu Lys Leu Ser Leu Lys Gln Lys Ile Glu Lys Phe Thr Arg Lys
 85 90 95
 Asn Ile Trp Ala Ser Leu Leu Gly Lys Asn Trp Glu Glu His Ser Val
 100 105 110
 Lys Asp Lys His Asn Thr Lys Glu Arg His Leu Ser Arg Asn Pro Arg
 115 120 125
 Val Glu Arg Pro Cys Lys Ser Ser Lys Gly Asn Lys Arg Gly Arg Thr
 130 135 140
 Phe Arg Lys Thr Arg Asn Cys Asn Arg His Leu Arg Arg
 145 150 155 157

<210> 1444
 <211> 53
 <212>Amino acid
 <213> Homo sapiens

<400> 1444
 Cys Val Cys Gly Phe Phe Val Cys Phe Glu Thr Lys Ser Cys Phe Val
 1 5 10 15
 Ala Gln Ala Gly Val Gln Trp His Asn Leu Ser Ser Leu Gln Ala Leu
 20 25 30
 Pro Pro Gly Phe Lys Gln Phe Ser Cys Leu Ser Leu Leu Ser Ser Trp
 35 40 45
 His Tyr Arg Arg Val
 50 53

<210> 1445
 <211> 106
 <212>Amino acid
 <213> Homo sapiens

<400> 1445

Gly Thr Arg Leu Arg Arg Arg Arg Glu Ala Val Trp Phe Glu Val Val
 1 5 10 15
 Asn Met Asp Phe Ser Arg Leu His Met Tyr Ser Pro Pro Gln Cys Val
 20 25 30
 Pro Glu Asn Thr Gly Tyr Thr Tyr Ala Leu Ser Ser Ser Tyr Ser Ser
 35 40 45
 Asp Ala Leu Asp Phe Glu Thr Glu His Lys Leu Asp Pro Val Phe Asp
 50 55 60
 Ser Pro Arg Met Ser Arg Arg Ser Leu Arg Leu Ala Thr Thr Ala Cys
 65 70 75 80
 Thr Leu Gly Asp Gly Glu Ala Val Gly Ala Asp Ser Gly Thr Ser Ser
 85 90 95
 Ala Val Ser Leu Lys Asn Arg Ala Ala Arg
 100 105 106

<210> 1446

<211> 95

<212>Amino acid

<213> Homo sapiens

<400> 1446

Asp Thr Met Gln Ala Val Val Pro Leu Asn Lys Met Thr Ala Ile Ser
 1 5 10 15
 Pro Glu Pro Gln Thr Leu Ala Ser Thr Glu Gln Asn Glu Val Pro Arg
 20 25 30
 Val Val Thr Ser Gly Glu Gln Glu Ala Ile Leu Arg Gly Asn Ala Ala
 35 40 45
 Asp Ala Glu Ser Phe Arg Gln Arg Phe Arg Trp Phe Cys Tyr Ser Glu
 50 55 60
 Val Ala Gly Pro Arg Lys Ala Leu Ser Gln Leu Trp Glu Leu Cys Asn
 65 70 75 80
 Gln Trp Leu Arg Pro Asp Ile His Thr Lys Glu Gln Ile Leu Glu
 85 90 95

<210> 1447

<211> 127

<212>Amino acid

<213> Homo sapiens

<400> 1447

Pro Ile Cys Leu Phe Ser Arg Pro Thr Leu Arg Pro Ser Arg Ser Lys
 1 5 10 15
 Val Ser Leu Ile Glu Gly Arg Gly Ala Asn Met Ala Ala Arg Trp Arg
 20 25 30
 Phe Trp Cys Val Ser Val Thr Met Val Val Ala Leu Leu Ile Val Cys
 35 40 45
 Asp Val Pro Ser Ala Ser Ala Gln Arg Lys Lys Glu Met Val Leu Ser
 50 55 60
 Glu Lys Val Ser Gln Leu Met Glu Trp Thr Asn Lys Arg Pro Val Ile
 65 70 75 80
 Arg Met Asn Gly Asp Lys Phe Arg Arg Leu Val Lys Ala Pro Pro Arg
 85 90 95
 Asn Tyr Ser Val Ile Val Met Phe Thr Ala Leu Gln Leu His Arg Gln
 100 105 110

Cys Val Val Cys Lys Tyr Glu Leu Gln Leu Arg Phe Lys Ile Lys
 115 120 125 127

<210> 1448
 <211> 143
 <212> Amino acid
 <213> Homo sapiens

<400> 1448
 Gln Met Arg Val Lys Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys
 1 5 10 15
 Arg Ser Lys Arg Pro Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp
 20 25 30
 Ile Ala Val Gly Leu Thr Cys Gln His Val Ser His Ala Ile Ser Val
 35 40 45
 Asn His Val Lys Arg Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser
 50 55 60
 Glu Cys Leu Lys Glu Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr
 65 70 75 80
 Ser Asp Ile Trp Leu Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys
 85 90 95
 Asn Ser Glu Ser Gln His Ser Leu Lys His Phe Lys Ser Ser Arg Thr
 100 105 110
 Glu Pro His Cys Ile Ile Ile Asn Leu Ser Thr Trp Ile Ile Trp Trp
 115 120 125
 Tyr Glu Trp Asp Glu Lys Ile Phe Thr Pro Leu Asn Lys Lys Gly
 130 135 140 143

<210> 1449
 <211> 121
 <212> Amino acid
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(121)
 <223> X = any amino acid or stop code

<400> 1449
 Ala Lys Glu Arg Gly Glu Glu Arg Gln Gly Glu Gly Gly Gly Trp Leu
 1 5 10 15
 Ser Gly Ser Arg Trp Pro Leu Val Arg Ser Ala Phe Val Pro Ala Pro
 20 25 30
 Ser Ser Leu Ile Leu Ser Met Cys Leu Ser Pro Gly Ile Pro Glu Ala
 35 40 45
 Ala Pro Asp Ser Pro Leu Thr Ala Ser Ala Pro Thr Pro Xaa Val Met
 50 55 60
 Leu Leu Gly Asp Thr Gly Val Gly Lys Thr Cys Phe Leu Ile Gln Phe
 65 70 75 80
 Lys Asp Gly Ala Phe Leu Ser Gly Thr Phe Ile Ala Thr Val Gly Ile
 85 90 95
 Asp Phe Arg Val Arg Trp Leu Gln Ala Leu Ala Ser Ser Arg Glu Pro
 100 105 110
 Gly Leu Trp Leu Arg His Gly Gly Val

115

120 121

<210> 1450
 <211> 76
 <212>Amino acid
 <213> Homo sapiens

<400> 1450
 Phe Tyr Pro Arg Ser Ser Ala Asp Leu Pro Phe Gln Thr Thr Arg Cys
 1 5 10 15
 Glu Phe Gln Thr Ser Val Met Glu Leu Ala His Ser Leu Leu Leu Asn
 20 25 30
 Glu Glu Ala Leu Ala Gln Ile Thr Glu Ala Lys Arg Pro Val Phe Ile
 35 40 45
 Phe Glu Trp Leu Arg Phe Leu Asp Lys Val Leu Val Ala Ala Asn Lys
 50 55 60
 Val Trp Tyr Cys Ser Phe Phe Pro Val Ala Leu Thr
 65 70 75 76

<210> 1451
 <211> 95
 <212>Amino acid
 <213> Homo sapiens

<400> 1451
 Met Asn Met Lys Gln Lys Ser Val Tyr Gln Gln Thr Lys Ala Leu Leu
 1 5 10 15
 Cys Lys Asn Phe Leu Lys Lys Trp Arg Met Lys Arg Glu Ser Leu Leu
 20 25 30
 Glu Trp Gly Leu Ser Ile Leu Leu Gly Leu Cys Ile Ala Leu Phe Ser
 35 40 45
 Ser Ser Met Arg Asn Val Gln Phe Pro Gly Met Ala Pro Gln Asn Leu
 50 55 60
 Gly Arg Val Asp Lys Phe Asn Ser Ser Ser Leu Met Val Val Tyr Thr
 65 70 75 80
 Pro Ile Ser Asn Leu Thr Gln Gln Ile Met Asn Lys Thr Ala Leu
 85 90 95

<210> 1452
 <211> 174
 <212>Amino acid
 <213> Homo sapiens

<400> 1452
 Ser Pro Gln Gly Asn Gly Cys Pro Asp Val Thr Gly Asp Ser Val Ile
 1 5 10 15
 Arg Val Pro Leu Thr Leu Leu Val His Asn Leu Ala Gly Leu Thr Gly
 20 25 30
 Leu Leu His His Cys Leu Ser Gly Pro Leu Pro Ala Pro Ser Pro Pro

	35						40					45				
Pro	Ala	Met	Ser	Ser	Ser	Arg	Lys	Asp	His	Leu	Gly	Ala	Ser	Ser	Ser	
	50					55					60					
Glu	Pro	Leu	Pro	Val	Ile	Ile	Val	Gly	Asn	Gly	Pro	Ser	Gly	Ile	Cys	
65					70					75					80	
Leu	Ser	Tyr	Leu	Leu	Ser	Gly	Tyr	Thr	Pro	Tyr	Thr	Lys	Pro	Asp	Ala	
				85					90					95		
Ile	His	Pro	His	Pro	Leu	Leu	Gln	Arg	Lys	Leu	Thr	Glu	Ala	Pro	Gly	
			100					105					110			
Val	Ser	Ile	Leu	Asp	Gln	Asp	Leu	Asp	Tyr	Leu	Ser	Glu	Gly	Leu	Glu	
		115				120						125				
Gly	Arg	Ser	Gln	Ser	Pro	Val	Ala	Leu	Leu	Phe	Asp	Ala	Leu	Leu	Arg	
	130					135					140					
Pro	Asp	Thr	Asp	Phe	Gly	Gly	Asn	Met	Lys	Ser	Val	Leu	Thr	Trp	Lys	
145					150					155					160	
His	Arg	Lys	Glu	His	Ala	Ile	Pro	His	Val	Val	Leu	Gly	Arg			
				165					170				174			

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<210> 1453
<211> 518
<212> Amino acid
<213> Homo sapiens
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<400> 1453															
Asn	Arg	Arg	Thr	Arg	Ala	Gln	Arg	Cys	Gln	Arg	Gly	Arg	Ser	Cys	Gly
1				5					10					15	
Ala	Arg	Glu	Glu	Glu	Val	Glu	Pro	Gly	Thr	Ala	Arg	Pro	Pro	Pro	Ala
			20					25					30		
Ala	Ser	Ala	Met	Asp	Ala	Ser	Leu	Glu	Lys	Ile	Ala	Asp	Pro	Thr	Leu
		35					40					45			
Ala	Glu	Met	Gly	Lys	Asn	Leu	Lys	Glu	Ala	Val	Lys	Met	Leu	Glu	Asp
	50					55					60				
Ser	Gln	Arg	Arg	Thr	Glu	Glu	Glu	Asn	Gly	Lys	Lys	Leu	Ile	Ser	Gly
	65				70					75					80
Asp	Ile	Pro	Gly	Pro	Leu	Gln	Gly	Ser	Gly	Gln	Asp	Met	Val	Ser	Ile
				85					90					95	
Leu	Gln	Leu	Val	Gln	Asn	Leu	Met	His	Gly	Asp	Glu	Asp	Glu	Glu	Pro
			100					105					110		
Gln	Ser	Pro	Arg	Ile	Gln	Asn	Ile	Gly	Glu	Gln	Gly	His	Met	Ala	Leu
		115					120					125			
Leu	Gly	His	Ser	Leu	Gly	Ala	Tyr	Ile	Ser	Thr	Leu	Asp	Lys	Glu	Lys
	130					135					140				
Leu	Arg	Lys	Leu	Thr	Thr	Arg	Ile	Leu	Ser	Asp	Thr	Thr	Leu	Trp	Leu
145					150					155					160
Cys	Arg	Ile	Phe	Arg	Tyr	Glu	Asn	Gly	Cys	Ala	Tyr	Phe	His	Glu	Glu
				165					170					175	
Glu	Arg	Glu	Gly	Leu	Ala	Lys	Ile	Cys	Arg	Leu	Ala	Ile	His	Ser	Arg
			180					185					190		
Tyr	Glu	Asp	Phe	Val	Val	Asp	Gly	Phe	Asn	Val	Leu	Tyr	Asn	Lys	Lys
		195					200					205			
Pro	Val	Ile	Tyr	Leu	Ser	Ala	Ala	Ala	Arg	Pro	Gly	Leu	Gly	Gln	Tyr
	210					215					220				
Leu	Cys	Asn	Gln	Leu	Gly	Leu	Pro	Phe	Pro	Cys	Leu	Cys	Arg	Val	Pro
225					230					235					240
Cys	Asn	Thr	Val	Phe	Gly	Ser	Gln	His	Gln	Met	Asp	Val	Ala	Phe	Leu
				245					250					255	
Glu	Lys	Leu	Ile	Lys	Asp	Asp	Ile	Glu	Arg	Gly	Arg	Leu	Pro	Leu	Leu
			260					265					270		
Leu	Val	Ala	Asn	Ala	Gly	Thr	Ala	Ala	Val	Gly	His	Thr	Asp	Lys	Ile

275 280 285
 Gly Arg Leu Lys Glu Leu Cys Glu Gln Tyr Gly Ile Trp Leu His Val
 290 295 300
 Glu Gly Val Asn Leu Ala Thr Leu Ala Leu Gly Tyr Val Ser Ser Ser
 305 310 315 320
 Val Leu Ala Ala Ala Lys Cys Asp Ser Met Thr Met Thr Pro Gly Pro
 325 330 335
 Trp Leu Gly Leu Pro Ala Val Pro Ala Val Thr Leu Tyr Lys His Asp
 340 345 350
 Asp Pro Ala Leu Thr Leu Val Ala Gly Leu Thr Ser Asn Lys Pro Thr
 355 360 365
 Asp Lys Leu Arg Ala Leu Pro Leu Trp Leu Ser Leu Gln Tyr Leu Gly
 370 375 380
 Leu Asp Gly Phe Val Glu Arg Ile Lys His Ala Cys Gln Leu Ser Gln
 385 390 395 400
 Arg Leu Gln Glu Ser Leu Lys Lys Val Asn Tyr Ile Lys Ile Leu Val
 405 410 415
 Glu Asp Glu Leu Ser Ser Pro Val Val Phe Arg Phe Phe Gln Glu
 420 425 430
 Leu Pro Gly Ser Asp Pro Val Phe Lys Ala Val Pro Val Pro Asn Met
 435 440 445
 Thr Pro Ser Gly Val Gly Arg Glu Arg His Ser Cys Asp Ala Leu Asn
 450 455 460
 Arg Trp Leu Gly Glu Gln Leu Lys Gln Leu Val Pro Ala Ser Gly Leu
 465 470 475 480
 Thr Val Met Asp Leu Glu Ala Glu Gly Thr Cys Leu Arg Phe Ser Pro
 485 490 495
 Leu Met Thr Ala Ala Gly Lys Pro Gly Leu Val Asp Ile Pro Cys Phe
 500 505 510
 Cys Ser Gly Ala Ala Gly
 515 518

<210> 1454

<211> 185

<212> Amino acid

<213> Homo sapiens

<400> 1454

Leu Cys Ile Met Asp Thr Lys Glu Glu Lys Lys Glu Arg Lys Gln Ser
 1 5 10 15
 Tyr Phe Ala Arg Leu Lys Lys Lys Lys Gln Ala Lys Gln Asn Ala Glu
 20 25 30
 Thr Ala Ser Ala Val Ala Thr Arg Thr His Thr Gly Lys Glu Asp Asn
 35 40 45
 Asn Thr Val Val Leu Glu Pro Asp Lys Cys Asn Ile Ala Val Glu Glu
 50 55 60
 Glu Tyr Met Thr Asp Glu Lys Lys Lys Arg Lys Ser Asn Gln Leu Lys
 65 70 75 80
 Glu Ile Arg Arg Thr Glu Leu Lys Arg Tyr Tyr Ser Ile Asp Asp Asn
 85 90 95
 Gln Asn Lys Thr His Asp Lys Lys Glu Lys Lys Met Val Val Gln Lys
 100 105 110
 Pro His Gly Thr Met Glu Tyr Thr Ala Gly Asn Gln Asp Thr Leu Asn
 115 120 125
 Ser Ile Ala Leu Lys Phe Asn Ile Thr Pro Asn Lys Leu Val Glu Leu
 130 135 140
 Asn Lys Leu Phe Thr His Thr Ile Val Pro Gly Gln Val Leu Phe Val
 145 150 155 160
 Pro Asp Ala Asn Ser Pro Ser Ser Thr Leu Arg Leu Ser Ser Ser

Pro Gly Ala Thr Val Ser Pro Ser Ser
 180 185 170 175

<210> 1455
 <211> 206
 <212> Amino acid
 <213> Homo sapiens

<400> 1455
 Ser Ala Gly Gly Asp Ser Cys Arg Ala Val Pro Met Leu Arg Phe Pro
 1 5 10 15
 Thr Cys Phe Pro Ser Phe Arg Val Val Gly Glu Lys Gln Leu Pro Gln
 20 25 30
 Glu Ile Ile Phe Leu Val Trp Ser Pro Lys Arg Asp Leu Ile Ala Leu
 35 40 45
 Ala Asn Thr Ala Gly Glu Val Leu Leu His Arg Leu Ala Ser Phe His
 50 55 60
 Arg Val Trp Ser Phe Pro Pro Asn Glu Asn Thr Gly Lys Glu Val Thr
 65 70 75 80
 Cys Leu Ala Trp Arg Pro Asp Gly Lys Leu Leu Ala Phe Ala Leu Ala
 85 90 95
 Asp Thr Lys Lys Ile Val Leu Cys Asp Val Glu Lys Pro Glu Ser Leu
 100 105 110
 His Ser Phe Ser Val Glu Ala Pro Val Ser Cys Met His Trp Met Glu
 115 120 125
 Val Thr Val Glu Ser Ser Val Leu Thr Ser Phe Tyr Asn Ala Glu Asp
 130 135 140
 Glu Ser Asn Leu Leu Leu Pro Lys Leu Pro Thr Leu Pro Lys Asn Tyr
 145 150 155 160
 Ser Asn Thr Ser Lys Ile Phe Ser Glu Glu Asn Ser Asp Glu Ile Ile
 165 170 175
 Lys Leu Leu Gly Asp Val Arg Leu Asn Ile Leu Val Leu Gly Gly Ser
 180 185 190
 Ser Gly Phe Ile Glu Leu Tyr Ala Tyr Gly Met Phe Lys Ile
 195 200 205 206

<210> 1456
 <211> 100
 <212> Amino acid
 <213> Homo sapiens

<400> 1456
 Pro Arg Asp Pro Val Thr Asp Arg Ala Arg Ala Met Pro Arg Arg Gly
 1 5 10 15
 Leu Val Ala Gly Pro Asp Leu Glu Tyr Phe Gln Arg His Tyr Phe Thr
 20 25 30
 Pro Ala Glu Val Ala Gln His Asn Arg Pro Glu Asp Leu Trp Val Ser
 35 40 45
 Tyr Leu Gly Arg Val Tyr Asp Leu Thr Ser Leu Ala Gln Glu Tyr Lys
 50 55 60
 Gly Asn Leu Leu Leu Lys Pro Ile Val Glu Val Ala Gly Gln Asp Ile
 65 70 75 80
 Ser His Trp Phe Asp Pro Lys Thr Arg Asp Val Ser Tyr Ala Gly Thr

Trp Asp Cys Gly 85 90 95
100

<210> 1457
<211> 159
<212> Amino acid
<213> Homo sapiens

<400> 1457
Arg Ile Pro Gly Arg Arg Phe Arg Ala Ala Phe Val Leu Gly Ser Ala
1 5 10 15
Asn Val Ala Ser Ser Val Arg Leu Arg Cys Ser Phe Pro Leu Ser Leu
20 25 30
Gly Gly Pro Ser Gly Pro Ala Ala Ala Ser Val Ala Leu Gly Pro Ala
35 40 45
Gly Pro Gly Arg Ser Leu Gly Arg Thr Pro Asp Thr Gly Asp Trp Glu
50 55 60
Met Asp Ser Val Ser Phe Glu Asp Val Ala Val Ala Phe Thr Gln Glu
65 70 75 80
Glu Trp Ala Leu Leu Asp Pro Ser Gln Lys Asn Leu Tyr Arg Asp Val
85 90 95
Met Gln Glu Ile Phe Arg Asn Leu Ala Ser Val Gly Asn Lys Ser Glu
100 105 110
Asp Gln Asn Ile Gln Asp Asp Phe Lys Asn Pro Gly Arg Asn Leu Ser
115 120 125
Ser His Val Val Glu Arg Leu Phe Glu Ile Lys Glu Gly Ser Gln Tyr
130 135 140
Gly Glu Thr Phe Ser Gln Asp Ser Asn Leu Asn Leu Asn Lys Ile
145 150 155 159

<210> 1458
<211> 154
<212> Amino acid
<213> Homo sapiens

<400> 1458
Ser Leu Ser Leu Ser Val Ser Pro Phe Leu Arg Leu Ser Leu Gly Arg
1 5 10 15
Val Gly Gly Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Ser Phe
20 25 30
Ser Ser Ser Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala
35 40 45
Arg Ser Arg Ile Phe Lys Ile Ile Val Ile Gly Asp Ser Asn Val Gly
50 55 60
Lys Thr Cys Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg
65 70 75 80
Thr Glu Ala Thr Ile Gly Val Asp Phe Arg Glu Arg Ala Val Glu Ile
85 90 95
Asp Gly Glu Arg Ile Lys Ile Gln Leu Trp Asp Thr Ala Gly Gln Glu
100 105 110
Arg Phe Arg Lys Ser Met Val Gln His Tyr Tyr Arg Asn Val His Ala
115 120 125
Val Val Phe Val Tyr Asp Met Thr Asn Met Ala Ser Phe His Ser Leu

130 135 140
 Pro Ser Trp Ile Glu Glu Cys Lys Gln His
 145 150 154

<210> 1459
 <211> 136
 <212> Amino acid
 <213> Homo sapiens

<400> 1459
 Arg Arg Pro Ser Pro Gly Ser Ile Val Ile Met Ala Ala Glu Ser Asp
 1 5 10 15
 Val Leu His Phe Gln Phe Glu Gln Gln Gly Asp Val Val Leu Gln Lys
 20 25 30
 Met Asn Leu Leu Arg Gln Gln Asn Leu Phe Cys Asp Val Ser Ile Tyr
 35 40 45
 Ile Asn Asp Thr Glu Phe Gln Gly His Lys Val Ile Leu Ala Ala Cys
 50 55 60
 Ser Thr Phe Met Arg Asp Gln Phe Leu Leu Thr Gln Ser Lys His Val
 65 70 75 80
 Arg Ile Thr Ile Leu Gln Ser Ala Glu Val Gly Arg Lys Leu Leu Leu
 85 90 95
 Ser Cys Tyr Thr Gly Ala Leu Glu Val Lys Arg Lys Glu Leu Leu Lys
 100 105 110
 Tyr Leu Thr Ala Ala Ser Tyr Leu Gln Met Val His Ile Ala Glu Lys
 115 120 125
 Arg Thr Glu Ala Phe Val Lys Phe
 130 135 136

<210> 1460
 <211> 219
 <212> Amino acid
 <213> Homo sapiens

<400> 1460
 Ala Glu Gly Leu Gln Ser Ala Ala Gly Ile Arg Ile Asp Thr Lys Ala
 1 5 10 15
 Gly Pro Pro Glu Met Leu Lys Pro Leu Trp Lys Ala Ala Val Ala Pro
 20 25 30
 Thr Trp Pro Cys Ser Met Pro Pro Arg Arg Pro Trp Asp Arg Gln Ala
 35 40 45
 Gly Thr Leu Gln Val Leu Gly Ala Leu Ala Val Leu Trp Leu Gly Ser
 50 55 60
 Val Ala Leu Ile Cys Leu Leu Trp Gln Val Pro Arg Pro Pro Thr Trp
 65 70 75 80
 Gly Gln Val Gln Pro Lys Asp Val Pro Arg Ser Trp Glu His Gly Ser
 85 90 95
 Ser Pro Ala Trp Glu Pro Leu Glu Ala Arg Gln Gln Arg Asp
 100 105 110
 Ser Cys Gln Leu Val Leu Val Glu Ser Ile Pro Gln Asp Leu Pro Ser
 115 120 125
 Ala Ala Gly Ser Pro Ser Ala Gln Pro Leu Gly Gln Ala Trp Leu Gln
 130 135 140
 Leu Leu Asp Thr Ala Gln Glu Ser Val His Val Ala Ser Tyr Tyr Trp

145 150 155 160
 Ser Leu Thr Gly Pro Asp Ile Gly Val Asn Asp Ser Ser Ser Gln Leu
 165 170 175
 Gly Glu Ala Leu Leu Gln Lys Leu Gln Gln Leu Leu Gly Arg Asn Ile
 180 185 190
 Ser Leu Ala Val Ala Thr Ser Ser Pro Thr Leu Ala Arg Thr Ser Thr
 195 200 205
 Asp Leu Gln Val Leu Ala Ala Arg Gly Ala His
 210 215 219

<210> 1461
 <211> 80
 <212> Amino acid
 <213> Homo sapiens

<400> 1461
 Arg Lys Lys Lys Met Pro Leu Pro Phe Gly Leu Lys Leu Lys Arg Thr
 1 5 10 15
 Arg Arg Tyr Thr Val Ser Ser Lys Ser Cys Leu Val Ala Arg Ile Gln
 20 25 30
 Leu Leu Asn Asn Glu Phe Val Glu Phe Thr Leu Ser Val Glu Ser Thr
 35 40 45
 Gly Gln Glu Ser Leu Glu Ala Val Ala Gln Arg Leu Glu Leu Arg Glu
 50 55 60
 Val Thr Tyr Phe Ser Leu Trp Tyr Tyr Asn Lys Gln Asn Gln Arg Arg
 65 70 75 80

<210> 1462
 <211> 176
 <212> Amino acid
 <213> Homo sapiens

<400> 1462
 Leu Gln Pro Leu Ser Ser Trp Glu Ser Ala Ser Glu Val Thr Arg Ser
 1 5 10 15
 Pro Val Ser Pro Glu Asp Val Lys Gln Ala Thr Ser Asn Phe Glu Asn
 20 25 30
 Leu Gln Lys Gln Leu Ala Arg Lys Met Lys Leu Pro Ile Phe Ile Ala
 35 40 45
 Asp Ala Phe Thr Ala Arg Ala Phe Arg Gly Asn Pro Ala Ala Val Cys
 50 55 60
 Leu Leu Glu Asn Glu Leu Asp Glu Asp Met His Gln Lys Ile Ala Arg
 65 70 75 80
 Glu Met Asn Leu Ser Glu Thr Ala Phe Ile Arg Lys Leu His Pro Thr
 85 90 95
 Asp Asn Phe Ala Gln Ser Ser Cys Phe Gly Leu Arg Trp Phe Thr Pro
 100 105 110
 Ala Ser Glu Val Pro Leu Cys Gly His Ala Thr Leu Ala Ser Ala Ala
 115 120 125
 Val Leu Phe His Lys Ile Lys Asn Met Asn Ser Thr Leu Thr Phe Val
 130 135 140
 Thr Leu Ser Gly Glu Leu Arg Ala Arg Arg Ala Glu Asp Gly Ile Val

```

145          150          155          160
Leu Asp Leu Pro Leu Tyr Pro Ala His Pro Gln Asp Phe His Glu *
          165          170          175

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<210> 1463
<211> 150
<212> Amino acid
<213> Homo sapiens
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[illegible]

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<210> 1464
<211> 86
<212> Amino acid
<213> Homo sapiens .
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<400> 1464
Phe Val Glu Arg Gly Leu Gly Asp Pro Ala Leu Pro Thr Leu Met Phe
  1                    5                10                  15
Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val Ala Ala Gly Leu Gly
          20                      25              30
Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser Ser Gln Asn Lys Val
      35                          40                  45
Ser Asp Ser Arg Glu Gln Trp Glu Leu Phe Gln Ala Ala Lys Arg Thr
    50                        55              60
Leu Val Asp Pro Ser Ala Val Cys Ile Ala Gly Arg Asp Thr Cys Gly
   65                     70             75               80
Thr Val Lys Gly Glu Ser
           85  86

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<210> 1465
<211> 286
<212>Amino acid
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<213> Homo sapiens

<400> 1465

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Val Val Glu Phe Leu Trp Ser Arg Arg Pro Ser Gly Ser Ser Asp Pro
1      5      10      15
Arg Pro Arg Arg Pro Ala Ser Lys Cys Gln Met Met Glu Glu Arg Ala
      20      25      30
Asn Leu Met His Met Met Lys Leu Ser Ile Lys Val Leu Leu Gln Ser
      35      40      45
Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala Asp His Ala Pro Leu Gln
      50      55      60
Gln Phe Phe Val Val Met Glu His Cys Leu Lys His Gly Leu Lys Val
      65      70      75      80
Lys Lys Ser Phe Ile Gly Gln Asn Lys Ser Phe Phe Gly Pro Leu Glu
      85      90      95
Leu Val Glu Lys Leu Cys Pro Glu Ala Ser Asp Ile Ala Thr Ser Val
      100     105     110
Arg Asn Leu Pro Glu Leu Lys Thr Ala Val Gly Arg Gly Arg Ala Trp
      115     120     125
Leu Tyr Leu Ala Leu Met Gln Lys Lys Leu Ala Asp Tyr Leu Lys Val
      130     135     140
Leu Ile Asp Asn Lys His Leu Leu Ser Glu Phe Tyr Glu Pro Glu Ala
145     150     155     160
Leu Met Met Glu Glu Glu Gly Met Val Ile Val Gly Leu Leu Val Gly
      165     170     175
Leu Asn Val Leu Asp Ala Asn Leu Cys Leu Lys Gly Glu Asp Leu Asp
      180     185     190
Ser Gln Val Gly Val Ile Asp Phe Ser Leu Tyr Leu Lys Asp Val Gln
      195     200     205
Asp Leu Asp Gly Gly Lys Glu His Glu Arg Ile Thr Asp Val Leu Asp
      210     215     220
Gln Lys Asn Tyr Val Glu Glu Leu Asn Arg His Leu Ser Cys Thr Val
225     230     235     240
Gly Asp Leu Gln Thr Lys Ile Asp Gly Leu Glu Lys Thr Asn Ser Lys
      245     250     255
Leu Gln Glu Arg Val Ser Ala Ala Thr Asp Arg Ile Cys Ser Leu Gln
      260     265     270
Glu Glu Gln Gln Gln Leu Arg Glu Gln Asn Glu Leu Ile Arg
      275     280     285 286

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<210> 1466

<211> 127

<212> Amino acid

<213> Homo sapiens

<400> 1466

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Gly Cys Tyr Ala Pro Ser Pro His Leu Gly Gly Ser Leu Thr Pro Arg
1      5      10      15
Phe Phe Pro Asn Gly Val Phe His Arg Arg Leu Pro Arg Pro Arg Pro
      20      25      30
Pro Gln Pro Pro Ser Val Ser Ser Ala Pro Thr Leu Arg Pro Leu Cys
      35      40      45
Ala His Phe Ser Leu Gly Lys Leu Arg Leu Arg Val Arg Lys Ser Ala
      50      55      60
Glu Val Ala Pro Pro Arg Thr Glu Lys Gly Trp Gly Ser Ala Glu Pro

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<210> 1467
<211> 146
<212> Amino acid
<213> Homo sapiens
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<210> 1468
<211> 44
<212> Amino acid
<213> Homo sapiens
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<210> 1469
<211> 198
<212> Amino acid
<213> Homo sapiens
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<400> 1469

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Ser Gly Asp Leu Ser Pro Ala Glu Leu Met Met Leu Thr Ile Gly Asp
 1           5           10           15
Val Ile Lys Gln Leu Ile Glu Ala His Glu Gln Gly Lys Asp Ile Asp
          20           25           30
Leu Asn Lys Val Lys Thr Lys Thr Ala Ala Lys Tyr Gly Leu Ser Ala
          35           40           45
Gln Pro Arg Leu Val Asp Ile Ile Ala Ala Val Pro Pro Gln Tyr Arg
          50           55           60
Lys Val Leu Met Pro Lys Leu Lys Ala Lys Pro Ile Arg Thr Ala Ser
          65           70           75           80
Gly Ile Ala Val Val Ala Val Met Cys Lys Pro His Arg Cys Pro His
          85           90           95
Ile Ser Phe Thr Gly Asn Ile Cys Val Tyr Cys Pro Gly Gly Pro Asp
          100          105          110
Ser Asp Phe Glu Tyr Ser Thr Gln Ser Tyr Thr Gly Tyr Glu Pro Thr
          115          120          125
Ser Met Arg Ala Ile Arg Ala Arg Tyr Asp Pro Phe Leu Gln Thr Arg
          130          135          140
His Arg Ile Glu Gln Leu Lys Gln Leu Gly His Ser Val Asp Lys Val
          145          150          155          160
Glu Phe Ile Glu Met Gly Gly Thr Phe Met Ala Leu Pro Glu Glu Tyr
          165          170          175
Arg Asp Tyr Phe Ile Arg Asn Leu His Asp Ala Leu Ser Gly His Thr
          180          185          190
Ser Asn Asn Ile Tyr Glu
          195          198

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<210> 1470

<211> 178

<212>Amino acid

<213> Homo sapiens

<400> 1470

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Trp Glu Ser Asp Val Gly Glu Gly Leu Arg Pro Pro Pro Pro Pro Pro
 1           5           10           15
Pro Pro Gly Arg Arg Arg Thr Gln Glu Pro Arg Ala Arg Asp Ala Ala
          20           25           30
Thr Val Ile Phe Ala Cys Pro Ala Ala Leu Leu Glu Thr Leu Ile Ala
          35           40           45
Tyr Gly Ser Ser Ser Pro Ser Phe Cys Lys His Arg Ala Ala Arg Pro
          50           55           60
Leu Ile Phe Leu Leu His Arg Leu Thr Ala Glu Ala Thr Ala Arg Cys
          65           70           75           80
Pro Ile Cys Ala Leu Glu Ala Arg Asn Pro Gly Arg Trp Gly Ile Cys
          85           90           95
Ala Ser Trp Pro Gly Met Lys Thr Pro Phe Gly Lys Ala Ala Ala Gly
          100          105          110
Gln Arg Ser Arg Thr Gly Ala Gly His Gly Ser Val Ser Val Thr Met
          115          120          125
Ile Lys Arg Lys Ala Ala His Lys Lys His Arg Ser Arg Pro Thr Ser
          130          135          140
Gln Pro Arg Gly Asn Ile Val Gly Cys Ile Ile Gln His Gly Trp Lys
          145          150          155          160
Asp Gly Asp Glu Pro Leu Thr Gln Trp Lys Gly Thr Val Leu Asp Gln

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Leu Leu 165 170 175
178

<210> 1471
<211> 253
<212> Amino acid
<213> Homo sapiens

<400> 1471
Arg Asp Leu Gly Val Ala Leu Glu Ala Phe Gln Trp Ala Arg Ala Gly
1 5 10 15
Asp Cys Gly Ser Gly Ala Gly Arg Ala Gly Gly Glu Gly Val Asp Ala
20 25 30
Gly Arg Arg Val Pro Glu Arg Gln His Arg Gly Arg Gly Gly Gly
35 40 45
Glu Pro Gly Arg Arg Gln Arg Gly Gly Arg Arg Gln Arg Ser Ser Ser
50 55 60
Arg Arg Ser Gly Gly Asp Gly Gly Asp Glu Val Glu Gly Ser Gly Val
65 70 75 80
Gly Ala Gly Glu Gly Glu Thr Val Gln His Phe Pro Leu Ala Arg Pro
85 90 95
Lys Ser Leu Met Gln Lys Leu Gln Cys Ser Phe Gln Thr Ser Trp Leu
100 105 110
Lys Asp Phe Pro Trp Leu Arg Tyr Ser Lys Asp Thr Gly Leu Met Ser
115 120 125
Cys Gly Trp Cys Gln Lys Thr Pro Ala Asp Gly Gly Ser Val Asp Leu
130 135 140
Pro Pro Val Gly His Asp Glu Leu Ser Arg Gly Thr Arg Asn Tyr Lys
145 150 155 160
Lys Thr Leu Leu Leu Arg His His Val Ser Thr Glu His Lys Leu His
165 170 175
Glu Ala Asn Ala Gln Glu Ser Glu Ile Pro Ser Glu Glu Gly Tyr Cys
180 185 190
Asp Phe Asn Ser Arg Pro Asn Glu Asn Ser Tyr Cys Tyr Gln Leu Leu
195 200 205
Arg Gln Leu Asn Glu Gln Arg Lys Lys Gly Ile Leu Cys Asp Val Ser
210 215 220
Ile Val Val Ser Gly Lys Ile Phe Lys Ala His Lys Asn Ile Leu Val
225 230 235 240
Ala Gly Ser Arg Phe Phe Lys Thr Leu Tyr Cys Phe Ser
245 250 253

<210> 1472
<211> 147
<212> Amino acid
<213> Homo sapiens

<400> 1472
Ser Leu Arg Ala Ala Ala Met Ala Asp Val Thr Ala Arg Ser Leu
1 5 10 15
Gln Tyr Glu Tyr Lys Ala Asn Ser Asn Leu Val Leu Gln Ala Asp Arg
20 25 30
Ser Leu Ile Asp Arg Thr Arg Arg Asp Glu Pro Thr Gly Glu Val Leu

```

      35      40      45
Ser Leu Val Gly Lys Leu Glu Gly Thr Arg Met Gly Asp Lys Ala Gln
  50      55      60
Arg Thr Lys Pro Gln Met Gln Glu Glu Arg Arg Ala Lys Arg Arg Lys
  65      70      75      80
Arg Asp Glu Asp Arg His Asp Ile Asn Lys Met Lys Gly Tyr Thr Leu
      85      90      95
Leu Ser Glu Gly Ile Asp Glu Met Val Gly Ile Ile Tyr Lys Pro Lys
      100      105      110
Thr Lys Glu Thr Arg Glu Thr Tyr Glu Val Leu Leu Ser Phe Ile Gln
      115      120      125
Ala Ala Leu Gly Asp Gln Pro Arg Asp Ile Leu Cys Gly Ala Ala Asp
      130      135      140
Glu Val Leu
145      147

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<210> 1473
<211> 139
<212>Amino acid
<213> Homo sapiens

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<400> 1473
Cys Asn Ser Ala Glu Ser Arg Met Asp Val Leu Phe Val Ala Ile Phe
  1      5      10      15
Ala Val Pro Leu Ile Leu Gly Gln Glu Tyr Glu Asp Glu Glu Arg Leu
      20      25      30
Gly Glu Asp Glu Tyr Tyr Gln Val Val Tyr Tyr Tyr Thr Val Thr Pro
      35      40      45
Ser Tyr Asp Asp Phe Ser Ala Asp Phe Thr Ile Asp Tyr Ser Ile Phe
  50      55      60
Glu Ser Glu Asp Arg Leu Asn Arg Leu Asp Lys Asp Ile Thr Glu Ala
  65      70      75      80
Ile Glu Thr Thr Ile Ser Leu Glu Thr Ala Arg Ala Asp His Pro Lys
      85      90      95
Pro Val Thr Val Lys Pro Val Thr Thr Glu Pro Gln Ser Pro Asp Leu
      100      105      110
Asn Asp Ala Val Ser Ser Leu Arg Ser Pro Ile Pro Leu Leu Leu Ser
      115      120      125
Cys Ala Phe Val Gln Val Gly Met Tyr Phe Met
      130      135      139

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<210> 1474
<211> 185
<212>Amino acid
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(185)
<223> X = any amino acid or stop code

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<400> 1474
Phe Val Arg Gly Pro Gly Glu Glu Gln Ala Pro Ala Phe Arg Lys Pro
  1      5      10      15

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Ala Pro Gly Ala Met Gly Ala Gln Val Arg Leu Pro Pro Gly Glu Pro
 20 25 30
 Cys Arg Glu Gly Tyr Val Leu Ser Leu Val Cys Pro Asn Ser Ser Gln
 35 40 45
 Ala Trp Cys Glu Ile Thr Asn Val Ser Gln Leu Leu Ala Ser Pro Val
 50 55 60
 Leu Tyr Thr Asp Leu Asn Tyr Ser Ile Asn Asn Leu Ser Ile Ser Ala
 65 70 75 80
 Asn Val Glu Asn Lys Tyr Ser Leu Tyr Val Gly Leu Val Leu Ala Val
 85 90 95
 Ser Ser Ser Ile Phe Ile Gly Ser Ser Phe Ile Leu Lys Lys Lys Gly
 100 105 110
 Leu Leu Gln Leu Ala Ser Lys Gly Phe Thr Arg Ala Gly Gln Gly Gly
 115 120 125
 His Ser Tyr Leu Lys Glu Trp Leu Trp Trp Val Gly Leu Leu Ser Ile
 130 135 140
 Leu Ser Trp Asn Ala Arg Glu Lys Val Asp Leu Xaa Asn Ile Thr Phe
 145 150 155 160
 Xaa Pro Gln Thr Ser Cys Ile Phe Phe Thr Ile Thr Ile Glu Lys Ser
 165 170 175
 Thr Phe Leu Ser Tyr Phe Pro Thr Ser
 180 185

<210> 1475

<211> 91

<212> Amino acid

<213> Homo sapiens

<400> 1475

Ala Arg Gly Ser Cys Pro Thr Arg Pro Arg Pro Ala Asn Gly Arg Met
 1 5 10 15
 Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp Val
 20 25 30
 Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala Gln
 35 40 45
 Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu Val
 50 55 60
 Ser Leu Gly His Arg Val Pro Lys Pro Glu Leu Val His Leu Leu Lys
 65 70 75 80
 His Gly Gln Glu Leu Trp Ile Val Lys Arg Gly
 85 90 91

<210> 1476

<211> 159

<212> Amino acid

<213> Homo sapiens

<400> 1476

Tyr Thr Met Leu Arg Gly Thr Met Thr Ala Trp Arg Gly Met Arg Pro
 1 5 10 15
 Glu Val Thr Leu Ala Cys Leu Leu Leu Ala Thr Ala Gly Cys Phe Ala
 20 25 30
 Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr Val
 35 40 45

Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu Pro Pro
 50 55 60
 Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu Asn Gly Ser
 65 70 75 80
 Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr Leu Val Ile Thr
 85 90 95
 Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln Cys Val Ala Arg Met
 100 105 110
 Pro Ala Gly Ala Val Ala Ser Val Pro Ala Thr Val Thr Leu Ala Ser
 115 120 125
 Glu Ser Ala Pro Leu Pro Pro Cys His Gly Ala Val Pro Pro His Leu
 130 135 140
 Ser His Pro Glu Ala Pro Thr Ile His Ala Ala Ser Cys Tyr Ser
 145 150 155 159

<210> 1477

<211> 139

<212>Amino acid

<213> Homo sapiens

<400> 1477

Trp Gly Arg Arg Arg Gln Leu Val Ser Glu Ala Ala Arg Ala Gln Gly
 1 5 10 15
 Asp Pro Val Cys Ser Thr Met Ser Glu Glu Ala Ala Gln Ile Pro
 20 25 30
 Arg Ser Ser Val Trp Glu Gln Asp Gln Gln Asn Val Val Gln Arg Val
 35 40 45
 Val Ala Leu Pro Leu Val Arg Ala Thr Cys Thr Ala Val Cys Asp Val
 50 55 60
 Tyr Ser Ala Ala Lys Asp Arg His Pro Leu Leu Gly Ser Ala Cys Arg
 65 70 75 80
 Leu Ala Glu Asn Cys Val Cys Gly Leu Thr Thr Arg Ala Leu Asp His
 85 90 95
 Ala Gln Pro Leu Leu Glu His Leu Gln Pro Gln Leu Ala Thr Met Asn
 100 105 110
 Ser Leu Ala Cys Arg Gly Leu Asp Lys Leu Glu Glu Lys Leu Pro Phe
 115 120 125
 Leu Gln Gln Pro Ser Glu Thr Val Val Thr Ser
 130 135 139

<210> 1478

<211> 331

<212>Amino acid

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(331)

<223> X = any amino acid or stop code

<400> 1478

Ala Lys Ala Phe Thr Met Ala Glu Ser Pro Gly Cys Cys Ser Val Trp
 1 5 10 15
 Ala Arg Cys Leu His Cys Leu Tyr Ser Cys His Trp Arg Lys Cys Pro

917 .

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(75) Inventors/Applicants (*for US only*): TANG, Y., Tom

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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/35017

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; C07H 21/02

US CL : 435/6; 536/23.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6; 536/23.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database EST, National Human Genome Institute (Bethesda, MD, USA), Accession Number AW068570, JIA et al., 'SGAP: The Skeletal Genome Anatomy Project,' 13 October 1999.	2-3 and 10 -----
---		6-9, 11 and 19
Y		6-9, 11 and 19
Y	WATSON et al. The Science Used in the Recombinant DNA Industry. Recombinant DNA; A Short Course. New York. W.H. Freeman and Company. 1983, pages 231-241, Chapter 18, see entire document.	6-9, 11 and 19

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T"

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&"

document member of the same patent family

Date of the actual completion of the international search

31 July 2001 (31.07.2001)

Date of mailing of the international search report

31 AUG 2001

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/35017

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-11, 19, and SEQ ID Number 1 (Claim 20 was in Group 1 but is not drawn to the elected sequence.)

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/35017

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-11, 19, and 20, drawn to a polynucleotide, a vector comprising the polynucleotide, a host cell comprising the vector, a polypeptide, a method of producing the polypeptide, and a composition comprising the polypeptide of Group I and a carrier.

Group II, claim(s) 12, drawn to an antibody specific for the polypeptide of Group I.

Group III, claim(s) 13-15, drawn to a method of detecting the polynucleotide of Group I.

Group IV, claim(s) 16, drawn to a method of detecting the polypeptide of Group I.

Group V, claim(s) 17 and 18, drawn to a method of finding a binding partner of the polypeptide of Group I.

Group VI, claim(s) 21, drawn to a polypeptide array.

Group VII, claim(s) 22-26, drawn to an array of polynucleotides comprising the polynucleotide of Group I.

Group VIII, claim(s) 27, drawn to a method of therapeutic treatment using the polypeptide of Group I.

Group IX, claim(s) 28, drawn to a method of therapeutic treatment using an antibody.

The inventions listed as Groups I-IX do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The polynucleotide of claim Group I lack a special technical feature because each polynucleotide is directed to a unique sequence which may give rise to a polypeptide with unique function. In addition, each additional group set forth has its own unifying feature which is distinct from that of the other. Finally, PCT Rule 13.1 and Annex B do not provide for unity of invention between two or more different products or methods of use that share a special technical feature.

In addition, each Group detailed above reads on distinct Groups drawn to multiple sequences. The sequences are distinct because they are unrelated sequences, and a further lack of unity is applied to each Group. The Applicants must further elect one sequence for examination in the elected Group detailed above. Payment of fees for an additional invention will entitle the Applicants to examination of one additional sequence.

The total number of invention was calculated based on the number of combination that exist between the SEQ ID Numbers and the total number of groups. The formula is recited below:

$$\begin{aligned}\text{Total Number of Inventions found} &= (\text{Total Groups} \times \text{Total SEQ ID Numbers}) - \text{Total Groups} \\ \text{Total Number for this Application} &= (9 \times 739) - 9 = 6642\end{aligned}$$

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/35017

Continuation of B. FIELDS SEARCHED Item 3:

Database EST, GenEmbl, GenBank;

Search terms: SEQ ID Number 1